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ACCESSION AX2111739
VERSION AX2111739.1 GI:15523950
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REFERENCE Streptomyces noursei
AUTHORS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Zotchev,S.B., Sekurova,O.N., Fjaervik,E., Brautaset,T.,
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Gulliksen,O.M.
TITLE Gene cluster encoding a nystatin polyketide synthase and its
manipulation and utility
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IND OG TEKNISK FORSKNING VED NORGES TEKNISKE HOGSKOLE (NO) ;
ALPHARMA AS (NO) ; Sirvent AS (NO) ; Zotchev, Sergey Borisovich
(NO) ; Sekurova, Olga Nikolayivna (NO) ; Fjaervik, Espen (NO) ;
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Db 33569 CTCGCGCTGCGCGCATTCATCTGCGCGGCGGCGAGCGCGGAATTCACCTGATCATCGG 33628  
Qy 24160 GGTGATGCGGCTCATGTTTACCTGGAAAGCGCGCATTTCTGCGATGAGCGACGCGATG 24219  
Db 33629 GCGGACGCGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 33688  
Qy 24220 GCGCTCGCGGCAATTCATCTGCGCGGCGGCGAGCGCGCGGAATTCACCTGATCATCGG 24279  
Db 33689 GCGCTGGGAAGCGCTCTGCGCGCTTGTTCGCGG---GAAGGAGCGCGCGCGGTGTCG 33745  
Qy 24280 GACATCTGAGTGGGAGCGCTTCTGCGCGCTTCACTGCTGACGCGCACAGCGCGCTCATC 24339  
Db 33746 GAGGTGGCGCTGGAACGGTTTCGCGCGCGCTTTCGCGGCGAGCGGACCGCGCGCTG 33805  
Qy 24340 GAGGACATTCGGAAGGTTTCGGAAGCGGCTCAGGAGCTGGAAGGAGCTGCTGCTGCA 24399  
Db 33806 CGGAGGTTCCCGGCTTACCGCGAGGCGC-----TCCGCGCGCC 33842  
Qy 24400 AAGACGACCAAGCTCAGCGCGATTTGGAGCTCTCTCGGTGAGGATTTGGCGCGGCTG 24459  
Db 33843 AGCGGAGAGCGCGCGGAGCGCGCG-----GGCTGGCGCGCGCGCTGCGCGCGCTG 33898

Qy 24460 TCCTCAAAGCAGAACCAAGTCTCTCGGCTGATTCGGACAGGCATCTGCACCGTCTCTC 24519  
Db 33899 CCGCGCGCGCTGGACACCGTTGTGCACTTGTGCGACCGCGCGCGCGAGTCTCTC 33958  
Qy 24520 GGCCTTCGTAACTCCGGAAGGATCGAGGACCAAGAGCTTTCGCGACCTTCGCGTTGAC 24579  
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Qy 24580 TCGCTGAGCTCGGCTCAGTTTCAAGCAAGAACTCCCAAGAAACCGGACTGCACTCC 24639  
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Qy 24640 CCGTCTCTGCTTTCGACTATCCCAACCGCGAGGAATGTGTGCGCA----- 24686  
Db 34079 GCGAGCTGCTGTTTCGACACCGACCGCGCGCTCTGCTCTCGGAGGACATCTCTCGG 34138  
Qy 24687 ----- 24686  
Db 34139 CTCTTCCCGGACGAGCGCGCGGTTCGACGACGAGACGGAGATCCGCGCGCTCTGCG 34198  
Qy 24687 -----TCTCGGACAC 24696  
Db 34199 TCGTCCCGCTCGACCACTTCGCGGAGATCGGGGTCTCTGAGCGCGCTCTCTCGCT 34258  
Qy 24697 CAACTCGTTCGACCTTAGACGAGAGGACGCGGCACTGTGGAATGTCTTCCGCAAGTG 24756  
Db 34259 GGACGCGCGCGCGCGCGCGGACGCGGAGTCCGTCGACTCGATGACAGTG 34318  
Qy 24757 GCGCATCGGCGTACCGTTCGAG----- 24778  
Db 34319 GCGACCTGCTGCGCGCGCGCGCTCAACGCGCGCTCGACCTGTAGCGGATGATGAG 34378  
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Db 34379 AGACGATGAACGCGCGCGGAGAACCCCGAGACCCCGGAGAACGTAAGTCCGCGACT 34438  
Qy 24779 ----- 24778  
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Qy 24779 ---ACGAAACCGATCGCATCATTCGTTATGGAATGTCGTTCCCGCGGCGGTACGTTCTG 24835  
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Qy 24836 CCGAGACCTGTCGGAATTCGCTTCGTTGGAAGGAGCTATCGGCTCTTCCGCGCG 24895  
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Qy 24896 ACCGCGGTGGGACCTTGGACACGCTCTACGACCCCGACCCCGACCCCGCGCACCTGCT 24955  
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Qy 24956 ACACCGGAAACGCGGATTTCTCTTACGCGGAGGCGCACTTTCGAGCGCGAATTTCTG 25015  
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Qy 25016 TCAGCGCGCGGAGCGCTCGCATGACCCCGAGCAACGACTCTCTCTGAAACCGGCT 25075  
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Qy 25076 GGGAAACCATCGAACAGCGCGGATCAACCCCGACACCTTCAGCGGACCCCGGAGAG 25135  
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Db 30789 CCCACTTGTCTACCGCCAGGACCCCGTGGCCGAC---TCGGGTGGCGCGCGCGCGCG 30845  
QY 21236 GAGTGTCTCATTTCCGGGTGACGGGACCAACAGCCACGTCATCTCTCAAGAGACACCG 21295  
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QY 21356 CTGCGCGGAGTCTCTGGGTGTGGCGGTGGTGTGGCGCAAGTCTGGCAGCGCGCCCTGC 21415  
Db 30946 -----GTTGCGGTTCTTGTCTCTCGGGCGCTTCGAGAAACGCCCTGC 30986  
QY 21416 GCGCCAGGCGCGAGCCCTGACGCGCCACCTCACGACACCGCGGCTCGACCTCGCGG 21475  
Db 30987 GCGCCAGGCGCGCGACTCTGTGGCCCGCTTACCGCCACCGCGGCGCGCG 31046  
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QY 21596 CCGCGTATCCACAGAGCGCCCGAGGGGACCGGAGCGGGGAGGCGCCAGGAAGA 21655  
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QY 21776 TCGACACCGCTCTCCCTCTCTACCCAAAGCAACGACCAACGAGGAG 21835  
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QY 21836 CCGCGCACTGCTCCAGCAGACCGGTACGCCAGCGCGCTTCTGGCTTTCAGGTG 21895  
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QY 22016 CCCTCATCACCAAGCGCGCACTCATGCAAAACAT---GCCCGCGGACCATGACCA 22072  
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QY 22193 AACACATCACCACTCTGCGCAACAAAGGACATCAAAACCAAAACCTCCCGCACCAAC 22252  
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31770 ACGCTTTCCACTCGCACTCATGACCGGACTTCCGACCGCTCGCGGAG 31829  
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22661 CCACCTCGACCTCCCGACCTTCCCAACCAACCACTACTGCTGCTGACTACCCA 22720  
32181 AGTGGTGGACCTTCCGACGTACCTTCCAGCGCGCGCTTCTGGCGG----- 32232  
22721 GCGCCAAAACGAGCGCGCTCAAGGCGTCTCGCGCTCGGC--TCAGACACCGCGGAG 22779  
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32411 GCGAGAGTCTCAACTGGGAGGTGCGCGCACCGCATGCTTGAAGGCTTACCGG 32470  
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23140 CGAACAAGCCCAACCAACCAACCGGAGCGGCTTCCCGGCTTCTTCTTCTTCTGCG 23199  
32639 -----GCCCGCACCGCGGACCGCGCTTGGCGGCGTAACTCTCCCTGTGCG 32689  
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32741 ACCCTCTTCCAGGCGCTTGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 32800  
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Db 28689 CCGCGCTCGGCCCGCGATCACCGTGTGGACACGACCCACCGCCCGGACGCGCTTCG 28748  
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Qy 19154 GCATCTCGACGACGCGACCTTACCAACTCACCACCTCACCACCGCACTCAACAGCTCTCC 19213  
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Qy 20036 GTGCGTTCGCGGCGGATGACTCGGCGGACGACTTCTGGGATCTGATCTCTCCCGAGC 20095  
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Qy 21116 TCCACGACTCTCCACGCGGATGAGCGGCTGCGCGCATGCTGCTGCTGCTGCTGCTGCTG 21175  
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QY	12536	CAGGCGGTATCTCTACAACTTCGGGCTCGAAGGCCCTCGGATCACTATCGACACCGCGT	12595	Db	23616	CCACCACGTCGGCTGACGGTCAACCAACCGACCGCGCGCGTGGCCGCCGGAATCA	23675
Db	22548	ACGCTTGACACTCTGTGTGCGCGCGCGCGCTCATGACGCGCTGCGCCGAGGCGCGCG	22607	QY	13655	TGCAAGCACTCCAGGCACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13714
QY	12596	GTTCTCTCTCGCTCGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	12655	Db	23676	CCGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23735
Db	22608	CGATGGTTCGCTTCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22667	QY	13715	CCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13774
QY	12656	CCATGGCGCTCGAGCGCGCGCGCTCGCTCATGGCCACTCCCTTCGCTTTCACGAGTTCT	12715	Db	23736	CGGGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23795
Db	22668	ACCGGGTGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22727	QY	13775	AGGCGACCCAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13831
QY	12716	CTCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	12770	Db	23796	AGGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23855
Db	22728	AGGAGTGTCTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22787	QY	13832	CCGCGCGCACTCAAGCACTCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13891
QY	12771	GGACGGGACCGCTGGTCCGAGGGTGTGGGATGTCTGTGTGGAGCGGCTCTCGAGCG	12830	Db	23856	CCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23915
Db	22788	GGGTGAGGCATGCTTCCACTCGCGCGCTGATGGACGCCATGCTGACGACTTCGCGCGCG	22847	QY	13892	CCCTCTCACCCAGGACCCCAACACCCAGGACACACACACCTCGAAGAGCGCGCGCGCG	13951
QY	12831	CCGCGCGCAACGGTCAACCGTGTCTTGGCGCGTCTGCGCGCGCGCGCGCGCGCGCGCGCG	12890	Db	23916	GGCGGTGCGCTCGGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23975
Db	22848	TGCGCGCGGGTGACTTACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22907	QY	13952	TGCTTCCAGCAGACCGCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14002
QY	12891	CGCAAGCAAGCGCTGACCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	12934	Db	23976	TGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24035
Db	22908	GCTTGGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22967	QY	14003	CCCTTCCACCGCGCTCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14062
QY	12935	AGGTATCCGCGAGCTTTGGCCAGCGCACACTCTCCCGCTGCGATGTGATGGCGTGG	12994	Db	24036	CGGTGGCGCTGCGCGCGCTTCCCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCG	24095
Db	22968	CGGTCCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23027	QY	14063	CCCTCGCGGAAATCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14122
QY	12995	AGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13054	Db	24096	CCGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24155
Db	23028	TGGAGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23087	QY	14123	CCCTTATCACCCAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14182
QY	13055	CCTACGSTCAGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13114	Db	24156	CCGCGCGCATC---GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24212
Db	23088	CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23147	QY	14183	TCCACACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14242
QY	13115	TGGGCACTTCCATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13174	Db	24213	TGCTGTCTTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24272
Db	23148	CCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23207	QY	14243	TGCGCGCGCATCAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14302
QY	13175	GGATGTGTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13234	Db	24273	TGAGGAACTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24332
Db	23208	ACCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23267	QY	14303	ACATCACCACTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14362
QY	13235	CCGCGGGTGTGCGGTGAGTGTGAGCGGAGACGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13294	Db	24333	TGGCGCGGTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24392
Db	23268	CCGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23324	QY	14363	CTTTCACCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14422
QY	13295	TACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13354	Db	24393	CCGCGGTGTGCGAGGACCACTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24452
Db	23325	TCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23384	QY	14423	TCACCTACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14482
QY	13355	AGGAAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13414	Db	24453	TGGCGCGCAAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24512
Db	23385	ACGCCACCGTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23444	QY	14483	TCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14542
QY	13415	CAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13474	Db	24513	CCGCTTTCGCGGTCTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24572
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QY	13475	GGCGGTGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	13534	Db	24573	ACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24632
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18289 Db CGTAGCCGCGACTGGCTGGACACCGCGGATGAGACGCGCGCTACTGGTTCGCAACT 18348  
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9189 QY GCACGAGTGGATGAGCTGACGCTGATGCGCGGTGCTGTGTCTGTGGATGGGGGT 9248  
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19129 Db GCTCGGACCGCGCTGACCTGGAGCTGATCCAGGCGCTCTCGCGCGCGGAAATCGACGC 19188  
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19489 Db GCGCGGCGCACACACTGTGTCAACCGCGCTCTCGGACCTCTCGCGCGCGCGCTCGCG 19548  
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19549 Db CTGCTGGCCAAACCGCGCGCGGAGCACCTGTCTGTATCAGCGCGCGCGCGCGCGCGC 19608  
9787 QY GTCGGCGGGG-----GGCGGGCGTGAGCGGTGTCTGGTGTGGT 9827  
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QY 4140 CCACACACCCACCCACCCACACGACCTCGACTGCGCACTACCCCTTCAACA 4199  
Db 13945 GCCTCGA-----CGCACCGACCTGCGGACCTAGCCCTTCAGCA 13983  
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QY 4320 GGGTTTCGGAGCGGGTGGCGCGGAGGACCTGGAACCGGTGCGGACCACTCGCGGT 4379  
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Db 15418 CATGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 15477  
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QY 6084 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6143  
Db 15838 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 15897  
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Db 64808 AGCGCGTGGCGAGGACCGAGCGCGGCGGCGCTGGCGACGAGCTCGCCGCTCTCG 64867

Qy 29113 CCAGCGTGGTGGCGCGCCACGCTGTCGCCACGCGGTACCGCGGTACCGCGCGTGGCC 29172

Db 64868 CCCCGG-TCGAGCAGGAGGCGGCTGCTGGAACACGCTCCGCGCCGACGCGCGTGGTC 64926

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RESULT 9

AF263912

LOCUS

DEFINITION Streptomyces noursei ATCC 11455 nystatin biosynthetic gene cluster, complete sequence.

ACCESSION AF263912

VERSION AF263912.1 GI:8050835

KEYWORDS

SOURCE Streptomyces noursei.

ORGANISM Streptomyces noursei

REFERENCE 1 (bases 1 to 123580) Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 123580)

AUTHORS Brattaset, T., Sekurova, O.N., Sletta, H., Ellingsen, T.E., Strim, A.R., Valla, S. and Zorchev, S.B.

TITLE Biosynthesis of the polyene antifungal antibiotic nystatin in Streptomyces noursei ATCC 11455: analysis of the gene cluster and deduction of the biosynthetic pathway

JOURNAL Chem. Biol. 7 (6), 395-403 (2000)

MEDLINE 20334850

PUBMED 10873841

REFERENCE 2 (bases 1 to 123580)

AUTHORS Brattaset, T., Sekurova, O.N., Sletta, H., Ellingsen, T.E., Strom, A.R., Valla, S. and Zorchev, S.B.

TITLE Direct Submission

JOURNAL Submitted (04-MAY-2000) Unigen, NTNU, O. Kyrres gt. 3, Trondheim N-7489, Norway

FEATURES

source

1..123580

Location/Qualifiers

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4714..5748

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4714..5748

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5930..34363

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5930..34363

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Qy 18234 AACCTGAAACCTTCACTTCCCACTCCCAACCAACCAACCAACCAACCTTGGCTATGCG 18293  
Db 53960 GTCTGGAAGAGGATACCCACCGCTCCGCGAGGCGCTTCCCGGATCGGTCTATGGCT 54019  
Qy 18294 CATCCCGAAGACCGAGACCCACCCCACTACCAACCACTCTTACCAACCTTCCACCA 18353  
Db 54020 GGTTCGCGTACGCGTGTGCGCAACTTGGGTCACCGCTTCCCGGGCT 54079  
Qy 18354 CCAGGTCATACCCCGCATCCCGCTTCCCGCTCAACCAACCAACCAACCAACCAACCT 18413  
Db 54080 GACCGAGGTGGCTTGGCGCGCTGCGGTCCCGGTGAGCGCGGCGACCGCGCTGAGG- 54138  
Qy 18414 CCACACACCGGACAAAGCCCAAAACCAACCAACCGGACCCATCAACCGGCTTGTCTC 18473  
Db 54139 --ACTGCGCGCGAGTCTACCCGAGCGCGGTGAGCAAAACCGTGTGGCGGCTCTGTC 54196  
Qy 18474 CTCTCTGCGCTTCAAGAAACACCCACCCCAACCAACCCCAACCAACCCCAACCT 18533  
Db 54197 GCTCTGCGGTGCGACTGTCGCGGGCGCGCGCGGAGCGCGGCTGCGGTCTGCGGCTGCG 54256



Db 47921 CTCCTCGCGAGCCGTCGCGTGGGTCTCTGTCCGGCAAGTCCGAGGCGCGACTGCGCGCCA 47980  
Qy 12138 ACTGTGGCATCTCGTCAAGTCCAGACGAGCGCTATCGGGGAGTTCCCGACCGACCGTGG 12197  
Db 47981 GGCCGAGCGCTGTGACCTTACCGCGCAGCGGCCGAAACCGTCCCTCACCAGAGCTCGG 48040  
Qy 12198 ATGGAACCTGAGCAGCTTACAGACCCGGAACCCCGACCGCTCAGGAACCAATTACAGCG 12257  
Db 48041 CTTCTCGTGGCCACACCCGCGCGCCTCGAGCACCGCGCGCGGTGCGGTGCCGA 48100  
Qy 12258 CAGCGGAGGTTTCTCTATGACGGGGCGACTTCGACGCCGG-----TTCTCTGAGTTGT 12313  
Db 48101 CCACGGCCGATCGCGAGGGCTGCGGGCCCTTGCCCTCGGGGGCGCCGCTCCCGGCG 48160  
Qy 12314 CACCGGTGAGCGCTGCGCAATGGAACCGCAGACGCGCTGCTGTCTGAAACCACTTGGG 12373  
Db 48161 CGTCTCGGCGCGCAGCGCGGCCAGGTGCGATTCTGTCTTCGCGGAGGGCTCGCA 48220  
Qy 12374 AAACGTTTGAACAGGGCGGAATCGAACCCGAGGTCCATGCG-----CGGAAGCCGGAACCG 12427  
Db 48221 CGGCATCGGCATGCGCGCGGCAACTGTACGAGCGCTTCCCGGTTCGCGGAGGGCTACGA 48280  
Qy 12428 GGGTTTCTGGGATCAATCCGAGGACTACACCCCGATACACACATCAGCCCTC-- 12485  
Db 48281 CGAGGTGTGACACACTCGACCCGCACTCGACCGGCCTCGACCGGACGTGCGGGACGTTCGG 48340  
Qy 12486 ---AAACGAGTTCGAGGCTACCTGCTCACTGGCAGCGCGCAAGACTTGGTTCAGGCGG 12542  
Db 48341 CGAGNATGTTACAGAGAGCGGGAGGAGCTGAAACCGACACCGCTTCACGACGCGCGCT 48400  
Qy 12543 TATCTCTAACATTCGCGGCTCGAAGGCCCTGCGATCAATTCGACACCGCGTGTCTC 12602  
Db 48401 GTTCGCGCACAGGTGCGCGTCCACCGCTGCTGAGTGTGGG---CGGTGCGCGCGGA 48457  
Qy 12603 CTCGCTCGCCCTGCTATCTGGCTGCGAGCGCTCGGTCGCGTGAATGCACCATGGC 12662  
Db 48458 CTACTGCGCGGCGCATCCGTTGGGCGAGATCGCGGCGCACACGTTGGCGCGGGCCCTGGC 48517  
Qy 12663 GCTCGAGCGCGGCTCCGCTCATGGCCACTCCCTTCGCTTCAACGAGTTCTCTCGCA 12722  
Db 48518 GCTGGAGACCGGCGCGCACTGGTGACGGCTGTCGCGCGCTGATGACAGGCCCTGCGCGC 48577  
Qy 12723 CGCGGCGCTGCGCGCAGACGCGCGTGAAGCGCTTTTCGCGCGCGCGGACGGAACCGG 12782  
Db 48578 CGCGGCGCGATGATCGCGCTCCAGGCCACCGAGGACGAGTGTGCGCGCACTTCAACCGA 48637  
Qy 12783 CTGCTCGAGGGTGTGGGAT-----CTGCTGTGTGAGGCGCTCTCGAGCGCCGCG 12836  
Db 48638 CGACGCGCGCATCGCGCGGATCAACGCGCCCGCAGTCCGCTGTGTTCTCCGGAACCGAGA 48697  
Qy 12837 CAACGGTCAACGTTCTCGGCGTCTGTCGCG-----GGCAGCGCGCTCAACAGGACGG 12890  
Db 48698 CGCGTAGCGCGCTCGCGGACTTCTTCGCGGGAGGCGCGAAGATTTCGCGGCTCAC 48757  
Qy 12891 CGCAAGAACCGGCTGACCGCACCAACCGGTGTTTCAAGTCAAGGTCAATCCGCCAGGC 12950  
Db 48758 GGTGAGCACCGGTTCCACTCGCGCTCATGSAACCCGCTGTGGAGGACTTTCGCCCGGT 48817  
Qy 12951 TTTGGCCAAACGACACTCTCCCTGCGCGATGTGATCGGTGGAGGCCACAGGACGCGG 13010  
Db 48818 GGTGCGCGGTCTGCGCTTCGAGACGCCCGCGACACCGGTGCTCTCGAACTTCAACCGGTGA 48877  
Qy 13011 GACCACTGGGCGACCGCGATCGAGGCTCAAGCCCTCGTCGAAGCTTACGGTTCAGGACCG 13070  
Db 48878 GCTCATCGACGGTACACGGCGGACTATTGGTTCGGGACGCTCCGAGGGCGGTCCGGTT 48937  
Qy 13071 CCCCAGCGCGCCCTCTGCTCGGAACCTTCAAGTCCAACATCGGGCACTTCCATGGC 13130  
Db 48938 CGCCAGCGCATCGGACCTCGGGGAGCTGCGGCTGACCACTGTTGTTGGAGACCGGGCC 48997  
Qy 13131 CGCTCGGGTGTGG-----CGGGGTATCAAGATGGTGTGATGGCTGCGGAATG 13180  
Db 48998 CGGCGCGTGTGAGTGCATGGGCCAGGGGCTGCTGGAGCGGCGTCCGCCCTTGCATC 49057

Qy 13181 GTCTGCTGCGCGGACGTTTGCATGTGTGATGAGCGCTGCGCGCATGTGGACTGTGTCCCGG 13240  
Db 49058 CGCCCGTTCGGCAGCCCCGAGCGCATACCGCGGCTCTTCGCGCAGCTCCACGT 49117  
Qy 13241 GTGCGGTGAGCTGTGTGACGAGACGCTGCTTGGCCCGCGGGAGGGGCGGTACGGC 13300  
Db 49118 GCAGCGTCTCCGCTGACCTGGCGGGGCTTCTTCGCGCGCGCGCGCGCGCGCG 49177  
Qy 13301 GGGCAGAGTGTATATATTTCGGGTGACGCG-----CACCAACCCCAACGTCAT 13349  
Db 49178 CTTGCCCACTACGCTTTCAGCACACGCGGTACTGCTGAGACACACCGCGCCACGCG 49237  
Qy 13350 CTTGAGAGAGCACCCGCCCAACATCCGCTCAGACACACCGCGCAGACGTCCTCGGG 13409  
Db 49238 CGCGCGGGGACCGACCGCGTGGAGACCGGTTCTGGGAGACGCTGAGCGCGGAGCGC 49297  
Qy 13410 AGAATCAGCGCGCAGAGATGCGGTAGTGGGGATGAGGCTGCTGCGCGAGTCCAGG 13469  
Db 49298 CCACTCTCTCGCGCCACCTTCGAACTGCGCTCGAGCAACTGAGACGCGTGTGCGCGC 49357  
Qy 13470 GGTGTGCGCGTGGTGTGTCGGCAGTGCAGCGCGGCTTCGCGCGCCAGGCGCCAGGC 13529  
Db 49358 GCTGTCCGCGTGGCGCGCGGAGACGCGCGGAGTCCGCGTGGAAAGCTGGTCTTACCG 49417  
Qy 13530 CTTGACGCGC---CACCTCACCGACCAACCCCGGCTTCGACCTTCGCGACGTCGGGTAC 13586  
Db 49418 CACGGGTGGAAGCGCTCAGCGGCTTCGCGCGCACGAACTGCGGGGCAACTGGCTGTT 49477  
Qy 13587 CTTGCGCCACGCGCGCGCTGTGTGACACACCGGCG-----ACCTCATTCGCGCGCA 13640  
Db 49478 CTTGCTCAGCGAGACACCGAGGCTTCGAGGCGCTTCGAGTGGACCGCGCGCTGCGCG 49537  
Qy 13641 CCGGACACCTTCTGCAAGCACTCCAGGCACTCGCGCGAGGCGAAGCCACACCGC 13699  
Db 49538 CGGCTCGCGCGCTGGGCGCGGCTGCTGCGGTGACGCTGACCGCGCGCGCGACCG 49597  
Qy 13700 TCATCCACAGCAGCGCGCCAGCGGAGCCGCGGAGCGCGAGGCGCAGGAAGACCGCAT 13759  
Db 49598 CGCGGCACTGCTGCGGAGCTCGCGGAGGCGCTCGGGAGAGCCCGCTCGACGCTGTGAT 49657  
Qy 13760 TCATCTGCTCG-----GACAGGGGACCCAAAGCGCGCGGATGCGCCACAGGCT 13808  
Db 49658 CTCCTCTCGGATCAGCAGAGGACCAACCGCGACACCCGCTCTGCTCGTGGCGAC 49717  
Qy 13809 CTACCACACCCCGCTCTTCGCGCGGCACTCAACGACATCTGCAACCAACCTCGACCC 13868  
Db 49718 CGTCTGACCTTCGCGCTGCTGCAAGGCGCTTGGGCGACGCGGGCATCGACGCCCTGTG 49777  
Qy 13869 CCACCTCGACACCCCTCTCTCCCTCTCACCCAGGACCCCAACACCCAGGACACCCAC 13928  
Db 49778 GCGCTGACAGGTTCGCCATGTCACCGCGCGGGCGGACGCGGTGCGGCGCGCGCA 49837  
Qy 13929 CACCTCGAAGAGCGCGCGCTGCTTCAGAGACACCGCTACGCGCCAGC-----CGCG 13982  
Db 49838 GAACCGCTCTGGGCTCTGGCGCGGCTGCGGCGCTGAGACACGCGCGCGCTGGGCGG 49897  
Qy 13983 CTTCTTCGCTTCAGGTGCGCTTCACCGCTCTTCAGCGAGGCTTACCAATACACCC 14042  
Db 49898 TCTGATCGACTTCGCGACACGCTTACGACCGGATCGCGCGGCTGCTGCGCGGTGCT 49957  
Qy 14043 CCACCTAGCGCGGACACTCTCTCGCGGAAATCACCGCGCGCCCACTTCGCGCGGATCT 14102  
Db 49958 CGCCAGTTCGCGCGGAGACCAAGTTCGCGATCCGCGACCGCGCGGTGTTCTGCTCGAG 50017  
Qy 14103 CACCTCAGCGACCGCACCTCTATC-----ACCCAAACCGCGCAC 14144  
Db 50018 GTCCACACCGCGCGCGCGCGGAAACACCGCGCGCGCTGCTGCGCGCGCGCGCAC 50077  
Qy 14145 CTTATCGAAACCATGCGCGCGCACCATGACCACTCCACCTCCACAC----- 14189  
Db 50078 CGTCTGATCACCGCGGTACGGGTGCTGGGCGGCGATCGTCCCGCTGGCTCGCGCGG 50137









QY 5706 GGGCCCGGCATATCTCGACGGCGCGGGTTTGAACCCATGTACCCAGATTGGCCACGGC 5765  
Db 41525 CGACGAAGGCACTTCGGCGCGCGCGTCTGTCACCTTCGCGCGCACTCGCGGTGAC 41584  
QY 5766 AGCGGTACGAGCGCATCGCGACACCGAAGCGGTATGCTCATCGCGACATCGA 5825  
Db 41585 CGCAGTCCAGCGGC---CTGAGTGCAGACACCGCGGTGCTGTCGGCGACATCGA 41641  
QY 5826 CTGGAGCAAGATC-----GAAACACACTCTCAGACCA 5857  
Db 41642 CTGGGAACGGTTCATCGGACCGTTACCTTCGGCGCGCGAGCGCTGCTCGAGCT 41701  
QY 5858 GCGACTGTGAGCGCGCGCGGAAAGGAGCAGCTGTCCAGGCGCCCACTCCACCGG 5917  
Db 41702 GCGCGAAGTTCGCGCGCGCGCGCGCTTCACAGCGCGCTTCACCGCGCGCGCGCGCT 41761  
QY 5918 CGGAGTTGCACAAACGCTG-----GCCCATCAGAGCTCGCGCGACCAAGCGCGC 5969  
Db 41762 CGCGGCCACGCCCTCGCGCGCGCGCTCGCGGACTTCGCGAGCTTCGCGAGCGCGAGCGCACACAC 41821  
QY 5970 ATTGCTCGAGCTCGTACGAGACCATGTGGCGCGAGTGTCTCCGGCAGCGGACCCGAAAGC 6029  
Db 41822 CCTGATCGACTGTTCGCGCGCAGCTCGCGCGCGCTGTGGGCCACTCTCGCGCGCGA 41881  
QY 6030 CATCGCGCCCGACAGTGTTCGTCGACTCGCGCTTCGATCACTACGCGCGCTCGAGTT 6089  
Db 41882 GGTTCAGCGCCGACCGCGCGCTTCAAGGCCCTCGGCTTCGACTCCCTGACCGCGCTCGAAT 41941  
QY 6090 CCGAAGCTGCTGATCAGGCAACAGGACTCGCGCTTCCTGTCTCGCTGGTCTTCAGCA 6149  
Db 41942 CCGGAACAAGGTCAACACGCGACCGCGCTCGCGCTTCGCGCCACGCTGTCTCGACTA 42001  
QY 6150 CCGGACCCCTGCGAAACTCGCGGTACACTGCGAGAACCAACTGCGGGGCACAGACGGA 6209  
Db 42002 CCCCAGCGCACGGCGCTCGCGCGCTCTCTGACAGAGAGCTGTCTGATCGCAGCGCT 42061  
QY 6210 GTGCGCTCTTCAGCGGACGCGTTACCGCGAGGCTTCTGTFCACGAGCGGATCGCCAT 6269  
Db 42062 CGTGGAGCAGGACGACGCGCGCGCGCGA-----CGAGCCCATCGCCAT 42109  
QY 6270 CGTGGCATGGCTGTCTGTTTCCCGCGGAGTGACTTCGGCGGACGACTTCGGGATCT 6329  
Db 42110 CGTGGCATGAGCTGCTGCTGCTGCGCGGCGTTCGACTCGCGCGAGGCGCTGTGGGACT 42169  
QY 6330 GATCTCTCCGAGCAGGACGCGATCGGGGATTCGCCACCGACCGCGCTGGGACTGGA 6389  
Db 42170 GGTGAGCTCGCGCGGAGCGCATCTCGAGTTCCCGTGCAGACCGCGCTGGGACTGGA 42229  
QY 6390 CACGCTCTACGACCCCGACCCCGACCAACCGGACCTGCTACACCCGAAACGGCGGATT 6449  
Db 42230 GCGCCCTCTACGACCCCGACCCCGATCGCCAGCAAGAGTACGCGCGCGCGGAGT 42289  
QY 6450 CCTCTACGACGAGCGCATTCGACCGCGAATTCCTGGCATACGCCCGCGGAGCGCT 6509  
Db 42290 CTTTATGCGCGCACCGACTTCGACCGCGGCTTCTTCGGGATCTCTCGCGCTGAGCGCT 42349  
QY 6510 CGCCATGACCCCGACGACGACTCTCTCGAAACCGCTGGGAAACCATCGAACACGC 6569  
Db 42350 GGCATGACCCCGAGAGCGCTGATGCTGGAGACCTCTGTGGAGGCTTCGAGCGGCG 42409  
QY 6570 CGGCATCAACCCCGACACCTTCACCGGACCCCGACCGGAGTCTTCACCGGACCAACGG 6629  
Db 42410 CGGGATCGCCCGCGCGAGCTGCGCGTAGCGGACCGCGCTTCTGCTCGGCATGGCCTA 42469  
QY 6630 ACAGACTACGCACTTCGCGTGCAACAGCGGGCGAGTCAACCGATGTTTTCGACTGAC 6689  
Db 42470 CAGGGCTACGAGCGGATGTGCGCGCACCGCGGAGCGGTGGAAGGACACCGGCTCGT 42529  
QY 6690 CGGAACCCCGCGAGCGTCTCTCGGTGCTATCTCGTACACGTTGTTTGGGGTCC 6749  
Db 42530 CGCGCGCGTTCAGCGTCTCTCGCGCGGGTGGCTTACACTTCGACTCGAGGGCC 42589  
QY 6750 TCGGTGTCTGGACACGCGTGTCTCTCGTGTGGTGTGCTTTCATCTGGGCTGTCA 6809

Db 42590 CGCCGCTCAGATCGACACGGCGTGTCTGCTGCTCCCTGCTGCTGCACTGCGCATGCA 42649  
QY 6810 GCGCTTGGTTCGGGTGAGTGTCTGATGGCGCTTCGCGGGGTGTGACGGTGTATGCTGTC 6869  
Db 42650 GTGCTGCGCAACCGCGAGTGCACATGGCGCTGCGCGCGCGCTCACCGTTCATGGCGG 42709  
QY 6870 TCGCGGTGCTTCGTGAGTTTTCGCGCAGCGGGGTTCGGCGCGGACGGGCAATTGCA 6929  
Db 42710 CCGAGAGCTTCTGTTGAGTTTCAGCGCGACGGCGGCTGTTCGCCGACGGCGCTGAC 42769  
QY 6930 GCGCTTTCGGCGCGCGCGGACCGGTCGGGTGAGGTGTGGGATGCTGCTGCT 6989  
Db 42770 GCGCTTCGGCGCGGACCGCGACCGCTGCGCTGGCGGAGCGCTGCGATCTCTGCT 42829  
QY 6990 GGAGCGGCTTCGAGCGGCCCATCGCAACGCTCACCGTCTTCGGCGGCTGCTGCTGGCAG 7049  
Db 42830 GGAGCGGCTGTCGAGCGGCCCGCGCAACGGGACCAAGGTGTTCGCGCTGCTCGCGGCG 42889  
QY 7050 TGCGGTCAACAGGACGCTGCGAGCAACGCTCTGACCGCGCCCAACGGCGCTGCCAGCA 7109  
Db 42890 GCGGTGAACAGAGAGTGTGCTCCACGGTCTGACCGCTCGAAGCGTTCGGCGCGCA 42949  
QY 7110 GCGTGTATCCCGCAGGCGCTTCGCCAACCGCGCTTGTTCGGCGGCTGATGTCAGCGCT 7169  
Db 42950 GCGGTGATCACCACTGCTGCGCTCGCGCGGCTGCTCGCGTGTGCTGAGCGCTGCG 43009  
QY 7170 GGAGGCCACCGCACCGGACCACTTTGGGCGACCGGATTCGAGGCCACGAGCGCTCTGCG 7229  
Db 43010 GGAGCGCACGCTACGGGACGAGGCTGGGTGACCCGATCGAGGCGCAGGCGCTGCTGCG 43069  
QY 7230 GACTACGACAGACCGTTCGCGCGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7289  
Db 43070 CACGTAACCGCAGGACCGGACCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43129  
QY 7290 TGTGCTCACAACAGGCTTCGCGCGGCGCTTCGCGGCTGATCAAGATGCTGATGGCGCT 7349  
Db 43130 CATCGCCACACGAGCGCGCGGCTGCTCGCGTGTGATCAAGATGCTGATGGCGAT 43189  
QY 7350 GCGCATGCTGCTGCTCGCGGCGGCTGCTGATGATGAGCGCTGCTGCTGCTGCTGCTGCTGCT 7409  
Db 43190 GCGCATGCTGCTGCTCGCGGCGGCTGCTGATGATGAGCGCTGCTGCTGCTGCTGCTGCTGCT 43249  
QY 7410 GTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7469  
Db 43250 GTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43306  
QY 7470 GCTACGCGGCGAGGAGTGTCTATTCGCGCTCAGCGGACCAACCGGCTGCTGCTGCTGCT 7529  
Db 43307 CCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43366  
QY 7530 CGAAGAACCGCGCGGACGCTTCGCGGGGACACCGCGCGGCGGAGGTGACGCGG 7589  
Db 43367 CGAGCGCGCGCGCGGAGCTTCGCGGAGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 43413  
QY 7590 CAGCGACGATGAGGCTGCTGCGCGGAGCTTCGCGGCTGCTGCGGCTGCTGCTGCTGCTGCT 7649  
Db 43414 -----GCGCGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43444  
QY 7650 GTCCAGCGCGGCTTCGCGCGCGCGGCTTCGCGCGGCTTCGCGCGGCTTCGCGCGGCTTCGCG 7709  
Db 43445 GGGGAGCGCGGCTGCTGCGGCTTCGCGCGGCTTCGCGCGGCTTCGCGCGGCTTCGCGCGGCTTCGCG 43504  
QY 7710 CGGCTCGACCTCGCGGATGTCGATACACCTTCGCGGACCGCGCGGCTGCTGCTGCTGCTGCT 7769  
Db 43505 CGGCTGAGCGGCTTCGCGGCTTCGCGGCTTCGCGGCTTCGCGGCTTCGCGGCTTCGCGGCTTCGCG 43561  
QY 7770 CCGCGCACCTCATCGCGGAGCGCGACGCTTCCTGCAAGCTTCGCAAGCTTCGAGGAGCTGCTGCT 7829  
Db 43562 CCGCGCGGCTGCTGCTGCAAGGCTCGGAGCTTCGCGGAGGCTTCGCGGAGGCTTCGCGGAGGCTTCG 43621  
QY 7830 CGCAGCGGAGCGCGCGCGCGCGCTTCATCCACAGCAGCGCGCGCGCGGAGCGGAGCGG 7889



QY	1341	CGCCGGCGCCTTTCGACCGCGCGGCTCGGCCACCTTCGACGAGGACACCGCGCCCGTACC	1400
Db	37430	GAACACGACAAAGCTCAGGGATTACCTCAAGCGCTGATGTGGAC-CTGAGCCAGACCC	37488
QY	1401	GGACTCACCGGCGGAGGACCGGACCGGCGGACCGACCGATCGCATCATCGG	1460
Db	37489	GAGGCGTGGGTGAGTGGG-----GGCGAAGGACACCGAGCCCATCGCCATCGTGG	37543
QY	1461	CATGCGATCCGCTTTCGCGGCGGAGTCCGCTCCCGAAGGACCTGTGGAGCTCGCGCG	1520
Db	37544	GATGCGCTCCGCTACCGCGGCGGCTCGCTCGCCGAGGAACTGTGGCACTGGTGC	37603
QY	1521	CTCGGCGGAGACGCGCATCGGCGCGTTCGCCACCGACCGCGCATGGCCACGAAACGCG	1580
Db	37604	CTCGGCGGCGGACGCGGCTCGCGGTTCCCAACCGACCGCGCTGGGACCTGACACGAT	37663
QY	1581	TCAGCGCCAGGACCCACGACGCGCGGACGTTCTTATCCGAGGAGGCGGTTCTTCA	1640
Db	37664	CTACGACCCCGAGCCCGGCGGACCGGCGCGCATGTCGCGAAGCGGCTTCTCTA	37723
QY	1641	CGACCGGCGCATTTTCGACCGCGGCTTCTTCGGAATCAGTCCACGTGAGGCACTGCGCAT	1700
Db	37724	CGACCGCGGAGTTTCGACCCCGCGTCTTCGCGATCTCCCGCGAGGCCCTGTCAT	37783
QY	1701	GGATCCGCGACGCGGCTGCTCGGACGCTCTCGGAGGCGTTTCGACCGGCGGGAAT	1760
Db	37784	GGACCCGCGACGCGGCTGCTTCGACGACCTCTCGGAGGCGCTTCGAACGCGCGGCAT	37843
QY	1761	CGATCCGCTGTCGTTACGGGTCGCTACGGGCTCTTCGGGCGGCCCTCTCTTCA	1820
Db	37844	CGACCCGCTACCGCACCGGACCCCGGCGCGGCTGTTCTGCGCACCAACCGGCGAGA	37903
QY	1821	CTACGGCGCGGTATGGACACCGCTGCTCGAGGCGCGCGGACGTGGAGGCGACAT	1880
Db	37904	CCAGCCTTACCTT-----CAGGCGAGGCGGACGAGGCGCCCACT	37951
QY	1891	CCTCACCGGTACACGCGGACGCTCTCTCGGCGCGTATCGCTACAGCTTCGGGCTGGA	1940
Db	37952	CGTACCCGGAACACCGCGCGTGTTCGCGCGCATCTCTACGCCCTCGGCTCGA	38011
QY	1941	AGGCGCGCGATCACCGTGGACACGGGCTGCTCGGCATCGTCTGACGCTGCTGGC	2000
Db	38012	AGGCGCGCGGTACCGTGGACACGGGCTGCTCTGCTCTGCTGTGGCGCTCCACCTGGC	38071
QY	2001	GTGCGAGTCTGCTGGGTGAGTGCACGCTGCGCTGCGCGCGGCGCTCTGCTCAT	2060
Db	38072	CGCCAGGCGTTCGCGCGGAGTGTCTGCTCGCCCTGCGGCGCGGTGACCGTAT	38131
QY	2061	GTCCACCTCGGCATGTTTCATCGATTTCTCCGCGAGCGCGGCTGTGCTGGAGCGGAG	2120
Db	38132	GGCCACGCGGAACACTTTCATCGGTTTCAGTGGCGAGCGCGGCTGTGCGCCGACGCGCG	38191
QY	2121	GTGCAAGCGGTACTCGGCTGACCGGACCGGCTGCGGCGGAGGCGCTCGGGATGCT	2180
Db	38192	CTGCGCGCGTCTCTCGACCGCGAGGTACGCGGCAATGTCGAAGGATCGGCGTCT	38251
QY	2181	GTGTGTGAGCGGTTGTGCGATGCGTCTGCGGATCGGCTGCTGCGGCTGGCGGTGACG	2240
Db	38252	CCTGCTGAGCGGTTGTCCGATGCCCCGTGCGCTCGGCCACAGGTGCTCGCCGTCATCCG	38311
QY	2241	CGGAGTTCGGTCAACAGGACGCGTGTGCGTCAATGCGGTGACGCGCGCGGACGCTCGCGC	2300
Db	38312	TGGCAGCGCGTCAACAGGACGCGGCTCTCAACGGGCTACGCGGCTCCGACGAGTCCCTC	38371
QY	2301	TCAGAGCGGTTGATTCGCGGAGGCTTGGCGAAACCGGGGTTGTCGTTGGCGGATGGGA	2360
Db	38372	GCAGAGCGGTTGATTCGCGGAGGCTTGGAGAAACCGCGGCTGACCGGCTCCAGGTCGA	38431
QY	2361	TGTGTGAGGCGGACGCGGACGCGGCTGCGTATCGGCTGCTGCGGTCGAGGACAGGCGTT	2420
Db	38432	CGCGTTCAGGCGGACGCGGACCGGCTCCACCGCTCGCGACCCGATTCAGGCGGAGGACT	38491
QY	2421	GCTCGCCACGTACCG---GCAGCGGCGGCTGACAGGCGGCTGTGGTGGGCTCTCTGAA	2477
Db	38492	GCTGCCACGTACGACAGGACCACTCGGACGACCGGCGCTGTGGCTGGATCCATCAA	38551
QY	2478	GTCCAAACATCGGACACCATCGGCTGCGCGGCTGTGGTGGGTTCATCAAGATGGTAT	2537
Db	38552	GTCCAAACATCGGTACACGACGCGCGCGGCTGTCCCGGTGTGATCAAGATGGTAT	38611
QY	2538	GGCGTTGCGGAGGCGGTGTTCCGCGGACGCTTGTCATGTGATAGCGCTCGCCAGGT	2597
Db	38612	GGCCATCGCAACAGGATCTTCCGCGACGCTGGACGTGGACGACCGCTCAGGT	38671
QY	2598	GGACTGTTCGCGGCGGCTGCGGCTGCTGACGAGCGGCTGCGTGGCGGCGGAGCGC	2657
Db	38672	CGACTGTTCGCGGCGGCTGAAAGCTGCTACGAGGCGGCTGCGCATGGCC-----CGA	38725
QY	2658	GGCAGGCGGTTGCGGCGGCGGAGTGTCTGCTGCTGGGATCGGCGGACGATGCGCA	2717
Db	38726	GTCGACACACCCCGCGGCGCGGCTCTGCTCTCGGCTGACGCGGAAACACGCGCA	38785
QY	2718	TGTGATTTTGAGAGGCGCGCGGCGGCGGCTGTGTTGCGGCGGTGGGTGTTGA	2777
Db	38786	CACGATCATCGACAGGCGCGCGGCTCGCCCTCGACCG-----38818	
QY	2778	GGGTGCTCCGGTCTTGCATTTCCGTGGCTGAGTTCGCTGCGGCTCCAGTGGCTGTCT	2837
Db	38819	-----GGAGCCCGCGCGGCGCGCGG	38842
QY	2838	TGCGCGGCTGCTGAGTTCGCTGCGGTCGCGGTCGCGGTCGCGGCTCTGCTGCGGCTCT	2897
Db	38843	GGCCCGCGCGCGCGGCTGCGGCTGCTCTGCGCGAAGAGCGACGCGGCGCTCGC	38902
QY	2898	GGTAGGTCTGAGGCTGGGTTGCGGCGGACGCGGAGCGTTCGCTAGTACGTGGCAGT	2957
Db	38903	.GCCCCAGGACGCGGCTGCTCTCTTCTTGAGAGAG-----GCCGAGCGGCGGAGC	38956
QY	2958	CCGCGCGGACGTTTTCGCTTCCGATGTGGGTGCGGCTGTGGCGTGTGGCGGCTGTCT	3017
Db	38957	CGGCGCGCGCTCGCGCGCGACATCGGCTTCTCCCTCGCCACGACGCGCACCGCTG	39016
QY	3018	GGACATCTGCTGCTGCTTCTGCGCGGAGACCGGTGAGGAGTGTGTCAGGCTGGGGGC	3077
Db	39017	GGACCGCGGCGCGGCTGCTGCGCGAGAGCTTCGAGAGAACTCACCGAAGCGCTAAGGC	39076
QY	3078	GCTCGCGCGGCTCAGCGCGGATCGCGGCTGACACGCTCATCGCGGCTGTGACCG	3137
Db	39077	ACTGCGCTCGGACCGC-----GTGCGCTGCGCTGCTCGCAACGCGCGCCCGCACCG	39130
QY	3138	GGCGGCTGCTGCTTCTGCTTCCCGACAGGCTGGGACGTGGGCGCGGATGGGTGTGCG	3197
Db	39131	CGACAAGACCGGCTTCTGCTTCTCGGCTCAGGCTTCGACGCGGTTGGGATGGGCGTGA	39190
QY	3198	TCTGCTCGCTCTCTCGGCTGTCGCGCGCGGATGAGGCGTTCGAGGAGGCTCTGCGC	3257
Db	39191	ACTTACGACGCTTCCCGGTTTCGCG-----GCC	39220
QY	3258	GCGTGGGTGAGTGTGCTGTGGTGACATCTCGCGCGGAGACGCGGCGGATGCGGTG	3317
Db	39221	GGCTACGACGAGATCGCGCCACCTCGAGCTCGCCCTCGACGCGGACGCGGAGCAGCT	39280
QY	3318	GGAGCGGCGGATGTGGTCCAGCCTGTGCTGTTTCAGCGCTCATGTGTCTTTTGGGTGCTCT	3377
Db	39281	CAACAGACCGTTGACCCAGCGCGGCTGTTGCTGCTGTCGAGGTGGCGCTGTTTCGCT	39340
QY	3378	GTGCGGTTCTTACGATCGAAACCGAGCGGCTCTTGGCGCATTCGACGCGGAGATCGC	3437
Db	39341	GTTGGAGTCTGGGCTGTCGCGCGGATATGTGGCGGCTCATTCGCTGGGTGAGATTGC	39400
QY	3438	GGCGCGCATGTGTGGGCGGCTGAGCCTGAGAGACGCGCGGAGACTGTGCGCTGCG	3497
Db	39401	GGCTGCTCATGTGGCGGCTGTTGCTGCTGGGAGTTCGCGGAGGCTGTGTGCGGCGC	39460
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Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.
Genome sequence of an industrial microorganism Streptomyces
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Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
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Ikeda,H.
Direct Submission
Submitted (01-SEP-2001) Haruo Ikeda, Kitasato University, Dept. of
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Shirokane, Minato-ku, Tokyo 108-8641, Japan
(E-mail: ikeda@mc.pharm.kitasato-u.ac.jp, Tel.: +81-3-5791-6242,
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CDS

FEATURES  
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CDS

CDS

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QY 26703 CGCGCCACATCTCGCGGCACTCAGCTCTGAAAGACGCGCCAAACCGTTGCACTGCG 26762  
Db 35614 GCGCGCATGTGGGGGGGTGTTCTCGTGGAGACCGCTCGCGTGTGGTGGCGGACG 35673  
QY 26763 CAGCGCGCATGCGCGCGGTACGAGGCGGGGCGCATGCGCTCACTGCGCCCTGCGCGC 26822  
Db 35674 TGCCGGGTGATGAGGGCGTTCGAGTGGTGGTCCATGTCTCGCGTGGAGGCGACCGA 35733  
QY 26823 CCAGAACGTGAGAGTCTATTTCCGAACGGTGGGAGGGGAGTGTGGGTGGAGCGCT 26882  
Db 35734 GGACGAGTGTGCGGTGTGACCGA-----GGGCGTGGGTGTGCGCGCGGT 35781  
QY 26883 CAAAGCGCCCACTCCACACCGTCTCGCGGACACCAAGCGGTGATGAGTGTGCGC 26942  
Db 35782 CAAAGCGCCGAGTGTGTGTCGTTTCGGGTGAGAGAGGCCAATCTCTCGCGGTGCGCGA 35841  
QY 26943 GCACTGCACGACACCGGCGCTACGGGGCAACAGCATCCCGCTGCACTACGCTCCCACTG 27002

Db 35842 GCAGTTGGCGCGAAGGGCGTCTGATCCAGCCGTCTGCGGGTGAGCCATGCTTCACTC 35901  
QY 27003 CCCCACGTCCAAACCCCTCCACGAGAACTCTCTGACCTGTGGGAGACATCACCCCA 27062  
Db 35902 GCGGTGATGACCCCATGCTCGACGATTCGCGCGGTTCGCGGAGACATCTCTCTACGA 35961  
QY 27063 GCGGTCCACCGTGGCTTCTTCTCCACCGTGGAAAGGACCTTGGGTGGACACCAACCT 27122  
Db 35962 CGAGCCACAGTCTCGGGTCTCTCCACCTGACCGGTACCTTCGCGCGGAGGCGAGTT 36021  
QY 27123 GGAACCGCC---TACTGGTACCGAACTCCACGAGCCCTTCGCTTTCAGCCAGCCAT 27179  
Db 36022 GACGAGCCGAGTACTGGGTGCTGTCTCCAGCTGACCGGTACCTTCGCGGTTCGCGAGCGT 36081  
QY 27180 CCAGACCTGACCGACGACGACACCGGCGCTTATCGAATTCAGCCCGGACCCACCT 27239  
Db 36082 CCGCGCTCTCGCGAGGCGCGCGCTCTCTCTCGAATTCGCGCGCGGAGTGTCT 36141  
QY 27240 CGTCCCGCCATCGAAGACACACCGAAACACACCGAAACATCACCGCGACCGGAG 27299  
Db 36142 CGCGCGCTGGCCAGAGTCTCGGCAACCGGCTCACCG-----TCCGTT 36186  
QY 27300 CCTCGCGCGGCGACAAACGACACCCACCGCTTCTTCAACCGCTTCGCGGACACCCAC 27359  
Db 36187 CCGCGAAGGACCGCCCGAGGAGCAAGCGCGTCAACCGGCTGGCGCGGTGACAC 36246  
QY 27360 CACCGCATCGGACACACCCACCTGGCACCACTAGACCAACCCAGCCCGGACCC 27419  
Db 36247 GCGCGGTCTACGGTCTGACGCGCGCTTCCACGAGGACCGGTGCGCGC 36300  
QY 27420 CAACCCACACCCACCTCGACCTGCGGCGCGCTTCCACGAGGACCGGTGCGCGC 36345  
Db 36301 -----CGCGGACTGCGCGCTTCCAGCGAGCGGCTTCTGCGGCTTCTGCGC 36345  
QY 27480 CCAACACCCACCAACAAACCGACTCACCAACCGGCTTCAACCCCGGCTTCAACCC 27539  
Db 36346 CAAGCGACCGGCGCTGTCGAGCGCACCGGCTCGGCTTCCGCGCGGACCATCC 36405  
QY 27540 CTTCTCACCGCACACTACCTTGGCGGACAAACACACAACTACTACCGCGCGCT 27599  
Db 36406 GCTGCTGGCGCGCGGATGTGCTGGCGGCTTCCAGCGAACTCTGCTTCAACCGGAC 36465  
QY 27600 CTCTTACGACACCCCTGCTCACGACCAACCGTTCGCGGCTTCTCTCTGCTTCTCC 27659  
Db 36466 GTGCTGCCACCAACCTTGGCTTGGCGGACCAAGGCTCGACGCGATGCTGCTTCTCC 36525  
QY 27660 GGGCACCGCTCTCGAACTCGCCCTTCAAGCGGCGGAAACGGGTGAGTCTGCTCGGGT 27719  
Db 36526 CGGTACCGGGTCTTCTGAGCTGGCGGTGCGCGCGCGACCGAGCGGCTCGGCGGCT 36585  
QY 27720 GGAGAACTGACCTGACCGACCGGTGTTGATCCCGGACACCGAGAGCTGAGTGTGA 27779  
Db 36586 CCAGAACTGACCTGCTGCCACCCCGCTGCTGCTGCGCGGCGCGGCTGAGATGCA 36645  
QY 27780 GGTCAACGTTGCGGACGCGATGAGTGGGCAATCGCGCGCTTCCGATCCACTGATCTC 27839  
Db 36646 GATCTCGTGGCGCGCGCGGAG-----GACCGCTTCCGTTGAGTGTGCTTCTTCC 36699  
QY 27840 CGGACCGCTGCTGCGCGGACCGGAGTGGACCGCTTCAACCGGCGCTTCTTCAACA 27899  
Db 36700 CCGCGCGGTGAGGACTTTCGAGCGCGGAGTGGACCGGACCGGCGCGGCGCATCGC--- 36756  
QY 27900 CCAGCCGACACCGATCACCGTGGCGGACGCGACCGAGCGGTGCTTGGCGGAGCTG 27959  
Db 36757 -----CTCGCGGAGCAGCTCTCGGCTTTCGACACCAACCGGTG 36795  
QY 27960 GCCCGCGCGCGCGGAGCCATCGAACTGGGCGAGTCTTACGGTGTGATGGCGGCGGA 28019  
Db 36796 GCGCGCGCGGACATTCGAGCGCGGTGACATCGAGGAACTGTTTCGACCGCTTCTCGA 36855  
QY 28020 CTGGAACATCGCTTACGGGCGGTCTTTCAGGGGCTGCAACCGCGCTTGGAGGTTTCGCG 28079



QY 21791 TCCCCCTCTCTACCCAAACGACAAACGACAAACGAGGACGCGCGCGACTGTCTCC 21850  
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QY 21851 AGCAGACCCGTAGCCAGCCGCGCTCTTGGCTTCCAGGTGCGCCTCCACCGCTCC 21910  
Db 30588 ---AGACGGGACACACCCAGCCGCGCTGTTCGCTTTCAGGTGCGCCTTACCGCTGG 30644  
QY 21911 TCACCGAGGCTTACCATCATCAACCCCACTACTACCGCGGACACTTCCCTCGCGCAATCA 21970  
Db 30645 T---GGAGTCTGGGAGTGAGCCCGGACTTCTGTCGCGGACATCTCCGTGCGGAGATCG 30701  
QY 21971 CGCGCGCCCACTCGCGCGGACATCTCAACCTTACCGAGCCACACCTCATCAACCCAAC 22030  
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QY 22031 GGGCACCTCATGCAAAACCATGCG---CCCGGACCATGACACCTTCCACACCAACC 22087  
Db 30762 GGGCCCGCTGATGACGACCTTGC CGCGCGCGCGCATGGTTCGCGTTCAGGCGCACCG 30821  
QY 22088 CACACCATCAACCCACCACTTCAACCGCCACGAAAGACCTCGCCATCGCGGCATCA 22147  
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QY 22148 AACCCCACTCTCTGTATAGCGGACGCCCCACACCGTCCAAACATCAACCAACC 22207  
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QY 22208 TCTGCCAACACAGGATCAAAACCAAAACGCTTCCCAACCAACGCGCTTCACTCCC 22267  
Db 30933 TCCTCGCGAGGTGCGCGCGCACTTCCCGCTCAAGGTGAGCGACACGCTTCACTCGG 30992  
QY 22268 CCCACCAACCCCACTCTCAACCAACTTCAACGACACACCAACCTCACTTACCAACC 22327  
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QY 22328 CACCCACACCCCTCTATACCGGCAACACC-----CCACCGACCAACTCC 22375  
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QY 22376 TCACCCCACTACTGGAGCCCAACGAGCCGGACACCGTGTGATAGCGGACGACGACC 22435  
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QY 22436 AAACCTTCCACCAACGCGGTTCACCATCATCGAACTCGGACCGCGGACCAACCTCA 22495  
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QY 22556 CCCACCAACCCCAACCACTTCTCAACCACTTCCCAACCAACCACTCACTTGGC 22615  
Db 31293 GCGAGGAGTGGAGACCTTGTGCGCGCTCTCGCGCGCTGCACTACACGCGCGCGGAC 31352  
QY 22616 ACCCCCACTTACACCAACCAACCAACCAACCAACCAACCACTTCACTTCACTTCC 22675  
Db 31353 CCGCTGGAGCGCTTCTGAC-----GCGCGCGCGGTCTCTGGCTGGACCTGCG 31403  
QY 22676 CCACCTACCTTCCAAACCAACCACTTCTGCTGAACTACCCAGCGCCCAACCAACGACC 22735  
Db 31404 CGACTACGCTTCCAGCGCGCGGTCTTGGCGGA-----CACCTGCGCCACCG 31454  
QY 22736 CCGGTAAAGGCTTCTCGCGCTCGGTTCAGACACCGCGGAGTTCGAGTTCGAGGACG 22795  
Db 31455 CCGCGAGGCGGCGCGGACCGCAGGGAGGCGGACCGGACGACGAGCGCTTCTGGAGC 31514  
QY 22796 CGGTGAACGAGAGACCTTCCAGAGCTTCCGCGGAAACCTCGACATCGAGCGCTCTGTC 22855  
Db 31515 CCGTGCACAGAGGACTTCCGCTGCTGGAGTTCGCTCTCGAGTTCGAGTTCGCGGCGGACGCCC 31574  
QY 22856 TGGACACGGTGTGCGGCACTCTCTCGCTGGCACCGCCACCAACGACCAAGCCGCGCA 22915

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Db 31635 TCGACAGTGGCGCACCGCATGCTCTGGAAGCGGTGACCGGCGCGGATGCGCCAC 31694  
QY 22976 CCACCAAACTGCTCATCGCATCCCGAAACCCAGACCCACACCCCAATCA 23035  
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QY 23036 ACATCTTCAACACTTCAACACCGCATCAACCGCATCCCGCATCCCTTACTGTCAACCA 23095  
Db 31755 GGGTGAACAGCGCTGAGCGCTTGGGCAACCGGCTGCTGCGCGGAGTTCGCGCGC- 31813  
QY 23096 CCACACAAACCCCAACACTTCAACCAACCTTCAACCAACCTTCAACCAACCAACCA 23155  
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QY 23156 ACACACACCGGACCCATCACCGGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 23215  
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QY 23216 ACCCCCAACCCCAACACACCGCATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 23275  
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QY 23276 ACACCAAAACCCCAACCAACCTTCTGTAAGCAACCAACCAACCAACCAACCAACCA 23335  
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QY 23456 CCACACCTTCAACCACTTCAACCAACCTTCAACCAACCAACCAACCAACCAACCAAC 23515  
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QY 23516 CCATCCGACACCGGACACACACCGCGCGCTTCAACCAACCAACCAACCAACCAACCA 23575  
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QY 23576 ACACCAACCCCAACCCCAACCGGAAACCACTTCTATCATCGCGGGAACCGCGCGCC 23635  
Db 32261 --CAGAGCGCGCTGGGACCGCGACCGGACCGGCTGTGTGATCATCGCGGCGCACCGGAGCGCA 32318  
QY 23636 TCGCCACCACTTCAACCACTTCAACCAACCTTCAACCAACCAACCAACCAACCAACCA 23695  
Db 32319 TCGCGCGCTTGTGGCGCGGCTGCGCTGCGCA---AGGACGGCTTCCAGACTTGTGTGCTG 32375  
QY 23696 CCAGCGGAACCGGCGCGCACACCGCGGACCAACCACTTCAACCAACCACTTCAACCA 23755  
Db 32376 TGAGCGCGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 32435  
QY 23756 AAGGCACTCACTTCAACCACTTCAACCACTTCAACCAACCAACCAACCAACCAACCA 23815  
Db 32436 TCGCGCGCGGCTCACCTTCCGCGCTGCGACGCTCCGACCGCGCGCGCGCGCGCGCGCG 32495  
QY 23816 TCCTCAACCACTTCCCAACCACTTCAACCACTTCAACCACTTCAACCACTTCAACCACT 23875  
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QY 23876 ATCTTTCGCGCGCTGTGGAACCGATGCGGAATCTTCTTCTTCTTCTTCTTCTTCTT 23935  
Db 32556 TCGACGAGCGGTTCATCGACCGGCTTACCCCGGAGCGGTACAGAGGTGTTCCGCGGGA 32615  
QY 23936 AGGCAACGCGCGCGGATTTCTGATGAGTTGCTGCTGGACCATGAAACGCTTGAACACT 23995





QY 17513 AAACCTCCCAACCAAAAGCCTTCCACTCCCCCAACACCAACCCGATCTCAACCAAC 17572  
Db 26319 CCCGGCTGGGGTGAGCATTCTTCATCTCGCCGCTCATGAGCCCGATGCTCAACGCT 26378  
QY 17573 TCACACGACACACCAAAACCTCTACCTACCAACCCCAACCCGCTCATC----- 17625  
Db 26379 TCGCCCGGCTCGCGAGTCCCTTCACTACACAGCCCGTATCCCGCTGGTCTCCACGG 26438  
QY 17626 --ACCGCAACACCCCAACCCGACCACTCTCACCCCACTTACTTGGACCCAAACAGCCC 17683  
Db 26439 TGACCCGGCTACCCGCGGAGCGCACTCTCAACCCCGGCTACTTGGGTGGGACAGTCC 26498  
QY 17684 GCAACACGCTGCACTAGCGACACCAACCAAAACCTTCAACCAACCGGCTACCACT 17743  
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QY 17744 ACATCGAAGTGGACCGGACCAACACCTTCAACACCTTCAACACCACTTCCCAACA 17803  
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QY 17975 AGCACTACTGGTTCGAAAGCAACAAGCCGGGTGCGGATCGGTTCCGGTTCGG 18034  
Db 26799 AGCGTACTGGCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 26858  
QY 18035 GCGGGGAGGACTGCGGGCGGAGCGGAGAGTGGAGTTCGGGACCGGCTG 18094  
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QY 18155 ACAGGTTGGTTCGGGCACTCTCCGCTTGGGACCGGACCAACCAACGACCGGCTCA 18214  
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QY 18215 ACACTGGACCTACAGGAAACCTGGAAACCCCTCAACCTCCCAACCAACCAACCC 18274  
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QY 18335 TCCTTCAACCACTTCAACCAAC-----ACGCACTCAC 18365  
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QY 18366 CCCATCCCTCACTCTCAACCAACCAACCAACCAACCAACCAACCACTTCAAC----- 18417  
Db 27216 CCGGTCGCGACGCGCGGACGCACTCTCGCGGACCGGCGGAAAGCCGAGTACGTCCA 27275  
QY 18418 -----CACACCGGACCAAGCCCAACCAACCAACCAACCAACCAACCAACCAAC 27275  
Db 27276 GTACGGGACTTTCGGGCGGACACCGGAGACGCAACCGGACCGGCTCTGGAGCGGC 27335  
QY 18471 CTCCCTCTCTCGCTTCAAGGAAACCAACCCCAACCCCAACCAAC-----CCCC 18514  
Db 27336 AAGCTACCTGCGGAGACTGAGACCGCGCGGCTGAGACCGTCTGCTGCTGCTGCTG 27395  
QY 18515 ACACCCCAACCGGACCGCTCTCAACCTCAACCTTCAACCAACCAACCAACCAACCAAC 18574

Db 27396 CCGCGGCGACCGGACCGCTTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 27455  
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Db 27456 TCGAGGCGCGCGCGCTGACGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27515  
QY 18623 CCAACGACCCCTTCAACACACCCCAACCAACCAACCAACCAACCAACCAACCAAC 18682  
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Db 27576 CCGTGTGACACCCCGAGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27635  
QY 18743 ACACCTTCAACCACTTCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 18802  
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QY 18803 TCCGACACCGGACCAACACCGCGCGCTTCAACCAACCAACCAACCAACCAACCAAC 18862  
Db 27696 TCCGCGCACCGGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27754  
QY 18863 AACCAACCAACCCCAACCGCGGACCAACCTTCAACCAACCAACCAACCAACCAAC 18922  
Db 27755 ----TCCGATGCGCGCGCACCGGACCGCTTGTGTGTGTGTGTGTGTGTGTGTGT 27809  
QY 18923 CCACCACTTCAACCACTTCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 18982  
Db 27810 GCGCGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27866  
QY 18983 GCCGAAACCGGCGCGCACACCGCGCGCTTCAACCAACCAACCAACCAACCAACCA 19042  
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QY 19043 GATTCACCTTCAACCACTTGTGACCAACCAACCAACCAACCAACCAACCAACCA 19102  
Db 27927 GCGCGGAGGTCAACGCTGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27986  
QY 19103 TCACACCACTTCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 19162  
Db 27987 TGA-----CGGACTGACCGGCTTCAACCGGCTGTGTGTGTGTGTGTGTGTGT 28037  
QY 19163 ACAGCGCACTTCAACCAACCTTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19222  
Db 28038 CGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 28065  
QY 19223 CCACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19282  
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QY 19283 TCTACTTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19342  
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QY 19343 ACCTTACCTTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19402  
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QY 19403 TCGCTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19462  
Db 28239 TCTTGTGAAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 28292  
QY 19463 GCGCGCGCGGATGTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19522  
Db 28293 GATGAAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 28352  
QY 19523 TCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19582  
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QY 19583 TTCTTCCAGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 19642



QY	13316	CATTGGCGTCAAGCGGCAACAGCGCCACGTCATCTCTGAGGAAGACCGCGCCCAACA	13375	Db	23214	CCGGCGAACTCCGGCGCGAACTGGAGGAGTCGGGCGCCGTCACGATCGCGCTCG	23273
Db	22137	CGGCGCAACCCCATGCTTCGACGTCGACGACCGCTGTTCCAGAGCGACGCGCGCC	22196	QY	14441	ACACCCCTCATCACCGCCCAACCCACCC	14482
QY	13376	TCCTCTCAGACACACCGCGGAGAGTCCCGGAG-----AATCAGCGCGAGGAG	13429	Db	23274	ACGCGCGCGACCGCGACGCGCTCGCGCACTCTCGCCACCGTGCCGAGCGCGCC	23333
Db	22197	GCGGGTGCCCTGCGCCACTACGCTTCCAGCGGAGCGGTACTGGCGCCGACACACCG	22256	QY	14483	TCACCCCG-----	14503
QY	13430	ATGCGGTAGTGGCGATGAGGTGTGTCGCGCAGTCCAGGGGTGTGGCGGTGGTGT	13489	Db	23334	TCA CGCGCTTTCACACACCGCGGCGTCTGAGACCATGTGGTGAAGAGTGACCC	23393
Db	22257	CGGCGCGCATACACGCGCCCGCGCTCGGCTCGGACTGGA CGCGAGTTCGTGGCGCGG	22316	QY	14504	AACAGCGCGCAACACCGTTCGACTACGCAACCAACCAACCAACCTTCCACCAACAGCG	14563
QY	13490	CGGCGAAGTTCGAGCGCGCTTCGCGGCGCAGCGCCAGCGCTGCAACCGCCACTCACCG	13549	Db	23394	CGGAGAGTTTCGCGCACCGTCTGATGCAAGAGCGTGGCGCGCGCATCTGACAGACC	23453
Db	22317	TGGAACAGCGCGACGTCGCTCGCTCACCGCTCTCGGCTGGCTGACGAGCGACCGTCA	22376	QY	14564	TCACACCTATCATGAACTCGACCGCAACACCTTACACACCTTACCCACGACCAAC	14623
QY	13550	ACCACCGGCTCGACCTTCGCGGAGTTCGGGTACACCTTCGCCACACCGCGCGCGTGT	13609	Db	23454	TCA CGCGCGCACGACCTCGCGCGTTCGCTCTCTCTCGACCGCGCGCTGATCG	23513
Db	22377	CGCGATGGTCCCGCGCTTCAACGCTGGCGGACGCGCGCGGCAACAGTCCCGCTCG	22436	QY	14624	TCCC-----CAACACCCCAACCAACCTTACCTTACCTTACCTTACCTTACCTTACCTT	14671
QY	13610	TCGACACCGCGCCACTTATCGCGCGCGACCGGACACCTTCTCTCAAGCACTTCCAGG	13669	Db	23514	GCGCGCGGACAGGCGAATACGCGCGCGCACTCCAGCTTGAAGCTTTCGCGGAGC	23573
Db	22437	ACTCTGGGCTTACCGCTTCACTTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCG	22496	QY	14672	ACCCCAAAACCACTCTCTCAACCTTTCGCAAAACCAACCAACCACTTGG-----	14721
QY	13670	CACTCGCGCAGGCGAAACCCACCGCGCTCATCCACGACGCGCGCCCGACGCGGACCG	13729	Db	23574	AGCGCGCGCGCGCGCTTCCCGCTTCTCGTGGCTTGGGGACCTTGGCGCGCTCG	23633
Db	22497	CGGACGCTGGTCTCTCTGTGTCGCGCGCGGACACCGGACGAGGCCACCGCGCTGG	22556	QY	14722	-----CACC-----CACC-----CACC-----CACC-----CACC-----	14725
QY	13730	GGACCGGGGCGCGCAGGAAGACCGCATTCATCTGCTTCGGGACGCGGACCCACCGCC	13789	Db	23634	GCATGTGCGCGCGCGCGCGGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23693
Db	22557	CGCGCGATGTTCGAGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22616	QY	14726	CCCACTACTACACCAACCAACCAACCAACCAACCAACCAACCAACCTTCCCGCA	14785
QY	13790	CGGCAATGGCCCAACCGCTTACCAACACCGCGCTTTCGCGCGCGCACTTCAACGACA	13849	Db	23694	TCGACCGCGCTCGGTGTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCG	23753
Db	22617	ACCGCGCGCTTCGCGCGCGCTTCAACGAGCGCGCGCGCGCGCGCGCGCGCGCG	22676	QY	14786	CCTACCCCTTTCACACCAACCACTTCTGCTTCAACCAACCGCGAAGCGCGACCGCT	14845
QY	13850	TCTGCAACCACTCGACCCCACTTCGACACCGCTTCTCTCTCTCTCTCTCTCTCTCT	13909	Db	23754	TGCGCTGCGCGACATCGACTGGGAACGCTTCTCTCGCGCGCTTTCGCGCGCGCG	23813
Db	22677	TGCTGTCTGTGCGCTGCGCGCGGTGAGCGCGGACACCC---CGGCGCGCGCGCG	22733	QY	14846	CACCGAGG-----AAGCGGTGAGCAAGCGCAGGA	14875
QY	13910	CGAACCCAGGACACGACGACCTTCGAAAGCGCGCGGCTGCTCAGCAGACCGCT	13969	Db	23814	TGCGCTGCTGCGCGACTTCCCGGAGACGCGCGCGCGCGCGCGCGCGCGCGCGCG	23873
Db	22734	CGCTCACCTTCAACCGCAACCGCTTCCAGCGGCTGCGCGGCTTATGACGCGCGCG	22793	QY	14876	CCCCATCAACCGCGCTCGGTGATGCTCTGTTGGCAAGTCTTCGACGAGCGAGCAAG	14935
QY	13970	ACGCCAGCGCGCTTTCGCTTTCAGGTGCGCTTCCACCGCTTCTTCAACGAGGCT	14029	Db	23874	GCACCGCTCAGGCTTCGCGAGGAGCTTCGCGCGCTTCGCGCGGAGCGCGCACGAC	23933
Db	22794	TGTGGAATCACCGCGGAGCGTTCGCGCGCTTCGCGCGCTTCGCGCGGAGCGCGCG	22853	QY	14936	AGCTTTCGCGCTGTCGCAACCACTTCGCGCGCTGCTGGGCGCATCCCACTCCCGAAG	14995
QY	14030	ACCAATCACCCCGCTACTACGCGGACACTTCTTCGCGGAAATCACCGCGCGCGCAC	14089	Db	23934	ATGTCCTCGATCTGCTCGGTACCCAGGTGGCGCGCTTCTCGGCGCATCCGACCGCG	23993
Db	22854	AACAGCGCGCTATGGGCGCTGTTTCGCGCGCGCGCGCTCGAACTGCGCGCGCGCTG	22913	QY	14996	TGATCTTCGCAACAGGCTTCAAGAGCTGGGTTTTGATCTCTCGCGCGAATTCAGC	15055
QY	14090	TGCGCGGATCTTCACTCTACGAGCGCACACCTTATCACCGAAGCGCGCACTTCA	14149	Db	23994	CCGTGCAAGCAGACTGGGCTTTCGCGGACCTTCGCTTTCGCTTTCGCTTTCGCTT	24053
Db	22914	CGCGAGGCTGCACTTCCCGGAGGACCTTCGACACCCAGCGCGCGCGCGCGCGCG	22973	QY	15056	TTGTAATCAGCTTGTGCTGAGTTCACCTTCGCGCTTCGCGCGCGCGCGCGCGCG	15115
QY	14150	TGCAAAACATGCCCCCGCGCATGACACCGCTTCCACACCGCGCGCGCGCGCGCG	14205	Db	24054	TGCGAAGCGCTTCAACCGCTTCAACCGCTTCAACCGCTTCAACCGCTTCAACCGCT	24113
Db	22974	TCCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23033	QY	15116	ACCCACTTCGATGGCGCTTTCGCGGCTTCGCGGCGCGGATCGTTCGCGCGGACACAG	15175
QY	14206	-----ACCCACCACTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14260	Db	24114	ACCGAGCGCGCGAGATGGCGGACTTCTGCTTCGCGCGGAACTCTCGGCTCGCTCG	24173
Db	23034	GCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23093	QY	15176	GCAGACCACTGCTCTGCGCGCTTAACTGCGGTTCGCGCGCGCGCGCGCGCGCGCG	15235
QY	14261	CCACTCTCTGATCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14320	Db	24174	AGTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	24233
Db	23094	GCACCGCTCTGATCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23153	QY	15236	GCATGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	15295
QY	14321	AACAAAGGATCAAAACCAAAACCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCG	14380	Db	24234	GCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	24293
Db	23154	CCCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23213	QY	15296	GTGTGGGCAATGACGCGGATCGCGGATTCGCGGAACTTCGCGGAGCGCTCGACACGC	15355
QY	14381	CCAAACCCCATCTCAACCAACTCCACGACACACCAAAACCTTCACTTACCGCGCG	14440				





Qy	9068	CAGGGCGGTGTCCTTTGAGGTCCGATCCGTGGCTGGCTGACATGCGCTGGCGGCACGG	9127
Db	17762	GCCGCCGTGTCGCCCGCGCTGTCTCTCTGGCGCGGGCCCGCAAGAGAGCGCTCCACCGTC	17821
Qy	9128	TGCTGCTGTGGGGCGCACCTTCTCGAACTCGCCCTTCATCGGGCACT--ACGTGG	9184
Db	17822	GACTCTTGGCGCTAACCGCCGACCTGGAAGCCCGTCAACAAGTCCCGCAGGCGACCTCG	17881
Qy	9185	GCTCGCACCGAGTGGATGAGCTGACGTGATGCGCGCTGGTGTCTCTGTGGATGGGG	9244
Db	17882	GACGGACCTGGCTGTGGTCCGCGA.CGGCGT.CGACGACACCAAGTCTGCGCAGGCG	17941
Qy	9245	GTGTGAGTGTGAGTTGGGTTTCGGCTCGCGATGGGAGGGCGCGCTTTGGTAGTG	9304
Db	17942	CTGAGACGGGCGCGCGAGGTGCGCGGCTCGTCTTGACGAGAGCTGCACCGACCGC	18001
Qy	9305	TGTATCGCGGGGTGGAGTGTCTTGTGTGGGGTGGTGGCTGGGTGGGTGTGGAGCT	9364
Db	18002	GCCGTGCTGGCGAGCGCCCTCACCGACCGCGACGGGCTG--ACCGCATCGTCTCGCTCT	18060
Qy	9365	GTCAATGCTCGGGGTCTGTTTGAAGCTCTCTGTGTGTGTGGTGGTGGTCTCTCGGGT	9424
Db	18061	CGCGGGCGCGAGCGGACCGTGGCGCTCCCGCGACCGGGCTCTCTCGGGTGGCTCTG	18120
Qy	9425	CGGGGTGTGGCCCGCGGGGTGCGGTGGCGTGGATGTTCGATGGTGTCCGTGACCGTT	9484
Db	18121	CACCGTCGCCCTGTTCCAGCGCTCGCGACACCGCGTATCGACACCCCGCTGTGGGCGCT	18180
Qy	9485	TGGCTGGGCTGTGTGTGTGTGGGCGGTGTGTTCGGGGCTGGTGGGTGTGGGTGG	9544
Db	18181	GACCGCGGGCGCGCTCTTCCACCGCGCGCTCCGACAAAGT.CACCGCGCGCTCCAGGCCA	18240
Qy	9545	ATGGGGGGGATTTGCTGGCTGAGTGTGTCGCGGAGGAGGGCTGGGGTGATGCGGCTG	9604
Db	18241	GGT.CACCGGATCGGCTGGACCGCG----CGTGGAGTGCCTGGGACGCTGGGGGTG	18296
Qy	9605	GTTTGGGCTGCATCCGGCGTTCTGATGGTGTGTCCAGCCGTTGTGCGTGTGCTTC	9664
Db	18297	TCGTCGACCTGCCGAGACACTGACGCCCGCGCGGGCCAGCGGCTCGCGCGCTCTCG	18356
Qy	9665	CGGTGGGA.CGGGGTTTGGGAGGGG--CGGGTTTCGGGAGGGTGTTCGGGTGCGGCT	9723
Db	18357	CGGCGCGCTCGGCGACACGACCCAGATCGCCCTTGGGCTCTCTCGGCGTCTT.CACCGCC	18416
Qy	9724	GTGTGGGTTGTTGTCTGCTT.CACCGGGGGGTGTACCCGTTGTGCGGTGCGTGTGTGCG	9783
Db	18417	GTA.TGTCGGCGGACCGCGCCCGACGCGCTCCGCCCGGACTGGGAAGCCCGCGGCA	18476
Qy	9784	GCTGT.CGGCGGGCGCGGCGGTGAGGGGTGTCCGTTGTTGTTCCGGGATGAGCGGGT	9843
Db	18477	CCACCTGTGTACCGGCGGCTCGGCACACTCGCCCGCACCTGGCGCGCTGGCTCGCG	18536
Qy	9844	GTGCGGTGCGTGTGTCGATTCGTTGAGTTTCGGGCTGTGGATATGGGT.CAGTTGGT	9903
Db	18537	AGCAGGGCGCGCAACACTGTTCTGTT.CAGCGCGCGCGGCCCGCAGGCGCCCGCGCGC	18596
Qy	9904	GCTGTCTCGTTTCGCGGGCGCGGGTT.CGCTGTATGCGGTGCAGTGGGCTGAGGTG	9963
Db	18597	CCGAATCCCGCGGAGCTGGCGGAACGGCGCACCGGACCGGACGACCTCTCGCGCTCG	18656
Qy	9964	GGTCTGTGCGGTGTGTGGG.CAGGGGTGGGGCT--GGCACGAGACGTGGGTGAGAGCG	10021
Db	18657	TCACCGACCGTGACCGGTGCGCGCTCTCTCGAAGCTTGAAGCCCGAGGGCGCACCG	18716
Qy	10022	GTGTTGGCCCTGTGTCGGGGGTGGTGGTGTGGGTGCCGATGCCGGTGCCTGTGGCG	10081
Db	18717	TCGCGACGTTGTGCACACCGCGGCCACCATCGAACTGCACACCTCTACGCGCACACCC	18776
Qy	10082	GTGCGGTGCGGTGTGGCGGTGGTGTGGTTGAGTTGTTGTTGGGTGTGGTGTGG	10141
Db	18777	TCGACGACTTCGACCGCGTCTCTCGCGCCCAAGGT.CACCGCGCGGAGATCTCTCGACGAAC	18836
Qy	10142	TGCAGGGGTGGCTGGGGCTGGAGCGGTTTTCGGGTTTCGGGCTGTGGTGTGACCCGGG	10201

18837	DB	TCCTCGACACGAGGAGCTGGACGACTTCGTCTCTACTCTCCACCGCCGGCATGTGGG	18896
10202	QY	GTGCGGTGTGCCGCGCCGGAGGACG--GCCCGGTGATGTGGTGGGTGCGTGGGT	10258
18897	DB	GCAGCGCGCGCACGCCGGTATGTCCGGGCAACGCTATCTGGCGGCCCTCCCGAGC	18956
10259	QY	GGGGCTGTGTTCGGCGCAGGCTGAGCATCCGACCGGTTTGTCTCTCTCCACCTCG	10318
18957	DB	ACCGGCGCCCGCGGCTGACCGCCCTGTGCTGTCTCTGGGCACTCTGGGCCGACGACC	19016
10319	QY	ACACGACACCGGCGACCGACTCTGACACCGGTCTGGTGTGGTGGGGCGTGTGATGGTG	10378
19017	DB	TCCAGCTCGCCGAGTCCGACCGCGAGATCCGCGCGACGCGCTTGAATTCATGGACC	19076
10379	QY	GGCGTGTGCGCGG--GTGGTGGCGTGTGTGAGCCGCACTTGGGCTGCGTGGGGACGG	10437
19077	DB	CGAGCTCGCGTGAAGCGGCTTAAAGCGGCGCTTCAGCAGCAGCAGCAGGTATCGCGG	19136
10438	QY	TTGCTGGCGCACGCTGAAACGACTTGAGTTCATCCGGTATGTTCCAGCCGACGCGTCC	10497
19137	DB	TCGCCGCGTGCAGCTGGGAGAGCTACCAACCCGCTTACACTCGGCCCGGCCACCCCGC	19196
10498	QY	GGTGACACAGAGCCCGCGCTCCGACGTGC-----CTGCCACGCTTCGGTGGCG	10549
19197	DB	TGTTCCAGAGGTTCCCGAGTGCAGCGGCTCACCGCGCTGCCGAGCAGAGCGCCGGG	19256
10550	QY	TGCCTGCTCGCGGTCTGGTTGATGATTCGGGTGGGAGGTGTGCCGTGTGTCTGGGTG	10609
19257	DB	ACCCGCGCGGGCGAGTTTCGCCCGCGCGCTGCTGGCCCTGCCCGCGCCGACAGCACC	19316
10610	QY	GTCGTGTGTGTGACGGTGGGACGGG-----TGTGCTGGGTTCGGCGGTGGCG	10660
19317	DB	GCAAGTCTGGAGACGCTCCGACCGAGGCGGCTTCGCTGCGGCTGTCTCCGCGG	19376
10661	QY	GGCACTGGGTGTGTGTGGGGTTCGGGA-----TCTGCTGTGTGTGACCGCGGTGG	10715
19377	DB	AGGACTTCACGACGCGGCTTCGCGGACGTCGGCTTCGACTCGCTGACCGCGCTCG	19436
10716	QY	TCCGATGCTCCGGGTGGGAGGCTTCGGGCGGAGCTGGCG-----	10759
19437	DB	GGCTGCGCAACCGGCTCCGCTCCGTCACCGGCTGACGTGCCGCTCCACGATGCTTCG	19496
10760	QY	-----CGTTGGGGCGGAGTGGGATGTTGCTGTGTGATGTGGGGGAGCGCG	10808
19497	DB	ACTACCGAAACCGGCGGCTTGCGGGTTCTTCCACTCCGAACTGGCCGACGTCCACT	19556
10809	QY	GGAGTGTTCGGCTGTCTGGAGGTTTCTTCCCGGGTTCGCTGACGGGTGTCTGTGCA	10868
19557	DB	CCGGGGCGCGTCCCGCTCACCGCGCGCGCCGTCGACGACGACCCGATCGCCATCG	19616
10869	QY	TGCGGTGTGTGTG--GACGATGCGAGATCGCTCTCTACGCCCGGAGCGGCTGGGCA	10927
19617	DB	TCGGCATGAGCTGCCGCTACCCCGCGGATACACTCCGCGGAGCTGTGGCGGCTCT	19676
10928	QY	CGGTGTTCCGCGCAAGGTGGATGCCGCTCTTTTGTGTGATGAGCTGACGCGGGTATGG	10987
19677	DB	CGTGGAGAGTCAACGGGTCTCCGTCTCCGGCCGACCGCGGCTGGGACCGCGAGG	19736
10988	QY	AGCTGTCCGCGTTCGTGTCTCTCTCGCCCGCGGGATCTCTGGGGTTCGGCCGGG--C	11044
19737	DB	CCCTCTACGACCCGACCGGACGCTTCGGCGCGCACTTACTCGTCCAGGGCGGCTTCC	19796
11045	QY	AGGGCACTACGCCCGCGCAATGCGCTCTGTGAGACGCGTGGCGTACCGCGCGGGCGG	11104
19797	DB	TGCGCGAGTGTCCGACTTCGACCCCGGTTCTTCGGCATCTCTGCCCGCGAGGCCCTGT	19856
11105	QY	CGGGTCTCCCGGGGTGTGCTGGGCTGTGGGAAGAGGCCACGGGATGACCG	11164
19857	DB	CGATGGACCGGACGAGCGCTTCTCTCGAGACGCGCTGGGAGGTCTTCGAGAACGCCG	19916
11165	QY	GGCACTGGCGCGGACCAACCGCGCGCATCATCGTTTCCGCTCTGCACTCCCATGTGCA	11224

Db 15605 TTCTGGCGTTTTCAGCCGACGCGCCCTCGCGCAGGACGCGCGGTGCAAGCGCTTCTCC 15664  
Qy 6940 GCGGCGCGGACGGACCGCTGGGGTGGGGATGCTGCTGGTGGAGCGGCTC 6999  
Db 15665 GAGACGCGGACGGATACCTCGCCGAGAGGTGCGGATCGTCTCGTGGAGCGGTG 15724  
Qy 7000 TCCGACGCCCATCGCAACGGTCAACCGTTCCTGGCGCGGTGGTGGAGTGGCGGTCAAC 7059  
Db 15725 TCCGACGCCCGCGCAACGGCACCGCGTCTCGCGGTGATCGCGGTCTCGGCCATCAAC 15784  
Qy 7060 CAGGACGGTGGAGCAACGGTCTGACCGCGGCCCAACGGGCGCTCCACGACGGGTGATC 7119  
Db 15785 CAGGACGGCGCTTCAACGGCGCTCAGCGGCCCAACGGGCGCTCCACGACGGGTGATC 15844  
Qy 7120 GCGCAGGCGCTCGCCAAACCGCGTGGTGGCGCGGTGATGTCGACGCGCGTGGAGGCCAC 7179  
Db 15845 GCGCAGGCGCTCGCCAAACCGCGGTGGTGGCGCGGTGATGTCGACGCGCTGGAGGCCAC 15904  
Qy 7180 GGCACCGGACCACTTTTGGGACCCGATCGAGGCCAGGCCCTCTCGCAGCCTTACGGA 7239  
Db 15905 GGCACCGGACCCCGCTCGCGGACCCATCGAGGCGCAGGCCCTGTTCCGCCACCTACGCG 15964  
Qy 7240 CAGGACGGTGGCGGAGGGCGCTGGCTGGCTGGCTGCTCAAGTCCAAATGTCGGTAC 7299  
Db 15965 GGCACCGGACCCCGGACCGCGTGTGCTGGCTGGTGAAGTCAATCGGGAC 16024  
Qy 7300 ACACAGGCTGCGCGCGGTGCGCGGGTGAATCAAGATGGTGAAGTGGCGCTCGCGATGGT 7359  
Db 16025 TCCAGTGGCGCGCGGTGCGGAGCATCATCAAGATGGTGAAGTGGCGCTGGCGCAGGT 16084  
Qy 7360 GTGCTGCGCGGACGTTGATGTGATGAGCGGTGCGCGCATGTGGATGTTGCGCGGT 7419  
Db 16085 GTGATGCCCGACAGCCCTGACCGCCAGAGCCCTCCAGCAGCTGCACTGGAGCCCGGGC 16144  
Qy 7420 GCGGTGACGTGCTGACGAGACGTTGCCCTGGCGCGGGGAGGGGCGCTAGCGGG 7479  
Db 16145 ACCGTACGGCTGCTCGGGAGAACACCGACTGGCC---GCAAGCGGGCGGTCCGGCGCGG 16201  
Qy 7480 GAGAGGTGTTCATCATTTGGGTGAGCGGCACCAACGCCACGTCATCTCGAAGAAGCA 7539  
Db 16202 GCGCGGTGTCTCTTTCGGCATCAGCGGTACCAACGCCACGTCATCTGGAGCAGGAG 16261  
Qy 7540 CCGCGCAGCAGCTTTCGGGGGACCAACCGCGCGGAGGGTGAACGCGGCGAGCGACGAT 7599  
Db 16262 ACCGAGG-----CGCCCGCGCGGAGGACGAGCAGCTCGCCCGC 16300  
Qy 7600 GAGGCTGTCGCGGAGTCTTGGGGTGGCGGTGGCTGGTGGTGGCTGGCAAGTGGAGCGG 7659  
Db 16301 GCGCCCTGTCGCGGTGCGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 16360  
Qy 7660 GCGCTGCGCGCCAGGCGCCAGGCGCTGACAGCGCCACCTC---ACGACCAACCGCGGCTC 7716  
Db 16361 GCGCTGCGGAGCAGGCGGACCGCTCTCTACCCATCTCTGACCGCGGACCGCGGCGCC 16420  
Qy 7717 GACTCGGGATGTCCGATACACCTTGGCCCAACCGCGCGGTGTTGCAACACCGCGCC 7776  
Db 16421 GCGCCGATGACATCGGTGTGCTGCTGGCACCTCCCGCGCTCTTTCGAGCACCGCGCC 16480  
Qy 7777 ACCCTCATCGCGGACCGGACAGTCTCTGCAAGCACTCCAGGCACTCGCGCAGGC 7836  
Db 16481 GTGGTGTGTCGCGCGCGGACCGACCGCTGGAGGCGCTGCGCGCGTGGCGCGGAC 16540  
Qy 7837 GAGCCCCACCGCGCTTATCACAAGCAGCGCGCGCGGAGCCGGGACCGGGAGGCC 7896  
Db 16541 GGGCCCTCGGGGTGTGTCGCCCGCGGTGTCG-----GAGCGTC 16579  
Qy 7897 GCGAAGAACCGCATTCATCTGCTCCGGAAGGGACCCCAACGCCCGGATGCGCCAC 7956  
Db 16580 GCGGCGCGCAGCGCTTCTGCTCTTCCCGCAGGGCTCCAGTGGCGGGCATGGCGCC 16639  
Qy 7957 GGCCTTACCAACCAACCGCTCTTGGCGCGGCACTCAACGACATCTGACACCACTC 8016  
Db 16640 CAGCTCTTGGAGTTCCTCGGTGTTCCCGGAGCGGATGCGCGGAATGCGCGCGCGCTC 16699

Qy 8017 GACCCACCTCGACCAACCCCTCTCCCTCTCTACCCCAAAACGACAAACGACGAG 8076  
Db 16700 GCGAGTTCAACGACTGGAACTCATCGAGTCT-----GCGGGCGCC 16744  
Qy 8077 GAGCGCGCGCATGTCTCAGCAGACCGGTAGCGCCAGCGCGGCTTCTTGGCTTCCAG 8136  
Db 16745 GAGGCGCGCGAGCTGGAGCGGTGAGCTGTCTCAGCGCGCTGTCTGCGCGTATG 16804  
Qy 8137 GTGCGCTCACCGCTCTCTCACCGAGCGGTACACATACCCCGCACTACTACGCGGA 8196  
Db 16805 GTCTCTCT---GGCGCGGTGTGGCGGCGCGAGGTGTGAAACCGAGCGGTGTGGC 16861  
Qy 8197 CACTCTCTCGCGGAATACACCGCGCGCACCTCGCGCGCATCTCACCTTACCGAGCGC 8256  
Db 16862 CACTCGAGGCGAGATCGCGCGCGGTGTCTCGCGCGCTGTCTGCTGCGCGAGC 16921  
Qy 8257 ACCACCTCATACCAACCGCGCACCTCATGCAAAACCATGCCCC-----CGGACC 8310  
Db 16922 GCGCGGTGTGAGCTCTCGCGCGCGAGCATCGCGCGAGCTCGCGCGCGCGCGC 16981  
Qy 8311 ATGACCACTTCCACACCAACCGCGCACCATACCCACCACTCACCGCGCGCAAAAC 8370  
Db 16982 ATGATGTGGTGGCGTGTGCGCGAGGTGGAGGCGCGTCTGGAGGCGTTGAGGGA 17041  
Qy 8371 GACCTGCGCATCGCGCGCATCAACACCCCGCACCTCTCTGTCATCAGCGCGACCCCGC 8430  
Db 17042 CGGCTGTCTGCGCGCGAGAACCGCGCGCGCTCTCTGTCGCGCGGCGAGCGCGC 17101  
Qy 8431 ACCTGCAACACATCACCGCTTGCACACCAAGCATCAAAACGCGCATCAAAACCAACCTCCC 8490  
Db 17102 GCGCTGACGAATGACGCGCAGCAGCTCACCGCGAGGAGTCCGGGCGCGCGCGCT 17161  
Qy 8491 ACCAACCGCTTCTCACTCCCGCACCAACCAACCGCATCTCAACCACTCCACGAG-- 8548  
Db 17162 GTGACTACGCTCGCACTCCCGCGAGATCGCGAGATCCGCTTCTCGACCGTCAACGCGAC 17221  
Qy 8549 -----ACACCCAAACCTCACCTACACCCACCCACACCCCGCTCATACCGCAAC 8601  
Db 17222 CTGCGCGAGGTGCGCGCGCGAGATCGCGAGATCCGCTTCTCGACCGTCAACGCGAC 17281  
Qy 8602 ACCCACCGACCACTCTCTACCCCGCATCTAGGAGCCCAACAAAGCGCGCGCAACCGTC 8661  
Db 17282 TGGCTCGACACCACTCATGAGCGCGGTCTGCTGACCGAGCTTGGTACCGAGCTTGGCGCGCGGTG 17341  
Qy 8662 GACTAGCGCACCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8721  
Db 17342 CTGTTGCGGAGCGAGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 17401  
Qy 8722 GGACCCGACCAACCTCACCGCGCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8778  
Db 17402 AGCTCCCGCGGTCTCGCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 17461  
Qy 8779 ACCACCTCAGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8838  
Db 17462 GGTGCTGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17521  
Qy 8839 GCCAAAACCAACCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8898  
Db 17522 GCGCGCGAGGTGTTGTCGCGCGGTTCAGGTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 17581  
Qy 8899 ACCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8958  
Db 17582 GGTGCGTCCCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17641  
Qy 8959 AGCACAGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 9018  
Db 17642 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17701  
Qy 9019 CTACTCGCGCGCATTTGGAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 9067  
Db 17702 GTCGAGCAGCGGAGCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17761



Db 11447 CACGGTGTACTGCCCCCGCACCTGTCACGTGACGCCCGCTCTCTCGCAGCTGCACTGGACC 11506  
Qy 2608 GCGGGGCGGTGCGGCTGCTGACGAGCGGTGCGGTGCGCGGGGAGCGCGGAGGGCGG 2667  
Db 11507 GAAGCGCGGTGAGCTGCTCAGCAGAGACCGCTCGGCC-----CGAACCGGCCGT 11560  
Qy 2668 TTGGGCGGGCGGAGTGTCTGTTCCGATCGGCGGACGAAATGCGCATGTGATTTTG 2727  
Db 11561 CCGGTGCGCGCGGTGCTCTCTTCCGTCATAGCGGACCAATGTCCACACCGTCTCG 11620  
Qy 2728 GAGAGGCGCGCGGCGGGGGGTGTGTTCCCGGGGTGGGGTGTGGAGGTGCTCCG 2787  
Db 11621 GAGAGGCGCG----- 11632  
Qy 2788 GGTCTTGCCATTTCGGTGGCTAGTTCGGTGGCGCTCTCAGTGGCTGTGTCGCGCGGTG 2847  
Db 11633 -----GGACACACCGTGGCC 11647  
Qy 2848 GCTGAGTCGGTGCCTGGTGCCTGGTGCCTGTCCTGTCGCGGTGTGGCTAGGTCT 2907  
Db 11648 GCGCGGCGCGCCCGAGCGCACCGCGCGCGCTCCGCTGCTGTCTCGGCGGCACC 11707  
Qy 2908 GAGGTGGTGTGCGGCGCAGCGGAGCGGTGCTGCTAGTACGTGGCAGTCCGGCGGAC 2967  
Db 11708 CGCAGCGCTGCGGCGCCAGCGCGCGCTGCTCACCCACTCCAGAACCAACCCCGAG 11767  
Qy 2968 GTTTCGCTTCCGATGTGGGTGCGGTCTGGCTGTGGCGGGTGTGCTCGAGCATCGT 3027  
Db 11768 CCGTCCCTCGCGACCTCGGCCACTCCCTGTGGCACACCCGCTCCGCTTCGAGCGCGC 11827  
Qy 3028 GCGGTGCTCTGCGCGCGACCGTGAAGAGCTGTGTGAAGGTGTGGGGCGCTGCGCGCG 3087  
Db 11828 GCGCGGTGATCGCGCAGACCGGAGGACTGCTCGCTCCCTCGGCTCCTCGCGCC 11887  
Qy 3088 GGTGAGCGGATCGCGGCGGTGACACCGGTGATGCGCGCGGTGTGACCGGGCGGTGTC 3147  
Db 11888 GGCGCGCGGACCGCGCGCTGCTGAGGGGTGAGCGCGCGCGGTGCGCG-----GTC 11941  
Qy 3148 GTCTTCGTGTTTCCGAGAGGGTGGGAGTGGCGGGGATGGGTGTGCGTCTGCTGCC 3207  
Db 11942 GCGGTGATGTTCTCGCGCAGGGGACGAGCGCGCGCCGTCATGGCGCGGAACTGTACGAG 12001  
Qy 3208 TCCTTCCTCGGTGTTCCGCGCGGATGACGAGGTGTCGAGAGGTCTGCGCGCGGTGGTG 3267  
Db 12002 ACCAGCCCCGTTCGCGCGCGCTTCGACGAGGTGTCGCGCGCTTCGACCGCTGCTC 12061  
Qy 3268 GACTGCTGTGTGGGATCATCTGCGCGCGGACGCGCG-----GGATGCGGTGTGG 3318  
Db 12062 GACCGCGCTGCGCGAGGTGCTGTTCCGCGCGAGGCGAGCGAGCGCGCTGCTC 12121  
Qy 3319 GAGCGGCGGATGTGTCAGCTGTGTTTCAGCGTTCATGGTGTCTTTGGCTGCTCG 3378  
Db 12122 GACCGACCGGTGACCGAGCGCGCTGTTTCGCGCTGAGGTGCGCCCTCTACCGACTT 12181  
Qy 3379 TGGCGTTCCTACGATATCAACCCGACCGGTCTTGGCCATTCCTCAGGCGGAGATCGCG 3438  
Db 12182 GTGAGAGCTGGGGGTTCGCGCGGCTTCGTCACCGGTCTCATCGTGGAGATCGCC 12241  
Qy 3439 GCGCGGATGTGTGGGGCGGTGAGCTGAAGGACGCGCGGAGACTGTTGCGGTGCGC 3498  
Db 12242 GCGCGCATATGCGCGGGGTGTTACCTCTCAGGACGCGCGCGGACTGTTGCGCGCGCG 12301  
Qy 3499 AGCGGGCGCTGCGCGCTGCGGGGCGGGCGGCGCATGGCTCAGTGCCTGCTGCC 3558  
Db 12302 GCCACCTCATGGAGCGCTGCCGTTCGCGCGCGCATGGTTCGCGGTGAGGCGACCGAG 12361  
Qy 3559 CAGGAGGTGGAGCAGCTCATTTGTGAGCGGTGGCGGGCGGTGTTGGGTGCGCGCGTTC 3618  
Db 12362 GAAGAGGTGCGCCGCTGCTCGCGA-----GGGCTGTGCTGCTCGCGCGCTC 12409  
Qy 3619 AACGCGCGCGCTCCACCGCGCTTCGCGGGGATGCGGAGGCGGTGAGCAGGTGCTGGCG 3678  
Db 12410 AACGCGCGCACCTCGCTGCTCTCGCGCAGAGGACCGCGCGGTGGAGTCTCGCGCGC 12469

Qy 3679 TACTGTGCGGCACCGGGGTGCGGGCCCGCGATCCGGTGCAGTATGCTTGCCTGCCTGC 3738  
Db 12470 GAGTTCCTCGGCGAGGGCGCGCCACCAAGCGTCTAGGGTGAAGCATGCTTCCACTCG 12529  
Qy 3739 CCCTATGTGAGCGCCCTGTCGGGAGGAGTTGCTGGAGTGTGGGGGACATCAGCCCGCAG 3798  
Db 12530 CCGCACAATGACGCAATGCTCGACGCGGTTCGACGCTCCCGAGAGCGTGTCTACGCC 12589  
Qy 3799 CCGTCCGGCGTGGCTTCTTCTCCAGGTGAGGGACCTGGGTGGACACACAAACCTG 3858  
Db 12590 GCGCCCGCATCCCGCTGCTCTCGACCTGACGGGCGGAGGCCGAGCGCGAGGTG 12649  
Qy 3859 ---GACCGCCCTACTGCTACCGCAACTCTGACAGCGCGTTCGTTTTCAGCGATGCCGTC 3915  
Db 12650 GGCACCGCGACTACTGGGTGCGCCACGTCGCTGAGGCGCTGCGTTTCGCGACTCGTC 12709  
Qy 3916 GAGCGCTGCGGATGAGACACCGGCTTCTGTCGAACTGAGCCCGCCACCCACCTC 3975  
Db 12710 CGCACCTGCGGACGCGCGCGCACCTCTTCTCGAACTGCGCCCGCGAGCTGCTG 12769  
Qy 3976 GTCCCGCCATCGAAGACACCGAGACACCGCGAAGACGTCACCGGATCGGAGC 4035  
Db 12770 ACCGCCATGCGGAGGACACCTTCGGCGAGCGGTTTACGACCAACACGCGACTGTC 12829  
Qy 4036 CTCCCGCGCGGACACGACACCGCGCGCTTCTCACCGCCCTTCGCGCCACACCCATACC 4095  
Db 12830 CCGCTGTGCGCGCGGACCGCGCGGAGAGCGCGCGCGCGCGCGCGCTC 12889  
Qy 4096 ACGGGATGCGGACACCCACACCTGCGACCACTACACCCACACACACACCGCGC 4155  
Db 12890 CAGATCCAGCGCTGCACTGAGTGCAGCGGTACCTGCGCGGACACCGCGCGCGC 12949  
Qy 4156 CACCCCGACGCGACTGCGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 4215  
Db 12950 G-----TCGACCTTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12994  
Qy 4216 GAGAGCTCACAGCGCGGTGCGGATCGGTTGCGGTGCGCGGTGCGGTGCGCGGT 4275  
Db 12995 CAGCTGCC----- 13003  
Qy 4276 TCCGGGCGGAGGAGATGCGGCGGAGAGTGTGAGTGTGCGGCGGTCTGGGAGCGC 4335  
Db 13004 TCCCGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13063  
Qy 4336 GTGCGCGCGGAGGAGTGTGAAACGCGTGCAGACACACTGCGCGTGCCTCCCGCGCGC 4395  
Db 13064 GCGCGCGAGCGCGCGGAACTGCGCGCGCTTCTCGGCGTTCGACGAGGAGAGCTCACCGC 13123  
Qy 4396 CTGAGACGCGTGTGTCGCGACTCTCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGC 4455  
Db 13124 CTGAGCTCTCTGTCGCGCGCTGAGCTCTTGGCGCGCGCGCGCGCGCGCGCGCGCTC 13183  
Qy 4456 ATCAACCTGAGGAGTGTGAGGAACTGAGAACTGAGAACTGAGTGTGCGCGCGCGCGCG 4515  
Db 13184 CTGAGACGCTGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 13243  
Qy 4516 CCGCACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4572  
Db 13244 CTGAGCGGACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13303  
Qy 4573 ACCAACTCTTCAACCACTTCAACCACTTCAACCACTTCAACCACTTCAACCACTTCAAC 4632  
Db 13304 CTGAGCGCTTGGCGGAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 13363  
Qy 4633 CACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 4692  
Db 13364 GAGCGGAGTGTGCGCGGAGTGTGCGCGGAGTGTGCGCGGAGTGTGCGCGGAGTGTGCG 13408  
Qy 4693 CAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 4752  
Db 13409 GACACCGAGACCGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13468









Db 39477 CCGCCCTCGCCCTCTGTCAGGACCTCTCTGCCCGCCACCGCCGACCAACCCGC 39418  
Qy 11365 ACCACCACTACCGGTGGTGGGACAAACGCGCCAGCTGCACGCCCGGCTGGCCGCCAG 11424  
Db 39417 ACCACCACTACCGGTGGTGGGACAAACGCGCCAGCTGCATGCCCGGCTGGCCGCCAG 39358  
Qy 11425 ACACAGAACAAACAGCACACCAACCCCTCTCGCCCTGGTCCGCTCCACATCGCCACCGTC 11484  
Db 39357 ACACAGAACAAACAGCACACCAACCCCTCTCGCCCTGGTCCGCTCCACATCGCCACCGTC 39298  
Qy 11485 CTGGGCGACACACCCCGGACACATATCCCGCCCGGACCGCGGTTCCGGAGCTTGGCTTC 11544  
Db 39297 CTGGGCGACACCGCCCGGAGATATCCCGCTTGACTCGCGGTTCCGGAGCTTAGGCTTC 39238  
Qy 11545 GACTCCCTCACCGCGTGGAACTACGCAACCGGCTCTCCCGCACACCGGACTCGCCCTC 11604  
Db 39237 GACTCTTTGACAGCGGTGGAACTCCGTAAACCGCTTGGGTGAGGCAACCGGACTGCGACTG 39178  
Qy 11605 CCCACCACTCGGCTTCGACCAACCCCAACCCACACCTCTCACCCACCACTCCACACA 11664  
Db 39177 CCGACCACTGGTCTTCGACACCGGAATGACGACCGCTGGCGGCTCACTT----- 39125  
Qy 11665 CAACTCCAGCCAAACCGGACAAACCGCTGTGCGCCCGCTGTTGGCGGAGCTCGACAAATC 11724  
Db 39124 ----- 39125  
Qy 11725 GAATCCGGCCCTCTCGCCCTCGACAAACCGACGCGCAAGAGTCACTCGCG 11784  
Db 39124 -----ACGTGAGCTGATGGCGACGACGCG 39096  
Qy 11785 CTGAAGTCACTCATGTTGAGGTGGAACGCCACCCAGCATTCGACAGCCGAAGCGCTGAT 11844  
Db 39095 AAGCGAGAGCGCATCGCAGGTGCGACTTCATCAGTTGCC----- 39055  
Qy 11845 GACGACGAGAGTTCACTCGGCAACAGAGGCTGAGATTTTCAAAATTCATTGACAAACGAC 11904  
Db 39054 ----- 39055  
Qy 11905 CTCGGCTGTCTGAACCGGACGCGCTGCCACTCGCCCGCTATCCGCTGGGCCCTGCTAGG 11964  
Db 39054 ----- 39055  
Qy 11965 ACGTGAATGCAATTGGCGAATGAAGCGAAGCTCTTGGAAATACCTCAAGCGGCTCACTGCG 12024  
Db 39054 ----- 39055  
Qy 12025 GACTGGACCGCACTCGCGCTGCGCTGTACGAGGTGTGCGAGCGTGAGAGGAGCGGATC 12084  
Db 39054 -----GCGATGAGCCGATT 39040  
Qy 12085 GCGATTGTGGGATGGCGTGTGTTTACCCAGCGGGGCGACGTCAACCCAGCGACTGTGG 12144  
Db 39039 GCGATTGTGGGATGGCGTGTGTTTCCGGGTGGGGTGTGTTCCCGGAGGAGTTGTGG 38980  
Qy 12145 CATCTCGTCAAGTCCAGACGAGCGCTATCGGGGAGTTCCCGACCGACCGCTGGATGGAAC 12204  
Db 38979 GAGTGGTTGCTCGGGTGGGATGCGATTGTGAAATTCGCGCGGTGGGGTGGAT 38920  
Qy 12205 CTGGAGCAGCTCTACGACCCGACCCCGACCGCTCAGGAAACAGTTTACACCGGACGCGA 12264  
Db 38919 CTGGAGGGGTGTTTGTATTCGACCCCTGACCCGCTCGGGAGCTGCTACCGCGGTATGCG 38860  
Qy 12265 GGGTTTCTATGACCGGGGCACTTCGACGCGGCTTCTTCGAGTTGTACCGGTGAG 12324  
Db 38859 GGGTTTGTATGAGCGGGGAGTTGATGCGGACTTCTTCGGATCATGTCGCGGTGAG 38800  
Qy 12325 GCGCTGGCAATGACCCCGCAGACGCGCTGTGCTCGAAACCACTTGGGAAACGTTTCGAA 12384  
Db 38799 GCGTTGGCGATGGATCCGACGACGCGTTGTTGCTGGAGACGTCTGGGAGCGTTTCGAG 38740  
Qy 12385 CAGGCGGGAATCGACCCGAGGTTCATGCGCGAAGCGGACCGGGTTCGTGGGGATC 12444  
Db 38739 CCGGCGGGGTATCGATCCGCTGTGATGCGTGGCTCCCGTACGGGTGTCTTTCGCGGGGTG 38680

Qy 12445 AATCCGAGGACTACACCAACCGGATACACATCAGCCCTCAAACGAGTCGAGGGCTAC 12504  
Db 38679 ATGTACCAACGACTACCGCGCGCGTCTC---CACCATGTCCCAGGGTTTCGAAGGCTC 38623  
Qy 12505 CTGCTCACTGGCAGCGGGCAAGATTGCTGAGCGGTATCTCTACAACTTCGGGCTC 12564  
Db 38622 ATGCCAAACGCGACGCGAGCGCTCGACCGCGGGTGGCTACAGCTTTGGGCTT 38563  
Qy 12565 GAGGGCTCGGATCACTATCGACACCGCGTGTCTCTCGCTCGTGGCCCTGCATCTG 12624  
Db 38562 GAGGGCTCGGCGGTGACCGCTCGATACGCGGTGTCTGCTGTGTGGGGTTCATTTGG 38503  
Qy 12625 GCCTGCCAAGCGTCCCGGTCCGGTGAATGCAACCATGCGCTCGCAGCGCGCTCCGTC 12684  
Db 38502 CGCGCGAGCGGTTCGTCGGGTGAGTGTTCGATGGCGCTTCCCGGGGTGTGACCGTG 38443  
Qy 12685 ATGGCCACTCCCTTCTTCAACCGAGTTCCTGCGCAGCGGGCTGTGGCGGACGCG 12744  
Db 38442 ATGTGCTCTCGGGTACGTTTGTGGAGTTTCACTGTCAGCGGGGTCTGGCGCGGACGG 38383  
Qy 12745 CGGTGAAGCGTTCGCGCGCGCGGACGCGGACCGGCTGCTCCGAGGGTGTGGGATG 12804  
Db 38382 CGGTGAAGCGCTATTCGGCGGCTGTGACCGGTACCGGCTGGCGCGAGGGTGTGGGATG 38323  
Qy 12805 CTGCTGTGAGGGGCTCTCCGACCGCCCGCGCAACCGGTCACTGCTGTCTTGGCGCTCGTC 12864  
Db 38322 CTGCTGTGAGCGGCTCTCCGACCGCCCGTCCGCAACCGGTCACTGCTGTCTTGGCGTGTG 38263  
Qy 12865 CGCGCAGCGCGTCAACAGGACGCGCGCAAGCAACCGGCTGACCGCACCCCAACCGTCTG 12924  
Db 38262 CGTGGAGTGGGTCAACAGGACGCGTGGAGCAACCGGTCTGACCGCGCCCAACCGGCCCC 38203  
Qy 12925 TCACAAGTCAAGTCACTCGCCAGGCTTTGCGCAACGACACCTCTCCCTGCGCGATGTC 12984  
Db 38202 TCCAGCAGCGGTGTATCTCCGTGAGGCCCTGCGCAATCGGGACTGACCCCGCGCGATGTC 38143  
Qy 12985 GATCGGTGAGGGCCCAACGCGGAGCAACCTCGGGCGACCCGATCGAGGCTCAAGGCC 13044  
Db 38142 GACGAGTGGAGGGCCACGCGACCGGGACCACTCTGGGGGACCCGATCGAGGCCCGGCA 38083  
Qy 13045 CTGCTGAAAGCTACGCTCAGGACCGCGCCCAACCGCGCGCCCTCTGCTGCTGGAACCTC 13104  
Db 38082 CTCTGCGCGCTACGAGCAACACCGCGCCACACCGCGCCCTTGTGGCTGGGATCCCTC 38023  
Qy 13105 AAGTCCAACTCGGCACTTCATGGCGCGCTGCGGGTGTGGCGGGGTCACTCAAGTGTG 13164  
Db 38022 AAATCCAACTCGGCGACGCAAGCGCGCGCGGGCTGTGGCGGAGTCACTCAAGTGTG 37963  
Qy 13165 ATGGCGCTGGGGAATGCTGTCTGCTGCGCGGACGTTGATGTGATGAGCGCTTCGCCGAT 13224  
Db 37962 ATGGCGCTGGCGAACGGGCTGTGCTCCACAGACCTCTCCAGTGGAGAGCCACCCCGAG 37903  
Qy 13225 GTGACTGTGCTCGCGGTGCGGTGACGTGTGAGGAGAGCGGTGCGCTTGGCCCGGGG-- 13282  
Db 37902 GTGACTGTGCTCACAGCGGAGTAACTCTCTGACAAACCGGTGCGCTTGGCCCGCGGAC 37843  
Qy 13283 -GGAGGGCGGCTTACCGCGGGCAGGAGTGTCACTATTTCGCGCTCAGCGGACCAACGCC 13341  
Db 37842 CCGCGCGCGCGGCGCACCGCCACGCGCGGTGTGTATCTTTCGCGGTGACGGGACCAACGCC 37783  
Qy 13342 CAGCTCATCTTCGAGGAAGCACCCCGCCCAACATCCCTCGTCAGACACACCCCGCGGAC 13401  
Db 37782 CATGTGATTTGGAGAGGCGCGCTG-----CGGCGCGGGCGGT 37744  
Qy 13402 GTCCCGGAGAAATCAGCCGCGACAGGATGCGGGTGTGCGGATGAGGCTGTGTCGCGC 13461  
Db 37743 GCTCCGCTGTGGGGTGTGCGGTGGGTCTCCGAATCCAGCCCTTCCGGTGGCTGAGTCT 37684  
Qy 13462 AGTCCAGGGGTGTGGCGTGTGCTGCGGCCAAGTCGAGCGCGGCTTCGCGCGCCAG 13521  
Db 37683 GAGCGGTGCGCGGTGCGCGGTGCGGTGCGGCGAGGCTGTGAGGCGGGGTTCGCGCGCGAG 37624

Qy	9160	GCCCTTATGCGGGCACAATAGTGGGCTGCGACCGAGTGTGATGAGCTGACGCTGCATGCGG	9219
Db	41499	GCCCTTATGCGCGAGAAAGTGTGGGTGGCGACCAACGTGACGAGCTGACGCTCCACACA	41440
Qy	9220	CCGCTGTGTGTTCCGTGTGATGGGGGTGAGTGTGCAAGTTGGGGTGGGGTTCGGCTCGGAT	9279
Db	41439	CCGTGTGTGTCATCTCTGAGGTTCGAGACGTCACCTTCAGGTTGCCATTCGGCGCCGAC	41380
Qy	9280	GGGAGAGGGCGCGCTTTTGGTGAAGTGTAATGCGCGGGTGGGAGTCTCTTGTGTGGGGGT	9339
Db	41379	GAGTGGGTGCCGCATGATGACCATCCACTACGCGGTGAGGCGGAGTGGTGAGCC	41320
Qy	9340	GGTCCGTCCGGTGGGGTGTGGAACGTGTCAATCCCTCGGGGGTGTGCTG---GTGAGGCTGCT	9396
Db	41319	GATGCGTCGGCCAGTGCCTGTGGAACGCGTCAATGCCCGGGTGTCTGAGCCCTGCCAAGGAC	41260
Qy	9397	GCTGGTGGTGTGGTGTGATGTCTGGCGGGGGTGTGACCGCGGGGGTTCGGGTGGGTGGG	9456
Db	41259	GATGACACTGCCTCCTGATCGAGCTGCTTTGCCGGGACCTCTGGCTCCCGGTGGAGCTACGCT	41200
Qy	9457	GTGGATGTGCATGTGTCCGTGACCGTTTCGGCTGGGGCTGTTGTGTCTTTTGGGGCCGGTG	9516
Db	41199	GTGCACCTGAACACGGCTTACGATCAAAATGGCCGACGCCGGCTTTCCTTATGGCTGGCA	41140
Qy	9517	TTTTCGGGGCTGCCTGCGGTGTGCGGTGATGCGGGGGGATTTGCTGCTGAGGTGTGTCTG	9576
Db	41139	TTCCAAGGTTGCGCGCGGCTTGGCGTACGGCGACGACATCTCTGTCGAGGCACGTCCT	41080
Qy	9577	CCGAGAGAGCGTGGGTGATGCGGCTGTTTGGGCTGCAATCCGGCGTTGCTGTGATGGT	9636
Db	41079	CCGAAAGAGTGTGGGAGACCGCGCGCGTACCGTCTGCAATCCCGGCCCTGCTTCGACGCT	41020
Qy	9637	GTGCTTCAGCCGTTGTCCGTTGTTGCTTCCGGGTGGGACCGGGGTTTGGGAGGGGGCGGG	9696
Db	41019	GCCCTTCA-----GGGACCGGCGCTCTTTCGTGTGGCGGG	40985
Qy	9697	TTCCGGAGAGGTGTTCCGGGTCCGGCTGTGTGGGGTGGTGTGTGCTTCAACCGGCGGGT	9756
Db	40984	TCCGGGACGCCGTC--GTGCCCATGTGTGAAACGGTCTGCGTTCGTACGACATGGT	40927
Qy	9757	GTGACCGGTGTGCGGTGCGTGTGTGCGCTGTGCGCGCGGGCGCGGGCGTGAAGCGGTG	9816
Db	40926	GCAATCTCCGTGCGCGCTGCCCTGTGCAC-----GCTTGGAGCGACAGGGCGGCCGTG	40873
Qy	9817	TCGGTCTGTGTCGGGATGAGGGGTTGTCGGCTGCGCTGCGTTCGATCGTCTCAGTTG	9876
Db	40872	TGCGTGGCAATACACGACGACACCGGGGTGCCGTGGCGTCCGTTCGATCTTGAGTTG	40813
Qy	9877	CGGCTGTGATATGGGTCAATTTGCTGCTCTCGGTTTCCGCGCGGGCGCGGGGTTCCG	9936
Db	40812	CGGCTGTGATATGGGTCAATTTGCGTGTCTCGGTTTCCGCGGGCGCGCGGGTTCG	40753
Qy	9937	CTGTATCCGGTGCATGTGGCTGAGTGGGTCTGTGCCCGTGTGTGGGACGGCGTGGCG	9996
Db	40752	CTGTATCCGGTGCATGTGGGTGAGAGTGGGTCTGTGCCCGTGTGTGGGACGGCGTGGCG	40693
Qy	9997	TGGACAGACCTGTGGTGAACCGTGTGGCCCTGTGCCCGGGGTGTGTGTGTGGG	10056
Db	40692	TGGACAGAGACCTGTGGTGAACCGTGTGGGCCCTGTGCCCGGGGTGTGTGTGTGGG	40633
Qy	10057	TGCCCGGATCCCGTGCCTGTGGCGGTGGCGGTGGCGGTGTGTGGCGGTGTGTGGGTGAG	10116
Db	40632	TGCCCGATCCCGTGC-----CGATGGCGGCGGTGGCGGTGTGTGGGTGAG	40585
Qy	10117	GTGTGTGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	10176
Db	40584	GTGTGTGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	40584
Qy	10177	TCCGGCTGTGTGTGTGACCCGGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	10236
Db	40524	TCCGGCTGTGTGTGTGACCCGGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	40465
Qy	10237	GATGTGGTGGGTGCGTGGTGTGGGGGCTGTGCTGTTCCGGCGAGGCTGAGCATCCGAC	10296

[illegible]

Db	43716	CTGCTGGTGGAGCGGCTCTCCGACGCCGCTCCGAAACCGGTCAACCGGTCTCTTGGCGGTGGTG	43657
Qy	7042	CGTGCAGTGGGTTCAACACGAGACGGTGGAGCAACGGTCTGACCGCGCCCAACGGGGCGG	7101
Db	43656	CGTGCAGTGGGTTCAACACGAGACGGTGGAGCAACGGTCTGACCGCGCCCAACGGGGCGG	43597
Qy	7102	TCCAGCAGCGTGTATCCGCGAGGCCCTCGCAACCGCGGCTTGTGGCGCGGTGATGTC	7161
Db	43596	TCCAGCAGCGTGTATCCGCGAGGCCCTCGCAACCGCGGCTTGTGGCGCGGTGATGTC	43537
Qy	7162	GACGCGTGGAGGCCCAACGAGACCGGACCACTTTGGCGAGCCCGATCGAGGCCAGGCC	7221
Db	43536	GATGCGTGGAGGCCCAACGAGACCGGACCACTTTGGCGAGCCCGATCGAGGCCAGGCC	43477
Qy	7222	CTCTTCGCGACCTACGAGCAGGACCGTGCAGGAGGGCGCTGTGGCTGGGCTCGGTC	7281
Db	43476	CTCTTCGCGACCTACGAGCAGGACCGTGCAGGAGGGCGCTGTGGCTGGGCTCGGTC	43417
Qy	7282	AAGTCCAATGTGGGTACACACAGGCTGCGCGGCGGTGCGCGGGTGATCAAGATGGTG	7341
Db	43416	AAGTCCAATGTGGGTACACACAGGCTGCGCGGCGGTGCGCGGGTGATCAAGATGGTG	43357
Qy	7342	ATGGCGCTGGCGATGGTCTGCTGCGGAGCTTGCATGTGGATGAGCGCTGCGCGCAT	7401
Db	43356	ATGGCGCTGGCGAATGGTCTGCTGCGGAGCTTGCATGTGGATGAGCGCTGCGCGCAT	43297
Qy	7402	GTGGACTGGTCCGCGGTCGCTGAGCTGTGACGAGACGGTGCCTGGCGCGGGGG	7461
Db	43296	GTGGACTGGTCCGCGGTCGCTGAGCTGTGACGAGACGGTGCCTGGCGCGGGGG	43237
Qy	7462	GAGGGCGGCTACGCGGGCAGGAGTGTATCATTTGGCGGTGAGGGGACCAACGCCAC	7521
Db	43236	GAGGGCGGCTACGCGGGCAGGAGTGTATCATTTGGCGGTGAGGGGACCAACGCCAC	43177
Qy	7522	GTACCTCTCGAAGAG-----GACCGCGGACGACGTT	7554
Db	43176	GTACCTCTCGAAGAGACCCGCCCAACATCCCGTCAGACACACCCGCGGACGACGTT	43117
Qy	7555	CGGGGGGACCAACCGCGGAGGGTGAACGGGCGAGCATGAGGCTGTGCGCGG	7614
Db	43116	CGGGGGGACCAACCGCGGAGGGTGAACGGGCGAGCATGAGGCTGTGCGCGG	43060
Qy	7615	AGTCTGGGGTGTGCGGTGTGTGTGCGCAAGTGCAGCGCGGCGCTTGGCGGCCAG	7674
Db	43059	AGTCTGGGGTGTGCGGTGTGTGTGCGCAAGTGCAGCGCGGCGCTTGGCGGCCAG	43000
Qy	7675	GCCAGGCGCTGCAGCGCCACTCAACGACACCGCGGCTCGACCTGCGGATGTCGA	7734
Db	42999	GCCAGGCGCTGCAGCGCCACTCAACGACACCGCGGCTCGACCTGCGGATGTCGA	42940
Qy	7735	TACACCTTCGCCACGCGCGCGCTGTTCGACACACCGCGCACCTCATTCGCGCGGAC	7794
Db	42939	TACACCTTCGCCACGCGCGCGCTGTTCGACACACCGCGCACCTCATTCGCGCGGAC	42880
Qy	7795	CGGACAGCTTCTCGAAGCACTCAGGACCTTCGCGAGGCGAGCCCAACCGCGCGTC	7854
Db	42879	CGGACAGCTTCTCGAAGCACTCAGGACCTTCGCGAGGCGAGCCCAACCGCGCGTC	42820
Qy	7855	ATCCACAGGCGCGCGGGGAGCGGAGCGGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	7914
Db	42819	ATCCACAGGCGCGCGGGGAGCGGAGCGGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	42760
Qy	7915	ATCTGCTTCGGAGGAGGACCAACCGCGCGCATGGCGCATTCACACACCGGAC	7974
Db	42759	ATCTGCTTCGGAGGAGGACCAACCGCGCGCATGGCGCATTCACACACCGGAC	42700
Qy	7975	CCCGTCTTCGCGCGCGCATCAACGACATCTGACACCACTCGACCCCGGACCTCGAGCC	8034
Db	42699	CCCGTCTTCGCGCGCGCATCAACGACATCTGACACCACTCGACCCCGGACCTCGAGCC	42640
Qy	8035	CCCGTCTTCGCGCGCGCATCAACGACATCTGACACCACTCGACCCCGGACCTCGAGCC	8079
Db	42639	CCCGTCTTCGCGCGCGCATCAACGACATCTGACACCACTCGACCCCGGACCTCGAGCC	42580
Qy	8080	GCGCGCAGCTGTCTCAGCAGAGCCCGCTACGCGCAGCCCGCGCTCTTGGCGTTCAGGTC	8139
Db	42579	GCGCGCAGCTGTCTCAGCAGAGCCCGCTACGCGCAGCCCGCGCTCTTGGCGTTCAGGTC	42520
Qy	8140	GCGCTCCACCGCTCTCTCAGCAGGCTACACATCAACCGCGCATCTACTAGCGCGGAC	8199
Db	42519	GCGCTCCACCGCTCTCTCAGCAGGCTACACATCAACCGCGCATCTACTAGCGCGGAC	42460
Qy	8200	TCCCTCGCGGAAATCAGCGCGCGCCACCTCATGCAAAACCATGTCGCGGATCTCACCCTCA	8259
Db	42459	TCCCTCGCGGAAATCAGCGCGCGCCACCTCATGCAAAACCATGTCGCGGATCTCACCCTCA	42400
Qy	8260	ACCCTCATCAACCAACCGCGCACCTCATGCAAAACCATGTCGCGGATCTCACCCTCA	8319
Db	42399	ACCCTCATCAACCAACCGCGCACCTCATGCAAAACCATGTCGCGGATCTCACCCTCA	42340
Qy	8320	CTCCACACACCGCGCACCATCAACCAACCATGTCGCGGATCTCACCCTCA	8379
Db	42339	CTCCACACACCGCGCACCATCAACCAACCATGTCGCGGATCTCACCCTCA	42280
Qy	8380	ATCGCGCGCATCAACCAACCGCGCACCTCATGCAAAACCATGTCGCGGATCTCACCCTCA	8439
Db	42279	ATCGCGCGCATCAACCAACCGCGCACCTCATGCAAAACCATGTCGCGGATCTCACCCTCA	42220
Qy	8440	CACATCAACCAACCGCGCACCTCATGCAAAACCATGTCGCGGATCTCACCCTCA	8499
Db	42219	CACATCAACCAACCGCGCACCTCATGCAAAACCATGTCGCGGATCTCACCCTCA	42160
Qy	8500	GCGTTCACCTCCGCGCACCAACCAACCATGTCGCGGATCTCACCCTCA	8559
Db	42159	GCGTTCACCTCCGCGCACCAACCAACCATGTCGCGGATCTCACCCTCA	42100
Qy	8560	CTGACCTTACCAACCGCGCACCAACCAACCATGTCGCGGATCTCACCCTCA	8619
Db	42099	CTGACCTTACCAACCGCGCACCAACCAACCATGTCGCGGATCTCACCCTCA	42040
Qy	8620	CTCACCCCGCGCACCAACCAACCATGTCGCGGATCTCACCCTCA	8679
Db	42039	CTCACCCCGCGCACCAACCAACCATGTCGCGGATCTCACCCTCA	41980
Qy	8680	CAAAACCTTCACCAACCGCGGTACCACTATGCAATCGGACCGCGGACCAACCGCTC	8739
Db	41979	CAAAACCTTCACCAACCGCGGTACCACTATGCAATCGGACCGCGGACCAACCGCTC	41920
Qy	8740	ACCAACCTTCACCAACCGCGGTACCACTATGCAATCGGACCGCGGACCAACCGCTC	8799
Db	41919	ACCAACCTTCACCAACCGCGGTACCACTATGCAATCGGACCGCGGACCAACCGCTC	41860
Qy	8800	CCCCACCAACCGCGGTACCACTATGCAATCGGACCGCGGACCAACCGCTC	8859
Db	41859	CCCCACCAACCGCGGTACCACTATGCAATCGGACCGCGGACCAACCGCTC	41800
Qy	8860	CACCCCAACCAACCGCGGTACCACTATGCAATCGGACCGCGGACCAACCGCTC	8919
Db	41799	CACCCCAACCAACCGCGGTACCACTATGCAATCGGACCGCGGACCAACCGCTC	41740
Qy	8920	CCGACCTTACCGGTACCAACCGGTACCTGCTGCAAGGACCAACCGGTGCGGTC	8979
Db	41739	CCGACCTTACCGGTACCAACCGGTACCTGCTGCAAGGACCAACCGGTGCGGTC	41680
Qy	8980	AACGCTGTCAGCAGCGCGGTACCGCGGTACCGCGGTACCGCGGTACCGCGGTAC	9039
Db	41679	AACGCTGTCAGCAGCGCGGTACCGCGGTACCGCGGTACCGCGGTACCGCGGTAC	41620
Qy	9040	CTGCGGACTGAGCGGTGAGCGGTCTTTCGAGGGGCGGTGCTTTCGAGGTGCGGTC	9099
Db	41619	CTGCGGACTGAGCGGTGAGCGGTCTTTCGAGGGGCGGTGCTTTCGAGGTGCGGTC	41560
Qy	9100	CTGCGTACCATGCGGTGCGGCGCGGTGCTGCTGCGGCGCGGTGCTGCTGCGGAC	9159
Db	41559	CTGCGGCGGTGAGCGGTGCTGCTGCGGCGCGGTGCTGCTGCGGAC	41500



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Db 48093 GACATCTCTGCGCGGGAACGCGGGGATGCGGTGTGGAGCGGGCGATGTGGTCCAGCCT 48034  
Qy 3343 GTGCTGTTACGCTCATGCTCTTTGCTGCTCTGTCGCGCTTCTACGGTATCGAACCC 3402  
Db 48033 GTGCTGTTACGCTCATGCTCTTTGCTGCTCTGTCGCGCTTCTACGGTATCGAACCC 47974  
Qy 3403 GACCGGTCTTTGGCCATTTCCAGGGCGAGATCGCGCGCGGCATGTGTGTGGGGCGCTG 3462  
Db 47973 GACCGGTCTTTGGCCATTTCCAGGGCGAGATCGCGCGCGGCATGTGTGTGGGGCGCTG 47914  
Qy 3463 AGCTGAAGAGACGCGCGGAGAGCTTTGCGCTGCGACCGGGCGCTGCGCGCTGTGCGG 3522  
Db 47913 AGCTGAAGAGACGCGCGGAGAGCTTTGCGCTGCGACCGGGCGCTGCGCGCTGTGCGG 47854  
Qy 3523 GCGCGGGCGGATGCGCTCAGTCCGCTGCTGCTCCAGAGAGTGGAGCAGCTCATTTGGT 3582  
Db 47853 GCGCGGGCGGATGCGCTCAGTCCGCTGCTGCTCCAGAGAGTGGAGCAGCTCATTTGGT 47794  
Qy 3583 GAGCGGTGGGGGGCGGTGTGGGTGGCGCGGTCAAAGCGCCCGCTCCACCGCGCTC 3642  
Db 47793 GAGCGGTGGGGGGCGGTGTGGGTGGCGCGGTCAAAGCGCCCGCTCCACCGCGCTC 47734  
Qy 3643 TCGGGGATGCGAGGCGGCTGAGAGAGTGTGGCTGCTGCGCGGCGACCGGGGTGCGG 3702  
Db 47733 TCGGGGATGCGAGGCGGCTGAGAGAGTGTGGCTGCTGCGCGGCGACCGGGGTGCGG 47674  
Qy 3703 GCCCGGCGATCCCGGTGACATATGCTCGCACTGCGCCCGCATGTGCAAGCCCTCGGGAG 3762  
Db 47673 GCCCGGCGATCCCGGTGACATATGCTCGCACTGCGCCCGCATGTGCAAGCCCTCGGGAG 47614  
Qy 3763 GAGTGTCTGGAGCTCTCGGGGACATAGCGCGGCGCTCGCGCTCGCGCTCTTTCTCC 3822  
Db 47613 GAGTGTCTGGAGCTCTCGGGGACATAGCGCGGCGCTCGCGCTCGCGCTCTTTCTCC 47554  
Qy 3823 ACGGTGAGGGGACCTGCTGCTGAGACCAACAACTGTGAGCGCGCTACTGTGACGCAAC 3882  
Db 47553 ACGGTGAGGGGACCTGCTGCTGAGACCAACAACTGTGAGCGCGCTACTGTGACGCAAC 47494  
Qy 3883 CTGACACGCGCTCGCTTTCAGCGATCGCTTTCAGGCGCTCGGGGATGAGCGACACCGC 3942  
Db 47493 CTGACACGCGCTCGCTTTCAGCGATCGCTTTCAGGCGCTCGGGGATGAGCGACACCGC 47434  
Qy 3943 GTCTTGTGTAAGTCAAGCCCGCCACCCCTCGTCCCGCATCGAAGACACCAACCGAA 4002  
Db 47433 GTCTTGTGTAAGTCAAGCCCGCCACCCCTCGTCCCGCATCGAAGACACCAACCGAA 47374  
Qy 4003 GACACGCGGAGAGCTCACCGGATCGGAGCTTCGCGCGGGGAGCAACGACACCGCG 4062  
Db 47373 GACACGCGGAGAGCTCACCGGATCGGAGCTTCGCGCGGGGAGCAACGACACCGCG 47314  
Qy 4063 CGCTTCTCACCGCGCTCGCCACACCATACCAACCGCATCGGCGACACCAACCGCTGG 4122  
Db 47313 CGCTTCTCACCGCGCTCGCCACACCATACCAACCGCATCGGCGACACCAACCGCTGG 47254  
Qy 4123 CACCACTACTACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCGC 4182  
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Qy	12745	CGGTGCAAGCGCTTTTCGCGCGCGGACGCGACCGGCTGCTCGAGGGTGTGGGGATG	12804
Db	26476	CGGTGCAAGCGCTATTTCGCGCGCTGCTGACGATACCGGCTGGCCGAGGGTGTGGGGATG	26535
Qy	12805	CTGCTGGTGGAGCGGCTCTCCGACGCCCGCCGCAACGGTCAACGCTGCTTGCGCGTCTGTC	12864
Db	26536	CTGCTGGTGGAGCGGCTCTCCGACGCCCGCTCGCAACCGGTCAACGCTGCTTGCGCGTCTG	26595
Qy	12865	CGCGGACGCCGTCAACGAGGACGGCGACGACGCGCTGACCGCACCCGACCGAAGCGTCTG	12924
Db	26596	CGTGGCAGTGCGGTCAACGAGACGGTGGAGCAACGGTCTGACCGCGCCCAACGGGCC	26655
Qy	12925	TCACAAGTCAAGTCACTCCGCGCAGGCTTTGGCCAAACGACACCTCTCCCTTCGCCATGTC	12984
Db	26656	TCCAGCAGCGTGTATCTCGTCAAGCCCTGGCCCAATGCGGGACTGACCCCGGCCGATGTC	26715
Qy	12985	GATGCGGTGAGGCCCAACCGGCAACGGGGACCACTCTGGGGGACCCGATCGAGGCTCAAGCC	13044
Db	26716	GAGCGAGTGGAGGGCCACGGCACCGGGACCACTCTGGGGGACCCGATCGAGGCCCAAGCA	26775
Qy	13045	CTGCTCGAAGCCTACCGTTCAGAGACCGCCCAACGGCGCGCCCTCTGGCTCGGAACCTCTC	13104
Db	26776	CTCTGCGCCCTACGGAACACCGCCGCCCACTACCGCCCTTGTGGCTGGGATCCCTC	26835
Qy	13105	AAGTCCAACATCGGGCACTTCATGCGCGCTGCGGGTGTGGGGGGTGCATCAAGATGTTG	13164
Db	26836	AAATCCAACATCGGGCACGACAGGCGCGCGGGCGTGGGCGGAGTCATCAAGATGTTG	26895
Qy	13165	ATGGCTCGGGAAATGTTCTGTCGCGGAGCTTGCAATGTGGATGAGCCGTGCGCGGAT	13224
Db	26896	ATGGCTCGGGCAACCGGGCTGTGCCACAGACCTTCCAGTGGACGAGGCCCAACCCCCAG	26955
Qy	13225	GTGGAATGTTGCCGCGGTGCGGTGCACTGCTGACGGGAGACGGTGCCTTCGGCGCGG--	13282
Db	26956	GTGCACTGGTCCACAGGCGAGTACAACCTCTTGACACACACCGTGCCTTCGGCGCGGAC	27015
Qy	13283	-GGGAGGGCGGCTACGGCGGGCAGAGTGTTCATATTCGGCGGTTCAGCGGCAACGACGCC	13341
Db	27016	CCGGCGGGCGGCGCACCGCACCGCGCGTGTATCATATTCGGCGGTTCAGGGCAACGACGCC	27075



Db	20962	GCCTGTGAGGGTTGCGTCCGGTGAGTGTCTGATGGCGCTTTGCGGGGGTGTGACGGTG	21021	Oy	7915	ATCTGCTCCGACAGGGACCCCAACGCGCCGGCATGGCCCAACGGCCTTACCAACACCCAC	7974
Oy	6862	ATGTCGTCTCCGGGTGCCTTCTGTGAGTTTTCGGCGAGCGGGTCTCGCGCGGACGGG	6921	Db	22099	ATCTGCTCCGACAGGGACCCCAACGCGCCGGCATGGCCCAACGGCCTTACCAACACCCAC	22158
Db	21022	ATGTCGTCTCCGGGTGCCTTCTGTGAGTTTTCGGCGAGCGGGTCTCGCGCGGACGGG	21081	Oy	7975	CCGCTTTCCGCGCGCGCATCAACGACATCTGCAACCATCTGACACCCGCCACTTCGACAC	8034
Oy	6922	CATTGCAAGGGTTCTTCGGCGCGCGCGACCGGACCGGCTGGGGTGGGGATG	6981	Db	22159	CCGCTTTCCGCGCGCGCATCAACGACATCTGCAACCATCTGACACCCGCCACTTCGACAC	22218
Db	21082	CATTGCAAGGGTTCTTCGGCGCGCGCGACCGGACCGGCTGGGGTGGGGATG	21141	Oy	8035	CCCTCTCTCCCTCTCTACCCCAAAACGACAAAGACAA-----CGAGGAC	8079
Oy	6982	CTGCTGTGGAGCGGCTCTCCGACGCCCTATCGCAACGGTCAACCGTCTCTGGCGGTG	7041	Db	22219	CCCTCTCTCTCTCTCTACCCAGGACCCCAACACCCAGGACACCAACCCCTCGAAGAA	22278
Db	21142	CTGCTGTGGAGCGGCTCTCCGACGCCCTATCGCAACGGTCAACCGTCTCTGGCGGTG	21201	Oy	8080	GGCGCGCGACTGTCTCCAGCAGACCCCGCTAGCGCCGAGCCCGCCCTCTTCGCGCTTCAGGTC	8139
Oy	7042	CGTGCACTGGCGTCAACAGGACCGGTGCGAGCAACGGTCTGACCGCGCCCAACGGGCGG	7101	Db	22279	GGCGCGCGACTGTCTCCAGCAGACCCCGCTAGCGCCGAGCCCGCCCTCTTCGCGCTTCAGGTC	22338
Db	21202	CGTGCACTGGCGTCAACAGGACCGGTGCGAGCAACGGGTGACCGCGCCCAACGGGCGC	21261	Oy	8140	GGCTCTCACCGCTCTCTACCGAGCGGTACACATACACCCGCCACTACTAGCGCGGACAC	8199
Oy	7102	TCCAGCAGCGTGTATCCGACAGCCCTTCGCCAAGCGCGGTGTCTGGCGCGGTGATGTC	7161	Db	22339	GGCTCTCACCGCTCTCTACCGAGCGGTACACATACACCCGCCACTACTAGCGCGGACAC	22398
Db	21262	TCCAGCAGCGTGTATCCGACAGCCCTTCGCCAAGCGCGGTGTCTGGCGCGGTGATGTC	21321	Oy	8200	TCCCTCGCGGAAATCACGCGCGCCACCTCATGCAAAACCATGTCGCCCGCGGACCATGACCA	8259
Oy	7162	GACCGGTGGAGGCCCAACCGGACCGGACCACTTTGGCGGACCCGATCGAGGCCAGGCC	7221	Db	22399	TCCCTCGCGGAAATCACGCGCGCCACCTCATGCAAAACCATGTCGCCCGCGGACCATGACCA	22458
Db	21322	GATCGGTGGAGGCCCAACCGGACCGGACCACTTTGGCGGACCCGATCGAGGCCAGGCC	21381	Oy	8260	ACCTCTATCAACCAACGCGCGCACCTCATGCAAAACCATGTCGCCCGCGGACCATGACCA	8319
Oy	7222	CTCTCGCGACCTACGCGACGACCGTGC CGCGGAGGGCGCTGTGGCTCGGTG	7281	Db	22459	ACCTCTATCAACCAACGCGCGCACCTCATGCAAAACCATGTCGCCCGCGGACCATGACCA	22518
Db	21382	CTCTCGCGACCTACGCGGAGGACCGTGC CGCGGAGGGCGCTGTGGCTCGGTG	21441	Oy	8320	CTCACACACCCCGCCACCATACCCACCATGTCGCCCGCGGACGAAAGAGACTCGCC	8379
Oy	7282	AAGTCAATGTGGTACACAGAGCTGCCCGGGCGTGC CGGGGTTGATCAAGATGTG	7341	Db	22519	CTCACACACCCCGCCACCATACCCACCATGTCGCCCGCGGACGAAAGAGACTCGCC	22578
Db	21442	AAGTCAATGTGGTACACAGAGCTGCCCGGGCGTGC CGGGGTTGATCAAGATGTG	21501	Oy	8380	ATGCGCGCATCAACACCCCGCCACCTCTGTCATACGCGGACCCCGCCACCGCTCCAA	8439
Oy	7342	ATGGCGCTCGGCATGGTCTGCTCGCGGAGCTTGTCATGTGGATGAGCGCTGCGCGCAT	7401	Db	22579	ATGCGCGCATCAACACCCCGCCACCTCTGTCATACGCGGACCCCGCCACCGCTCCAA	22638
Db	21502	ATGGCGCTCGGCATGGTCTGCTCGCGGAGCTTGTCATGTGGATGAGCGCTGCGCGCAT	21561	Oy	8440	CACATCAACACCCCTCTGCGCAACAAAGGATCAAAACCAAAACCCCTCCCGCCACCAAC	8499
Oy	7402	GTGACTGTGCGGGTGGGTGAGTGTGCTGACGAGAGCGGTGCCCTGGCGCGCGGG	7461	Db	22639	CACATCAACACCCCTCTGCGCAACAAAGGATCAAAACCAAAACCCCTCCCGCCACCAAC	22698
Db	21562	GTGACTGTGCGGGTGGGTGAGTGTGCTGACGAGAGCGGTGCCCTGGCGCGCGGG	21621	Oy	8500	GCCTTTCACCTCCCGCCACACCAACCCCATCTCTCAACAACTTCACAGCAGCAGCAACCA	8559
Oy	7462	GAGGGCGGTACCGCGGGCAGGAGTGTATCATTTCCGCGTACGCGGACCAACGCCAC	7521	Db	22699	GCCTTTCACCTCCCGCCACACCAACCCCATCTCTCAACAACTTCACAGCAGCAGCAACCA	22758
Db	21622	GAGGGCGGTACCGCGGGCAGGAGTGTATCATTTCCGCGTACGCGGACCAACGCCAC	21681	Oy	8560	CTACCTTACCAACCAACCCCGCCACCTCTATACCGCGCAACCCCGCCACCGCAACCTC	8619
Oy	7522	GTATCTCTCGAAGAG-----GACCGCGGACGACGTT	7554	Db	22759	CTACCTTACCAACCAACCCCGCCACCTCTATACCGCGCAACCCCGCCACCGCAACCTC	22818
Db	21682	GTATCTCTCGAAGAGACCCCGCCACCAACATCCCGTCAAGACACACCCCGCGACGCTT	21741	Oy	8620	CTACACCCCGCTACTTGGACCCCAACAGCCCGCAACACCGTTCGACTAGCGCCACCAAC	8679
Oy	7555	CCGGGGGACACACCCCGCGGAGGGTGAACGGGGCAGCAGATGAGGCTGCTGCGCGC	7614	Db	22819	CTACACCCCGCTACTTGGACCCCAACAGCCCGCAACACCGTTCGACTAGCGCCACCAAC	22878
Db	21742	CCGGGGGACACACCCCGCGGAG--GATGCGGTAGTGGGAGGAGGCTGCTGCGCGC	21798	Oy	8680	CAAAACCTTCACCAACAGGGGTACCACTTACATCGAACTTCGGAGCGGACCAACACCTC	8739
Oy	7615	AGTCTGGGGTGTGCGCGTGTGTGTGCGCAAGTGCAGCGCGCGCTTCGCGCGCGAG	7674	Db	22879	CAAAACCTTCACCAACAGGGGTACCACTTACATCGAACTTCGGAGCGGACCAACACCTC	22938
Db	21799	AGTCTGGGGTGTGCGCGTGTGTGTGCGCAAGTGCAGCGCGCGCTTCGCGCGCGAG	21858	Oy	8740	ACCACTTACCAACCAACCTCCCAACCCCGCCACCGCCACCGCTTACCGCTTACCGCAC	8799
Oy	7675	GCCAGGCGCTGCAGCGCCACTTACAGACCAACCCCGCGCTTCGACTTCGCGATGCGGA	7734	Db	22939	ACCACTTACCAACCAACCTCCCAACCCCGCCACCGCCACCGCTTACCGCTTACCGCAC	22998
Db	21859	GCCAGGCGCTGCAGCGCCACTTACAGACCAACCCCGCGCTTCGACTTCGCGATGCGGA	21918	Oy	8800	CCCCCACCACCCCGCCCAACCTCTCTACCAACCTTCGCGCAAAACCCACCAACCTCTGG	8859
Oy	7735	TACACCTTCGCGCGCGCGCTGTGTGACACCAACCGCGCACCGCTTATGCGCGCGGAC	7794	Db	22999	CCCCCACCACCCCGCCCAACCTCTCTACCAACCTTCGCGCAAAACCCACCAACCTCTGG	23058
Db	21919	TACACCTTCGCGCGCGCGCTGTGTGACACCAACCGCGCACCGCTTATGCGCGCGGAC	21978	Oy	8860	QACCCCAACCACTACACCCACGAGCAACCAACCCCGCCACCGCCACCGCTTACCGCTC	8919
Oy	7795	CGCGACAAGTCTTCTCAAGCACTCAGGACCTTCGCGGAGGCGAGCCCGCCCGCGTC	7854	Db	23059	CACCCCAACCACTACACCCACGAGCAACCAACCCCGCCACCGCCACCGCTTACCGCTC	23118
Db	21979	CGCGACAAGTCTTCTCAAGCACTCAGGACCTTCGCGGAGGCGAGCCCGCCCGCGTC	22038	Oy	8920	CCCACTTACCGCTTTCGAGACCACTTCTGCTCGAAAGCACACAGCGCGGTCGCGC	8979
Oy	7855	ATCCACAGCGCCCGCGGAGCCCGGACCGGAGCCCGGAGGCGGAGGAGCAAGACCGCATTC	7914	Db	23119	CCCACTTACCGCTTTCGAGACCACTTCTGCTCGAAAGCACACAGCGCGGTCGCGC	23178
Db	22039	ATCCACAGCGCCCGCGGAGCCCGGAGCCCGGAGGCGGAGGCGGAGGAGCAAGACCGCATTC	22098				



Db 16585 CGGTTGACACGGGTGTCGCGCGGGTGGTGACCGGGGGGTGTCGTCCTTGGTGTTC 16644  
Qy 3163 GACAGGGTGGGACGTGGGCGGGGATGGGTGGCGCTGCTGCGCTCTCTCCGGGTTC 3222  
Db 16645 GACAGGGTGGGACGTGGGCGGGGATGGGTGGCGCTGCTGCGCTCTCTCCGGGTTC 16704  
Qy 3223 GCCCGCGGATGACAGCGGTGCGAGAGGCTCTGGCGCGGTGGGTGGACTGGTGTGGTG 3282  
Db 16705 GCCCGCGGATGACAGCGGTGCGAGAGGCTCTGGCGCGGTGGGTGGACTGGTGTGGTG 16764  
Qy 3283 GACATCTGCGCGCGGACCGGGGATGGGTGGGTGGAGCGGCGCGATGGTTCAGGCT 3342  
Db 16765 GACATCTGCGCGCGGACCGGGGATGGGTGGGTGGAGCGGCGCGATGGTTCAGGCT 16824  
Qy 3343 GTGCTGTTGAGGTCATGGTGTCTTGGTGTCTGCTGGCGGTCTACGGGTATCGAACCC 3402  
Db 16825 GTGCTGTTGAGGTCATGGTGTCTTGGTGTCTGCTGGCGGTCTACGGGTATCGAACCC 16884  
Qy 3403 GACCGGTCCTTGGCCATTCACAGGCGAGATCGCGCGCGCATGTGTGGGCGCTG 3462  
Db 16885 GACCGGTCCTTGGCCATTCACAGGCGAGATCGCGCGCGCATGTGTGGGCGCTG 16944  
Qy 3463 AGCTGAAGAGCGCGGAGAGCTGTGGCTGCGCGAGCGGCGCTGCGCTGTGCGG 3522  
Db 16945 AGCTGAAGAGCGCGGAGAGCTGTGGCTGCGCGAGCGGCGCTGCGCTGTGCGG 17004  
Qy 3523 GSCCGGCGGATGCGCTCAGTGGCGCTGCTGCGCGCGAGGAGTGGAGCTCAATTGGT 3582  
Db 17005 GSCCGGCGGATGCGCTCAGTGGCGCTGCTGCGCGCGAGGAGTGGAGCTCAATTGGT 17064  
Qy 3583 GACCGGTGGCGGGCGGTGTGGGTGGCGCGGTCAACGGGCGCGCTCACCGCGCTC 3642  
Db 17065 GACCGGTGGCGGGCGGTGTGGGTGGCGCGGTCAACGGGCGCGCTCACCGCGCTC 17124  
Qy 3643 TCGGGGATCGCGAGCGGTGACAGAGTGTGGGTGCTGCGCGGACCGGGTGGG 3702  
Db 17125 TCGGGGATCGCGAGCGGTGACAGAGTGTGGGTGCTGCGCGGACCGGGTGGG 17184  
Qy 3703 GCCCGGCGATCCCGTGCAGTATGCTGCGCACTGCCCGCATGTGAGCGGCGCGGAG 3762  
Db 17185 GCCCGGCGATCCCGTGCAGTATGCTGCGCACTGCCCGCATGTGAGCGGCGCGGAG 17244  
Qy 3763 GAGTGTCTGGAGTCTCTGGGAGCATAGCCCGCAGCGCTCGCGGTGCCGTTCCTCC 3822  
Db 17245 GAGTGTCTGGAGTCTCTGGGAGCATAGCCCGCAGCGCTCGCGGTGCCGTTCCTCC 17304  
Qy 3823 ACGGTGGAGGACCTTGGCTGACACACCAACCTCTGGAGCGCGCTACTGTACCGAAC 3882  
Db 17305 ACGGTGGAGGACCTTGGCTGACACACCAACCTCTGGAGCGCGCTACTGTACCGAAC 17364  
Qy 3883 CTGCACGACCGGTCCGTTTACCGATGCGGTCCAGGCGCTCGCGGATGACGACACCGC 3942  
Db 17365 CTGCACGACCGGTCCGTTTACCGATGCGGTCCAGGCGCTCGCGGATGACGACACCGC 17424  
Qy 3943 GTCTTCTGTAAGTCAAGCCCCACCCACCTCTGTCGCGCATCGAAGACACCCGAA 4002  
Db 17425 GTCTTCTGTAAGTCAAGCCCCACCCACCTCTGTCGCGCATCGAAGACACCCGAA 17484  
Qy 4003 GACACCGCGAAGAGTCAACCGGATCGGAGCTCTCGCGCGGCGAACAAGACACCGC 4062  
Db 17485 GACACCGCGAAGAGTCAACCGGATCGGAGCTCTCGCGCGGCGAACAAGACACCGC 17544  
Qy 4063 CGCTTCTCACCGCTCGGCCACACCCATACACCGGATCGGACACCCACACCTGG 4122  
Db 17545 CGCTTCTCACCGCTCGGCCACACCCATACACCGGATCGGACACCCACACCTGG 17604  
Qy 4123 CACCACTACACCCACACCAACCCACCCACCCACCGATCGACCTCGACCTGCC 4182  
Db 17605 CACCACTACACCCACACCAACCCACCCACCCACCGATCGACCTCGACCTGCC 17661  
Qy 4183 ACTTACCTTCAACACAGGACTACTGGCTGGA----- 4217  
Db 17662 ACTTATCCCTTCAACAGGAGACTACTGGCTCGAGCTTCCACCGGAGAGGTGACGCTC 17721

Qy 4218 ----- 4217  
Db 17722 GCCGCTCTGGCTTGGAGCGCGGACACCCCTCTGCTCGCGGCAACAGTCCAACTCGCA 17781  
Qy 4218 -----GAGCTCACAGCCG----- 4230  
Db 17782 GACACGACGCTGCTTACTGACGGGTGCGCTGTCTCTTGGCTCGCATCCGCTGGCTGGGC 17841  
Qy 4231 ----- 4230  
Db 17842 GATTACGAGTGGGGGTGCGGCTCTCTCTGCGGGTCTGGGTTCGTGGAGCTGGCGGTC 17901  
Qy 4231 ----- 4230  
Db 17902 CAGGTTGGCGAACGCGTGGGCTGCACCCGAATCGAGCAACTCACTGTGATGCGCCGCTG 17961  
Qy 4231 --GGTGGCGGATCCGGTTCGGGTGCGCGGTTCGGGTGCGCGGTTCGGGGGGGCGAG 4288  
Db 17962 GTGTTCTCTGTTGGGTGGGGGTGTGAGTGTGAGGTTGGGGTTCGGCTGCGGATGGGGAG 18021  
Qy 4289 GGACTGCG-----G 4297  
Db 18022 GGGCGGCTTGTGTGATGTGTATGCGCGGGGTGGAGTGTCTGTGTGGGGTGGTGGC 18081  
Qy 4298 CCGGGACGCGAGGTTGAGTGTGCGCGGTCTCTGGGACGC----- 4334  
Db 18082 TCGGTTGGGTGTGAGAGTGTGATGCTCGCGGGGTGCTGTGAGGCTGTCTGTGGTGGT 18141  
Qy 4335 ----- 4334  
Db 18142 GGTGTGTGTGATGTGTGCGCGGGGTGTGGCGCGGGGTGCGGTGGCGTGGAT 18201  
Qy 4335 ----- 4334  
Db 18202 GTGATGGTGTCTGTGACCGTTTGGCTGGGCTGTGTGTGGGGCGCGGTGTTTCG 18261  
Qy 4335 -----GGTGGCCCGCCAGGAC 4350  
Db 18262 GGGCTGCTGCGGTGTGCGGTGTGAGGGGGAATTGTGTGGCTGAGGTGTGTCTCCGAG 18321  
Qy 4351 CTGGAACGGTTCGCGACACACTGCGCGTGGCCCCCTCGCGGCGCTGGACACCGTGGTG 4410  
Db 18322 GAGCGTGGGTGTGTCGGGTGTGTTGGGTGATCGCGGTGCTGGATGGTGTGGTC 18381  
Qy 4411 CCCCACTCTCCG----- 4423  
Db 18382 CAGCGTTGTGCGGTGTGCTTCCGGGTGGAGCGGGGTGGGGAGGGGGCGGGTTCGGG 18441  
Qy 4424 -----CCTGGCAGCGCCACCAACAGCACCAAGCCCGCATCAACACCTTGACCTACCA 4475  
Db 18442 GAGGTTGTTCGGGTGCGCGGTGTGTGGGTGTGTGTGCTTACCGGGGGGTGTGACC 18501  
Qy 4476 GGAACCTGGAACCCCTCACCTCCCAACCCACCAACCCACCAACCCCTGGCTCAT 4535  
Db 18502 GGTGTGGGTGTGCTGTGGGTGTAGGGCGGGCGCGGGGTGAGGGGTGTGGTC 18561  
Qy 4536 CGCCATCCCCGAACCCAGACCCACCCACCCACATCACCAACATCTCAACCACTTCCA 4595  
Db 18562 GTGTGCGGGATGAGGCGGGTGTGCGGGTGGCTGTGATCTGTGATGTTGGGCT 18621  
Qy 4596 CCACGAGGATCACCCCTCACCCCTCAACCCACCAACCCACCAACCCCTTGTAT 18681  
Db 18622 GTGATATGGTGTGCTGTGCTGTGCTGTGCTGTGCGGGGGCGGGGTTCGTGTAT 18681  
Qy 4656 CCTCCACACACCTCTCACACACAC-----GACAAAGCCCAAAACAC 4701  
Db 18682 CCGGTGAGTGGGTGAGGTGGGTCTGTGCGGTGTGTGGGCGAGGGGTGGCGTGGCAG 18741  
Qy 4702 ACACCGGAGCCATCAGCGGCTGTCTCCCTCTCGCCCTCGACGAAACCCACCCGCC 4761  
Db 18742 GAGGACGTGGGTGAGAGCGGTGGTGGGCTGTGCGGGGGTGGTGGTTCGGGTGGCCG 18801





Db 9044 CCTACCCCTTCCAAACACCACTACTGGCTGAAAGCACACAGACCCCGGTGCGGCAACG 9103  
Qy 9894 TGTACAGACGGGACTCGACCCACCCGAAACACCCCTACTCTGGGCGCCACATTGGAACTGG 9043  
Db 9104 TGTACAGACGGGACTCGACCCACCCGAAACACCCCTACTCTGGGCGCCACATTGGAACTGG 9163  
Qy 9044 CGACTGACGGGTGGAGCGCTTCTTTCAGGGCGCTTGTCTTTGAGGTGCGATCCGTGGCTGG 9103  
Db 9164 CGACTGACGGGTGGAGCGCTTCTTTCAGGGCGCTTGTCTTTGAGGTGCGATCCGTGGCTGG 9223  
Qy 9104 CTGACCATGCGGTGCGGCGGACCGGTGCTGCTGTCGGGCGCCACCTTCTCGAATCGGCC 9163  
Db 9224 CTGACCATGCGGTGCGGCGGACCGGTGCTGCTGTCGGGCGCCACCTTCTCGAATCGGCC 9283  
Qy 9164 TTTCATGCGGGCACATACGTTGGGCTCCGACCGAGTGGATGAGCTGACGCTGATGCGCCG 9223  
Db 9284 TTTCATGCGGGCACATACGTTGGGCTCCGACCGAGTGGATGAGCTGACGCTGATGCGCCG 9343  
Qy 9224 TGGTGGTTCTGTGGATGGGGGTGAGTGTGCAGGTTGGGTTGCGGCTCGGATGGGG 9283  
Db 9344 TGGTGGTTCTGTGGATGGGGGTGAGTGTGCAGGTTGGGTTGCGGCTCGGATGGGA 9403  
Qy 9284 AGGGCGGCGCTTGGTGAAGTGTATGCGCGGGGTGGAGTGCCTTGTGCTGGGGTGGTG 9343  
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Qy 9404 GTGTGGTGGTGGATGGTTCGCGGGGTGTGCGCGCGCGGGTGCCTGCGGTGGATG 9463  
Db 9524 GTGTGGTGGTGGATGGTTCGCGGGGTGTGCGCGCGCGGGTGCCTGCGGTGGATG 9583  
Qy 9464 TCGATGCTGCTCGTACCGCTTGGCTGGGCTGGTGTGTTTGGGCGCGGTGTTTCGG 9523  
Db 9584 TCGATGCTGCTCGTACCGCTTGGCTGGGCTGGTGTGTTTGGGCGCGGTGTTTCGG 9643  
Qy 9524 GCTCCGCTGGGTGGCTGTGATGGGGGGGATTTGCTGGCTGAGGTGTCTGCCGAGG 9583  
Db 9644 GCTCCGCTGGGTGGCTGTGATGGGGGGGATTTGCTGGCTGAGGTGTCTGCCGAGG 9703  
Qy 9584 AGGCGTGGGTGATGCGGCTGGTTTTGGGCTGCATCCGCGCTGCTGAGTGGTGGTCC 9643  
Db 9704 AGGCGTGGGTGATGCGGCTGGTTTTGGGCTGCATCCGCGCTGCTGAGTGGTGGTCC 9763  
Qy 9644 AGCGCTGTGCTGCTTCCGGTGGGACCGGGTGTGGGAGGGGCGGGGTTCCGGG 9703  
Db 9764 AGCGCTGTGCTGCTTCCGGTGGGACCGGGTGTGGGAGGGGCGGGGTTCCGGG 9823  
Qy 9704 AGGGTGTTCGGGTGCGGCTGTGCGGGTGTGCTGCTTACCGGCGGGTGTGACCG 9763  
Db 9824 AGGGTGTTCGGGTGCGGCTGTGCGGGTGTGCTGCTTACCGGCGGGTGTGACCG 9883  
Qy 9764 GTGTCCGGTGCCTGTGTCGGCTGTGCGGCGGGCGCGGCGCTGAGCGGCTGCTGGTCCG 9823  
Db 9884 GTGTCCGGTGCCTGTGTCGGCTGTGCGGCGGGCGCGGCGCTGAGCGGCTGCTGGTCCG 9943  
Qy 9824 TGGTCCGGGATGAGCGGGTGTCCGGTGGGCTGCGGTGCACTGCTTGAATGGGCGCTG 9883  
Db 9944 TGGTCCGGGATGAGCGGGTGTCCGGTGGGCTGCGGTGCACTGCTTGAATGGGCGCTG 10003  
Qy 9884 TGGATATCGGTGAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9943  
Db 10004 TGGATATCGGTGAGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10063  
Qy 9944 CGGTGAGTGGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10003  
Db 10064 CGGTGAGTGGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10123  
Qy 10004 AGGACGTGGGTGAGAGCGGTGTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10063  
Db 10124 AGGACGTGGGTGAGAGCGGTGTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10183

Qy 10064 ATGCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 10123  
Db 10184 ATGCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 10243  
Qy 10124 GTGGGGTGTGGGTGCTGCTGCAAGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGT 10183  
Db 10244 GTGGGGTGTGGGTGCTGCTGCAAGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGT 10303  
Qy 10184 TGGTGGTGTGACCCCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10243  
Db 10304 TGGTGGTGTGACCCCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10363  
Qy 10244 TGGTGGTGTGACCCCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10303  
Db 10364 TGGTGGTGTGACCCCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10423  
Qy 10304 TCCTTCCTGACCTTCGACACCGACACCGGACCGGACCTTCGACACCGGACCTTCGACACCGGAC 10363  
Db 10424 TCCTTCCTGACCTTCGACACCGACACCGGACCGGACCTTCGACACCGGACCTTCGACACCGGAC 10483  
Qy 10364 GGGGCGTGGATGGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10423  
Db 10484 GGGGCGTGGATGGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10543  
Qy 10424 TGCGTGGGGAGCGGTTGCTGCGCGCGCACCGCTGAAACCGACTTTCGAGTTCATTCGCGTTCATTC 10483  
Db 10544 TGCGTGGGGAGCGGTTGCTGCGCGCGCACCGCTGAAACCGACTTTCGAGTTCATTCGCGTTCATTC 10603  
Qy 10484 CAGCCAGCGGTCGCTGCAACAGAGCCCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGG 10543  
Db 10604 CAGCCAGCGGTCGCTGCAACAGAGCCCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGG 10663  
Qy 10544 GTGGCGTCCCTGCTCGCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGT 10603  
Db 10664 GTGGCGTCCCTGCTCGCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGT 10723  
Qy 10604 CCGGTGGGTGCGTGTGCTGCAAGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10663  
Db 10724 CCGGTGGGTGCGTGTGCTGCAAGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10783  
Qy 10664 ATCTGGTGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10723  
Db 10784 ATCTGGTGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10843  
Qy 10724 CTCCGGTGGGAGGGTCTCGGGCGGAGCTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10783  
Db 10844 CTCCGGTGGGAGGGTCTCGGGCGGAGCTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10900  
Qy 10784 TTGGCTGTGATGTGGGGAGCGCGGAGGTGGGTCCCGGCGGCTGCGGAGGGTGTTCCTGCGG 10842  
Db 10901 TTGGCTGTGATGTGGGGAGCGCGGAGGTGGGTCCCGGCGGCTGCGGAGGGTGTTCCTGCGG 10960  
Qy 10843 GGGTGTCCGTGACG--GGTGTGCTGATGCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGG 10900  
Db 10961 GGGTGTCCGTGACG--GGTGTGCTGATGCGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGG 11020  
Qy 10901 CCTCTCTCAGCCCGAGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 10960  
Db 11021 CCTCTCTCAGCCCGAGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGGGGTGTGG 11080  
Qy 10961 TGCTGGAT 10968  
Db 11081 ACCTCGAT 11088

RESULT 5

E38021

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

E38021 31422 bp DNA linear PAT 31-JAN-2002  
Avermectin aglycon synthase gene.

E38021

E38021.1 GI:18626910

JP 2000245457-A/2.

QY	6765	CACGGCTTGTTCCTCGTTCGTTGGTGGCTTTCGATCTGGCCCTGTCAAGCGTTGCGTTCGGG	6824
DB	6885	CACGGCTTGTTCCTCGTTCGTTGGTGGCTTTCGATCTGGCCCTGTCAAGCGTTGCGTTCGGG	6944
QY	6825	TGAGTGCTCGATGGCGCTTCGCGGGGTGTGACGGTGATGTCGTCGCGGTGCTTCGT	6884
DB	6945	TGAGTGCTCGATGGCGCTTCGCGGGGTGTGACGGTGATGTCGTCGCGGTGCTTCGT	7004
QY	6885	GGAGTTTTTCGGCGCAGCGGGGTCTTGGCCGCGGACGGGCATTTGCAAGGCTTCTCGCGCGC	6944
DB	7005	GGAGTTTTTCGGCGCAGCGGGGTCTTGGCCGCGGACGGGCATTTGCAAGGCTTCTCGCGCGC	7064
QY	6945	GGCGGACGGGACCGGCTGGGCTGAGGGTGTGGGATGCTGTGTGTGAGCGGCTCTCCGA	7004
DB	7065	GGCGGACGGGACCGGCTGGGCTGAGGGTGTGGGATGCTGTGTGTGAGCGGCTCTCCGA	7124
QY	7005	CGCCCATCGCAACGGTCAACGCTGTCTTGGCCGCTGGTGGCGAGTGGGTCAACACGGA	7064
DB	7125	CGCCCATCGCAACGGTCAACGCTGTCTTGGCCGCTGGTGGCGAGTGGGTCAACACGGA	7184
QY	7065	CGGTGCGAGCAACGGTCTGACCGCGGCCCAACGGGCGGTCCCGACGAGCGTGTCAATCCGCCA	7124
DB	7185	CGGTGCGAGCAACGGTCTGACCGCGGCCCAACGGGCGGTCCCGACGAGCGTGTCAATCCGCCA	7244
QY	7125	GGCCCTTCGCCAAACCGCGGCTTGTTCGGCCGCTGTGTCGACGCGGTGAGAGCCCAACGGCAC	7184
DB	7245	GGCCCTTCGCCAAACCGCGGCTTGTTCGGCCGCTGTGTCGACGCGGTGAGAGCCCAACGGCAC	7304
QY	7185	CGGCACACATTTGGGCGACCGATCGAGGCCCGAGGCCCTCTCTCGGACCTTACGGACAGGA	7244
DB	7305	CGGCACACATTTGGGCGACCGATCGAGGCCCGAGGCCCTCTCTCGGACCTTACGGACAGGA	7364
QY	7245	CCGTGCGCGGACGAGGGCGCGCTGTGGCTTGGGCTCGGTCAAGTCCAATGTCGGTCAACACA	7304
DB	7365	CCGTGCGCGGACGAGGGCGCGCTGTGGCTTGGGCTCGGTCAAGTCCAATGTCGGTCAACACA	7424
QY	7305	GGTGCCGCGGCGCTCGCCGGGTGTATCAAGATGGTGTGATGGCGCTGCGGATGGTCTGTCT	7364
DB	7425	GGTGCCGCGGCGCTCGCCGGGTGTATCAAGATGGTGTGATGGCGCTGCGGATGGTCTGTCT	7484
QY	7365	GC CGCGGACGTTGATGTGATGATGACCGTTCGCCCGCATGTGAGACTGCTTCGCGGTGCGGT	7424
DB	7485	GC CGCGGACGTTGATGTGATGATGACCGTTCGCCCGCATGTGAGACTGCTTCGCGGTGCGGT	7544
QY	7425	GCAGCTGCTGACGGAGACGGTGCCTTGCCCGCGGGGAGGGCGGCTACGGCGGGGCGG	7484
DB	7545	GCAGCTGCTGACGGAGACGGTGCCTTGCCCGCGGGGAGGGCGGCTACGGCGGGGCGG	7604
QY	7485	AGTGTCATCATTTGGCGCTGACGGCACCAACGCCACGTATCTCTGAAAGAACGCCCGC	7544
DB	7605	AGTGTCATCATTTGGCGCTGACGGCACCAACGCCACGTATCTCTGAAAGAACGCCCGC	7664
QY	7545	CGACGACGTTCCGGGGGGAACAACCGCGGGGAGGGTGAACGGGCGACGACGATGAGGC	7604
DB	7665	CGACGACGTTCCGGGGGGAACAACCGCGGGGAGGGTGAACGGGCGACGACGATGAGGC	7724
QY	7605	TGCTGCGCGGACGTCCTCGGGGTGTGGCGTGTGGCTCGGCCCAAGTTCGAGCGCGGCCCT	7664
DB	7725	TGCTGCGCGGACGTCCTCGGGGTGTGGCGTGTGGCTCGGCCCAAGTTCGAGCGCGGCCCT	7784
QY	7665	GC CGCGCCGAGCCGAGGCCCTTGACGCGCCACCTCACCGACACCCCGGCCCTCGACCTCGC	7724
DB	7785	GC CGCGCCGAGCCGAGGCCCTTGACGCGCCACCTCACCGACACCCCGGCCCTCGACCTCGC	7844
QY	7725	GGATGTCGGATACACCTTCGCCACGCGCGCGCGGTGTTGGAACAACCGCGCCACCTCAT	7784
DB	7845	GGATGTCGGATACACCTTCGCCACGCGCGCGCGGTGTTGGAACAACCGCGCCACCTCAT	7904
QY	7785	CGCCGCGGACCGGACACGTTCTCTGCAAGCACTTCCAGGCACTCGCCGAGGCGAGCCCA	7844
DB	7905	CGCCGCGGACCGGACACGTTCTCTGCAAGCACTTCCAGGCACTCGCCGAGGCGAGCCCA	7964
QY	7845	CCCGCGCTCATCCACAGCAGCGCCCGCGGGGACCGGGACCGGGGAGGCCCGACGAAA	7904

Db	7965	 CCCCCGCGTTCATCCACAGCAGCGCCCGGGCGGGACCGGGAGCGCGCAGAGAAA	8024
Qy	7905	GACCGCATTCATCTGCTCGGACAGAGGCAACCCAAACGCCCGGCATCGCCACAGGCGCTCTA	7964
Db	8025	GACCGCATTCATCTGCTCGGACAGGAGCACCCAAACGCCCGGCATCGCCACAGGCGCTCTA	8084
Qy	7965	CCACACCCACCCCGTCTTTGCGCCGCGCACTCAACAGCATCTGCACCCACTCGACCCCCA	8024
Db	8085	CCACACCCACCCCGTCTTTGCGCGCGCACTCAACAGCATCTGCACCCACTCGACCCCCA	8144
Qy	8025	CCTCGACCAACCCCGTCTTCCCTCTCTACCCAAAAGCAACAGAGAGAGCGCGC	8084
Db	8145	CCTCGACCAACCCCGTCTTCCCTCTCTACCCAAAAGCAACAGAGAGAGCGCGC	8204
Qy	8085	CGCACTGCTCCAGCAGACCGCTACGCCGAGCGCGCTCTTCGCTTCACAGTGCCTCT	8144
Db	8205	CGCACTGCTCCAGCAGACCGCTACGCCGAGCGCGCTCTTCGCTTCACAGTGCCTCT	8264
Qy	8145	CCACCGGCTCCTCAACCGACGGCTACCACTACACCCCGCACTACTAGCGCGACACTCCCT	8204
Db	8265	CCACCGGCTCCTCAACCGAGGCTACCACTACACCCCGCACTACTAGCGCGACACTCCCT	8324
Qy	8205	GGCGGAAATCACCGCGCGCACTCGCGCGCACTCTCACCCCTCACGAGCCACCACTCT	8264
Db	8325	GGCGGAAATCACCGCGCGCGCACTCGCGCGCACTCTCACCCCTCACGAGCCACCACTCT	8384
Qy	8265	CATCACCCACGCGCGCACCTCATGCAAAACCATGCCCCCGGCAACCATGACCACTCTCA	8324
Db	8385	CATCACCCACGCGCGCACCTCATGCAAAACCATGCCCCCGGCAACCATGACCACTCTCA	8444
Qy	8325	CACACCCCCCACCATCACCCACCACTCACCGCGCCACGAAAGACACTCGCATCGC	8384
Db	8445	CACACCCCCCACCATCACCCACCACTCACCGCGCCACGAAAGACACTCGCATCGC	8504
Qy	8385	GGCCATCAACACCCCACTCTCCTGCTCATGAGGSCACCCCGCCACACGTCGTCACACAT	8444
Db	8505	GGCCATCAACACCCCACTCTCCTGCTCATGAGGSCACCCCGCCACACGTCGTCACACAT	8564
Qy	8445	CACACCGCTCTGCCAACACAGGCAATCAAAACCAAAACCTCTCCGACCAACAGCCTTT	8504
Db	8565	CACACCGCTCTGCCAACACAGGCAATCAAAACCAAAACCTCTCCGACCAACAGCCTTT	8624
Qy	8505	CCACTCCCCCAACACAAACCCCATCTCAACCAACTCCACAGCAGACACCCAAACCTCAC	8564
Db	8625	CCACTCCCCCAACACAAACCCCATCTCAACCAACTCCACAGCAGACACCCAAACCTCAC	8684
Qy	8565	CTACCAACCAACCCCAACACCCCTCATACCGCCCAACACCCCAACCGACCAACTCCTCAC	8624
Db	8685	CTACCAACCAACCCCAACACCCCTCATACCGCCCAACACCCCAACCGACCAACTCCTCAC	8744
Qy	8625	CCCCCACTACTGGAACCAACAGCGCGGAGACACGCTGACTAGGCAACACACCCCAAC	8684
Db	8745	CCCCCACTACTGGAACCAACAGCGCGGAAACACCGCTGACTAGGCAACACACCCCAAC	8804
Qy	8685	CTTCACCAACAGCGGCTCACCACCTACATCGAACTCGGACCGGACACACCTCACCAC	8744
Db	8805	CTTCACCAACAGCGGCTCACCACCTACATCGAACTCGGACCGGACACACCTCACCAC	8864
Qy	8745	CCTCACCCACCAACACTCCCCCAACCCCGCCACCACTCTCACCTCTCACCCACCCCA	8804
Db	8865	CCTCACCCACCAACACTCCCCCAACCCCGCCACCACTCTCACCTCTCACCCACCCCA	8924
Qy	8805	CGACGACCGCGAAAACCACTCTTACGAACTCGCGCAAAACCAACCACTTGGAACCC	8864
Db	8925	CGACGACCGCGAAAACCACTCTTACGAACTCGCGCAAAACCAACCACTTGGAACCC	8984
Qy	8865	CCACCACTACCCACCAAG - ACAACCAACCCCAACCCCAACCACTCTGACCTCCCA	8923
Db	8985	GCACCACTACCCACCAAGCAACCAACCCCAACCACTCTGACCTCTCCCA - CTTGACCTCTCCCA	9043
Qy	8924	CCTTACCCCTTCAACACCACTACTTGCTCGAAAGCACAGCGCCCGTGCAGCAACG	8983

Db	4665	AACCCAGACCACACACCCCCACATCAACCAATCTTCAACCAACCTTCAACATCAAGGAT	4724
Qy	4608	CACCCCATCCCTCTCAACCTCAACACACACACCAACCCCAACACCTTCAACACAC	4667
Db	4725	CACCCCATCCCTCTCAACCTCAACACACACACCAACCCCAACACCTTCAACACAC	4784
Qy	4668	CCTCACACACACCCGACAAAGCCCAAAACACACACACCGAGCCATCAACCGCTGCT	4727
Db	4785	CCTTCAACACACCGACAAAGCCCAAAACACACACACCGAGCCATCAACCGCTGCT	4844
Qy	4728	CTCCCTCTCCCTCTCAACGAAACACACCCACCCCGACACACCCACACACCGGAC	4787
Db	4845	CTCCCTCTCCCTCTCAACGAAACACACCCACCCCGACACACCCACACACCGGAC	4904
Qy	4788	CCTCTCAACCTCAACCTCAACCAACACACCAACCAACCAACCAACCAACCAACCAAC	4847
Db	4905	CCTCTCAACCTCAACCTCAACCAACACACCAACCAACCAACCAACCAACCAACCAAC	4964
Qy	4848	GTACGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	4907
Db	4965	GTACGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	5024
Qy	4908	AGCCCAACCTGGGACTCGCCGACACACCTCTCGAACAACCGACCGACCGGCGG	4967
Db	5025	AGCCCAACCTGGGACTCGCCGACACACCTCTCGAACAACCGACCGACCGGCGG	5084
Qy	4968	AATCATGACCTCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCT	5027
Db	5085	AATCATGACCTCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCT	5144
Qy	5028	CACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	5087
Db	5145	CACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	5204
Qy	5088	CCTACCCCAACCAACCTTACCCCAACCAACCAACCAACCAACCAACCAACCAAC	5147
Db	5205	CCTACCCCAACCAACCTTACCCCAACCAACCAACCAACCAACCAACCAACCAAC	5264
Qy	5148	CACCTCATACCGCGGAACCGGCGCTCGCAACCAACCAACCAACCAACCAACCAAC	5207
Db	5265	CACCTCATACCGCGGAACCGGCGCTCGCAACCAACCAACCAACCAACCAACCAAC	5324
Qy	5208	CCACCAACCAACCAACCTTCTTCAACGAGCGAAACCGGCGCCCAACCAACCAAC	5267
Db	5325	CCACCAACCAACCAACCTTCTTCAACGAGCGAAACCGGCGCCCAACCAACCAAC	5384
Qy	5268	ACAACACCTACACCAACCTTCAACCAACCAACCAACCAACCAACCAACCAACCT	5327
Db	5385	ACAACACCTACACCAACCTTCAACCAACCAACCAACCAACCAACCAACCAACCT	5444
Qy	5328	CACCAACCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTTCAAC	5384
Db	5445	CACCAACCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTTCAAC	5504
Qy	5385	CCTCACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAAC	5444
Db	5505	GGTCAACCACTTCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAAC	5564
Qy	5445	CCCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAAC	5504
Db	5565	CCCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAAC	5624
Qy	5505	ACTACCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTTCAAC	5564
Db	5625	ACTACCAACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTTCAAC	5684
Qy	5565	CGGCGCACCCGCGCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTT	5624
Db	5685	CGGCGCACCCGCGCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTT	5744
Qy	5625	CCACCGCACACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTT	5684
Db	5745	CCACCGCACACCAACCTTCAACCAACCTTCAACCAACCTTCAACCAACCTT	5804

Qy	5685	CGACCTCGCTGATTCGACAAAGCCCGCGCATATCTCGACCGCGCGGGTTTGACCCAT	5744
Db	5805	CGACCTCGCTGATTCGACAAAGCCCGCGCATATCTCGACCGCGCGGGTTTGACCCAT	5864
Qy	5745	GTACCCGAGTTGGCCACCGGACAGCGGTACGAGGCGATCGCGGACACCGAAAGCGCGTA	5804
Db	5865	GTACCCGAGTTGGCCACCGGACAGCGGTACGAGGCGATCGCGGACACCGAAAGCGCGTA	5924
Qy	5805	TGTGCTCATCGCCGACATCGACTGGAGCAAGATCGAACACACCTCTCAGACGAGCACT	5864
Db	5925	TGTGCTCATCGCCGACATCGACTGGAGCAAGATCGAACACACCTCTCAGACGAGCACT	5984
Qy	5865	GGTGAGCGCGCCCGGAAAGGAGCGAGCTGTCCAGCGGCCCACTCCACCGCGCGAGTT	5924
Db	5985	GGTGAGCGCGCCCGGAAAGGAGCGAGCTGTCCAGCGGCCCACTCCACCGCGCGAGTT	6044
Qy	5925	GCACAAACCGCTGGCCCATCAGAGCTCGGCGGACCAAGCGGCGCGCATTTGCTCGAGCTCGT	5984
Db	6045	GCACAAACCGCTGGCCCATCAGAGCTCGGCGGACCAAGCGGCGCGCATTTGCTCGAGCTCGT	6104
Qy	5985	ACGAGACCATGTGGCGGAGTGTCCGCGACCGGACCCGAAAGCCATTCGGCGCCGACCA	6044
Db	6105	ACGAGACCATGTGGCGGAGTGTCCGCGACCGGACCCGAAAGCCATTCGGCGCCGACCA	6164
Qy	6045	GTGCTTCCGTGCACTCGGCTTCGATTCATCTCAGCGGCGTTCGAGTTCCGAAACCTTGCTGAT	6104
Db	6165	GTGCTTCCGTGCACTCGGCTTCGATTCATCTCAGCGGCGTTCGAGTTCCGAAACCTTGCTGAT	6224
Qy	6105	CAAGGCAACAGGACTCGGCTTCGATTCATCTCAGCGGCGTTCGAGTTCCGAAACCTTGCTGAT	6164
Db	6225	CAAGGCAACAGGACTCGGCTTCGATTCATCTCAGCGGCGTTCGAGTTCCGAAACCTTGCTGAT	6284
Qy	6165	ACTCGCGTACACTCGGACCAACCTTCGCGGCGGACAGCAGCGAGTTCGCTCTCAGC	6224
Db	6285	ACTCGCGTACACTCGGACCAACCTTCGCGGCGGACAGCAGCGAGTTCGCTCTCAGC	6344
Qy	6225	GGCAGCGTTTACCGCCGAGGCTTCTGTACCGAGCGCATCGCCATCGTTGCGCTGGCTG	6284
Db	6345	GGCAGCGTTTACCGCCGAGGCTTCTGTACCGAGCGCATCGCCATCGTTGCGCTGGCTG	6404
Qy	6285	TGCTTCCCGCGGAGTACCTCGGCGGAGGACTTCTGGGATCTGATCTCTCTCGAGCA	6344
Db	6405	TGCTTCCCGCGGAGTACCTCGGCGGAGGACTTCTGGGATCTGATCTCTCTCGAGCA	6464
Qy	6345	GGACCGCATCGGCGGATTTCCCAACCGCGCTGGGACCTGGACAGCTCTACGACCC	6404
Db	6465	GGACCGCATCGGCGGATTTCCCAACCGCGCTGGGACCTGGACAGCTCTACGACCC	6524
Qy	6405	CGACCCCGACACCCCGGACCTGCTACACCCGAAACCGGCGGATTCCTCTACGACGAGG	6464
Db	6525	CGACCCCGACACCCCGGACCTGCTACACCCGAAACCGGCGGATTCCTCTACGACGAGG	6584
Qy	6465	CCACTTCGACCGCAATTTCTTGGGATCAGCCCGCGGAGGCGCTCGGATTCGACCCCA	6524
Db	6585	CCACTTCGACCGCAATTTCTTGGGATCAGCCCGCGGAGGCGCTCGGATTCGACCCCA	6644
Qy	6525	GCACGACTCTCTCGAAACCGCTCGGAAACCATCGAACACCGCGGATTCACACCCCA	6584
Db	6645	GCACGACTCTCTCGAAACCGCTCGGAAACCATCGAACACCGCGGATTCACACCCCA	6704
Qy	6585	CACCTTCGACGAGACCCCGGAGTCTTCAACCGGACCAACCGGACGAGTACGCACT	6644
Db	6705	CACCTTCGACGAGACCCCGGAGTCTTCAACCGGACCAACCGGACGAGTACGCACT	6764
Qy	6645	TGCGGTGCAACACCGGCGGAGTCAACGATGTTTTCGACTGACCGGAAACCGCGGAG	6704
Db	6765	TGCGGTGCAACACCGGCGGAGTCAACGATGTTTTCGACTGACCGGAAACCGCGGAG	6824
Qy	6705	CGTACCTCGGTCGATCTCGTACGATTTGTTTGGGGTCTCGGTCGCTGGA	6764
Db	6825	CGTACCTCGGTCGATCTCGTACGATTTGTTTGGGGTCTCGGTCGCTGGA	6884

QY 2451 TGGCTGGGGTCTCTGAAGTCCAACTCGGGGCACCATGGTGC CGCGGGGTGTGGGTGGG 2520  
Db 2572 TGGCTGGGGTCTCTGAAGTCCAACTCGGGGCACCATGGTGC CGCGGGGTGTGGGTGGG 2631  
QY 2521 GTCAATCAAGATGGTATCGCGTTCGGGAGGGGGTTCGCCGCAAGCTTCGATGTGGAT 2580  
Db 2632 GTCAATCAAGATGGTATCGCGTTCGGGAGGGGGTTCGCCGCAAGCTTCGATGTAGAT 2691  
QY 2581 AAGCGCTCGCGCAGGTGGAATCGCTCCGCGGGGGCGGTCCGCTCTCAACGAGGCGGTG 2640  
Db 2692 GAGCGCTCGCGCAGGGG---CTGGCGCGGGGGCGGTCCGCTCTCAACGAGGCGGTG 2748  
QY 2641 CCGTGGCCCGGGGACCGCGCAAGGCGGTTCGGCGGGCGGGAGTGTCTGTTCGGGATC 2700  
Db 2749 CCGTGGCCCGGGGACCGCGCAAGGCGGTTCGGCGGGCGGGAGTTCGTCTCGGTTCGGGATC 2808  
QY 2701 GGCGGCAGGAATCGCATGTGATTTTGGAGAGGCGCGGGGGGGGGGGGGGGGGTGTTC 2760  
Db 2809 GGCGGCAGGAATCGCATGTGATTTTGGAGAGGCGCGGGGGGGGGGGGGGGGGTGTTC 2868  
QY 2761 GGGGGTGGGGGTGTGGAGGGGTCTCCGGGTCTTGCCATTTCCGTGGCTGAGTCCGGTGCC 2820  
Db 2869 GGGGGTGGGGGTGTGGAGGGGTCTCTGGTCTTGCCATTTCCGTGGCTGAGTCCGGTGCC 2928  
QY 2821 GCTCCAGTGGTGTGTCTGCGCCGGTGTCTGAGTGGTTCGGTTCGGTTCGGTTCGGTTCGG 2880  
Db 2929 GCTCCAGTGGTGTGTCTGCGCCGGTGTCTGAGTGGTTCGGTTCGGTTCGGTTCGGTTCGG 2988  
QY 2881 GTTCTGTGCGGTGTCCGTAGTCTGAGCTGGGTTCGGGCGCAGCGCGGAGCGGTG 2940  
Db 2989 GTTCTGTGCGGTGTCCGTAGTCTGAACTGGGTTCGGGCGCAGCGCGGAGCGGTG 3048  
QY 2941 CGTCAGTACGTGGCAGTCCCGCGGACGTTTCGCTTTCGGTTCGGTTCGGTTCGGTTCGG 3000  
Db 3049 CGTCAGTACGAGCAGTCCAGCGGACGTTTCGCTTTCGGTTCGGTTCGGTTCGGTTCGG 3108  
QY 3001 TGTGGGGGGGTGTCTGAGCATGTGCGGTGTCTGCTGGCGC----- 3044  
Db 3109 TGTAGGCGAGGTGTCTGAGCATCATGTGTCTATCTCTGCGCGCTGCACCGACTCTCTCA 3168  
QY 3045 -----GGACGTGAGGAGCTGTGTCA----- 3065  
Db 3169 CGGTCCGCGGCGAGACACCGCAGAGCTCCAGCACAGCGCCGCCACAGGCGCAGACCC 3228  
QY 3066 -----AGGGTGGGGCGCTGCGCGGGGTGAGCGGATCGCGGGTG 3108  
Db 3229 GCACCCACATCGGCAGGCGAATGGGGCGCTGGCGCGGGTAGCGGATCGCGGGCGCTG 3288  
QY 3109 ACCACGGGTCAATCGCGCGGGTGGTGAACCGGGCGGTGTCTGTTTCCCGGACAG 3168  
Db 3289 ACCACGGGTCAATCGCGCGGGTGGTGAACCGGGCGGTGTCTGTTTCCCGGACAG 3348  
QY 3169 GGTGGGCAGTGGCGGGGATGGGTGTGCTGTCTGCTGCTCTCCGCTCTCTCCGCGG 3228  
Db 3349 GGTGGGCAGTGGCGGGGATGGGTGTGCTGTCTGCTGCTCTCCGCTCTCTCCGCGG 3408  
QY 3229 CGGATGACAGGCGTGCAGGAGGCTCTGGCGCGGTGGGTGAGTGTCTGTGGTGCACATC 3288  
Db 3409 CGGATGACAGGCGTGCAGGAGGCTCTGGCGCGGTGGGTGAGTGTCTGTGGTGCACATC 3468  
QY 3289 CTGCGCGGGACGCGGGGATGCGGTGTGGAGCGGGCGGATGTGGTCCAGCTGTGCTG 3348  
Db 3469 CTGCGCGGGACGCGGGGATGCGAGTGTGGAGCAGGCGCGGATGTAGTCCAGCTGTACTG 3528  
QY 3349 TTCAAGCTCATGTGTCTTTGGCTGTCTGTGGGTTCCTACGGTATCGAATCCGACGCG 3408  
Db 3529 TTCAAGCTCATGTGTCTTTAGCTGTCTTTGGGGTTCTTACGGTATCGAATCCGACGAG 3588  
QY 3409 GTCTTGGCCATTCCAGGGGAGATCGCGCGCGCATGTGTGGGGCGCTCAGCGCTG 3468  
Db 3589 GTCTTGGCCATTCCAGGACGAGATCGCGCGCGCATATATATATATATATATATATAT 3648  
QY 3469 AAGGACGCGGCGAAGACTGTTGCGCTGCGAGCGCGGGCGTGGCGGTGTGCGGGGCGG 3528

Db 3649 AAGGACGCGGCGAAGACTGTTGCGCTC----- 3675  
QY 3529 GGGCGCATGGGCTCAGTGCCTCAGTGCCTGCCAGAGAGTGGAGCAGCTCATTTGGTGAAGCGG 3588  
Db 3676 -----CCTCCCGAGAGGTGGAGCAGCTCATTTGGTGAAGC--- 3709  
QY 3589 TGGCGGGGGCGGTGTGGGTGGCGCGGTCAACGGCCCCCGCTCCACCGCGCTCTTCGGGG 3648  
Db 3710 -GTGGCGGGCGGTGTGGGTGGCTCGCGTCAACGGCCCCCGCTCCACCGCGCTCTTCGGGG 3768  
QY 3649 GATGCCAGGCGGTGGAGAGGTGTGGCTGTCTGTGTCGGCACCGGGGTGCGGGCCCGG 3708  
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QY 3709 CGGATCCCGGTTCGACTATGCTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 3768  
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QY 3769 CTGAGCTGTCTGGGGGACATCAGCCCGCAGCGGTCCGGCGTTCGGTCTTCTTCTCACCGGTG 3828  
Db 3886 CTGAGCTGTCTGGGGGACATCAGCCCGCAGCGGTACGGCGTTCGGTCTTCTTCTCACCGGTG 3945  
QY 3829 GAGGGCACCTGGCTGGACACCAAACTTGAACCGCGCTTACTGTACTCGCAACTGTGCAC 3888  
Db 3946 GAGGGCACCTGGCTGGACACCAAACTTGAACCGCGCTTACTGTACTCGCAACTGTGCAC 4005  
QY 3889 CAGCCGGTCCGTTCAGCGATGCGTTCAGGCGCTTCAGGCGTTCAGGCGTTCAGGCGTTCAGG 3948  
Db 4006 CAGCCGGTTCAGCGATGCGTTCAGGCGCTTCAGGCGTTCAGGCGTTCAGGCGTTCAGG 4065  
QY 3949 GTCAAGTCAAGCCCCCACCACCTCTGCTCCCGCCATCGAAGACACACACCGAAGACACC 4008  
Db 4066 CTAGAAGTCAAGCCCCCACCACCTCTGCTCCCGCCATCGAAGACACACCGAAGACACC 4125  
QY 4009 G-CCGAAGAGTCAACCGCATTCGGAGCTTCGGCGCGGCGCAACAGACACCCCGCGTT 4067  
Db 4126 GCCGAAGAGTCACTCGCATCGGAGCTTCGGCGCGGCGGAGAAAGACACACCGCTTCTT 4185  
QY 4068 CCTCACCGCTTCGCCACACCCATACACGGGATCGGACACCGACACCGACCTTGGCACCA 4127  
Db 4186 CCTCAGCGCTTTAGCTAGACCCCATATACCGGATCGGCGAGACCCACCGTGGCACCA 4245  
QY 4128 CCATACACCCACACACACCCACCCACCGCCACACCGACCTCGACCTCGCCACCTA 4187  
Db 4246 CTACTAGACCCACACACACCTACCCCGCCATCGAAGACCTTGCACCTTGCACCT- 4304  
QY 4188 CCCCTTCCAAACACAGCACTACTGGTTCGAGAGTCAACAGCGGTGCGCGATCCGGTTC 4247  
Db 4305 CCCCTTCCAAACACAGCACTACTGGTTCGAGAGTCAACAGCGGTGCGCGATCCGGTTC 4364  
QY 4248 GGGTCCGGTCCGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGG 4307  
Db 4365 GGGTCCGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGG 4424  
QY 4308 AGAGTGGAGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGG 4367  
Db 4425 AGAGTGGAGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGG 4484  
QY 4368 CACACTCGCGTCCCGCTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGG 4427  
Db 4485 CACACTCGCGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGG 4544  
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## RESULT 4

AF275943

LOCUS

DEFINITION

Streptomyces avermitilis avermectin polyketide synthase gene,

partial cds.

ACCESSION

AF275943

VERSION

AF275943.1

KEYWORDS

SOURCE

ORGANISM

Streptomyces avermitilis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 11096)

Hong, Y.-S. and Lee, J.J.

Targeted Gene Disruption of the avermectin O-methyltransferase gene

and polyketide synthase gene from Streptomyces avermitilis

Unpublished

2 (bases 1 to 11096)

Hong, Y.-S. and Lee, J.J.

Direct Submission

Submitted (07-JUN-2000) Anticancer Agent Research Laboratory, Korea

Research Institute of Bioscience and Biotechnology, P.O. Box 116,

Yusong-Gu, Taejeon 305-600, South Korea

Location/Qualifiers

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Qy	10081	GCTGGCGTGGCGGTGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	10140	Qy	11161	ACCGGGACCTGGCGGGACCGACACCGCGGCGATCATCCGTTCGGTCTGTCATCCCATG	11220
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Qy	10141	GTGAGGGGTGGTGGGGCTGAGACGGTTCGGGGTTCGGGGTTCGGGGTTCGGGGTTCGG	10200	Qy	11221	TCGACCCCGAGACGATGGGGCTCTTTCGATGGGGCTTCGGCTTCGGAGCGGGCGGGTTCG	11280
				Db	12038	TCGACCCCGAGACGATGGGGCTCTTTCGATGGGGCTTCGGCTTCGGAGCGGGCGGGTTCG	12097

Qy	6901	CGGGTCTGTGGCGCGGACGGGCAATTGCAAGGGTTTCTCGGGCGCGCGGAGCGGACCGGC	6960
Db	7118	CGGGTCTGTGGCGCGGACGGGCAATTGCAAGGGTTTCTCGGGCGCGCGGAGCGGACCGGC	7777
Qy	6961	TGGGGTAGGGGTGTGGGATGCTGTGTGTGAGCGGCTCTCGAGCGCCATCTGCAACGGT	7020
Db	7778	TGGGGTAGGGGTGTGGGATGCTGTGTGTGAGCGGCTCTCGAGCGCCATCTGCAACGGT	7837
Qy	7021	CACCGTCTCTGGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	7080
Db	7838	CACCGTCTCTGGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	7897
Qy	7081	CTGACCGGCGCCAAACGGGCGGTCCGACGACGGTGTCTCCGCGCAGGCGCTCTCGCAACGCC	7140
Db	7898	CTGACCGGCGCCAAACGGGCGGTCCGACGACGGTGTCTCCGCGCAGGCGCTCTCGCAACGCC	7957
Qy	7141	GGCTGTGTGGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	7200
Db	7958	GGCTGTGTGGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	8017
Qy	7201	GACCGATCGAGGCGCGGCGCTCTCGGACCTACGACGAGGCGGTGCGGCGGAGGG	7260
Db	8018	GACCGATCGAGGCGCGGCGCTCTCGGACCTACGACGAGGCGGTGCGGCGGAGGG	8077
Qy	7261	CCGCTGTGGCTGGGCTCGGTCAAAGTCCAAATGTCTGTCACACAGGCTGCGCGGCGGCTC	7320
Db	8078	CCGCTGTGGCTGGGCTCGGTCAAAGTCCAAATGTCTGTCACACAGGCTGCGCGGCGGCTC	8137
Qy	7321	CGCGGGTGATCAAGATGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	7380
Db	8138	CGCGGGTGATCAAGATGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT	8197
Qy	7381	GTGATGAGCGGTGCGCGCANGTGACCTGCTCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT	7440
Db	8198	GTGATGAGCGGTGCGCGCANGTGACCTGCTCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT	8257
Qy	7441	ACGGTGTGGCTGGCGGGGAGGGGCGGCTTACGGCGGGGAGGAGTGTCTATCATTTGGC	7500
Db	8258	ACGGTGTGGCTGGCGGGGAGGGGCGGCTTACGGCGGGGAGGAGTGTCTATCATTTGGC	8317
Qy	7501	GTGACGGGCAACAGCCCAAGTATCTGCAAGAGCAACCGCGCGAGAGTGTTCGGGG	7560
Db	8318	GTGACGGGCAACAGCCCAAGTATCTGCAAGAGCAACCGCGCGAGAGTGTTCGGGG	8377
Qy	7561	GGACACCGCGCGGGGTGACGCGGGGAGCGGAGGAGTGTGCTGCGCGGAGTCTT	7620
Db	8378	GGACACCGCGCGGGGTGACGCGGGGAGCGGAGGAGTGTGCTGCGCGGAGTCTT	8437
Qy	7621	GGGGTGTGGCGGTGGCTGTGGGCAAGTGTGGGCGGCGGCTTGGCGCGGCGGCGGCGG	7680
Db	8438	GGGGTGTGGCGGTGGCTGTGGGCAAGTGTGGGCGGCGGCTTGGCGCGGCGGCGGCGG	8497
Qy	7681	GGCTGTGACGGCCACTTACCGACCAACCGCGGCTGTGACCTGTGGGATGTGCGATACAC	7740
Db	8498	GGCTGTGACGGCCACTTACCGACCAACCGCGGCTGTGACCTGTGGGATGTGCGATACAC	8557
Qy	7741	CTCGCCACGCGCGCGGTGTGGACACCGCGGCGGCGGCTTATGCGCGGCGGCGGCGG	7800
Db	8558	CTCGCCACGCGCGCGGTGTGGACACCGCGGCGGCGGCTTATGCGCGGCGGCGGCGG	8617
Qy	7801	ACGTTCTGTGCAAGCACTTCCAGGCACTTCCGCGAGCGGCGGCGGCGGCGGCGGCGG	7860
Db	8618	ACGTTCTGTGCAAGCACTTCCAGGCACTTCCGCGAGCGGCGGCGGCGGCGGCGGCGG	8677
Qy	7861	AGCAGCGCGCGGGGACCGGAGCGGGGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGG	7920
Db	8678	AGCAGCGCGCGGGGACCGGAGCGGGGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGG	8737
Qy	7921	TCCGAGAGGCGACCCCAACCGCGCGGATGCGCGGCGGCGGCGGCGGCGGCGGCGG	7980
Db	8738	TCCGAGAGGCGACCCCAACCGCGCGGATGCGCGGCGGCGGCGGCGGCGGCGGCGG	8797

Qy	7981	TTTCGCGCGCGCACTCAACGACATCTGACACCACTTGCACCCCGCCACTTGCACCCCGCTC	8040
Db	8798	TTTCGCGCGCGCACTCAACGACATCTGACACCACTTGCACCCCGCCACTTGCACCCCGCTC	8857
Qy	8041	CTCCCGCTCTTCAACCCAAACGACAAACGAGAGGCGGCGGCGGCGGCGGCGGCGGCGG	8100
Db	8858	CTCCCGCTCTTCAACCCAAACGACAAACGAGAGGCGGCGGCGGCGGCGGCGGCGGCGG	8917
Qy	8101	ACCGCTACGCGCGGCGGCGGCTTCTGCGCTTTCAGAGTGTGCGCTTCCACCGCTCTCTACC	8160
Db	8918	ACCGCTACGCGCGGCGGCGGCTTCTGCGCTTTCAGAGTGTGCGCTTCCACCGCTCTCTACC	8977
Qy	8161	GACGGTACCAATCAACCCCGGCTTACTACGCGGAGACCTCTCTGCGGGAATCAACCGCC	8220
Db	8978	GACGGTACCAATCAACCCCGGCTTACTACGCGGAGACCTCTCTCTGCGGGAATCAACCGCC	9037
Qy	8221	GCCACCTCGCGGAGTCTTACCGCTTACCGAGCGGACCACTCTCATCAACCGAGCGGCG	8280
Db	9038	GCCACCTCGCGGAGTCTTACCGCTTACCGAGCGGACCACTCTCATCAACCGAGCGGCG	9097
Qy	8281	ACCTCTATGAAACCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	8340
Db	9098	ACCTCTATGAAACCATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9157
Qy	8341	ATCACCCACCACTTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	8400
Db	9158	ATCACCCACCACTTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9217
Qy	8401	ACCTCTCTGTCTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	8460
Db	9218	ACCTCTCTGTCTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9277
Qy	8461	CAACAAGGATCAAAACCAAAACCTTCCCAACCAACGCGCTTCCACTCTCTCTCTCTCTCT	8520
Db	9278	CAACAAGGATCAAAACCAAAACCTTCCCAACCAACGCGCTTCCACTCTCTCTCTCTCTCT	9337
Qy	8521	AACCCCTCTCTCAACCACTTCCACGACACACCAACCTTCACTTACACCCCGGCGGCGG	8580
Db	9338	AACCCCTCTCTCAACCACTTCCACGACACACCAACCTTCACTTACACCCCGGCGGCGG	9397
Qy	8581	ACCCCTCTCTATCAGCGGCAACACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	8640
Db	9398	ACCCCTCTCTATCAGCGGCAACACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9457
Qy	8641	CAACAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	8700
Db	9458	CAACAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9517
Qy	8701	GTCAACCACTTACATCGAACTCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	8760
Db	9518	GTCAACCACTTACATCGAACTCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9577
Qy	8761	CTCCCGAACCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	8820
Db	9578	CTCCCGAACCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9637
Qy	8821	CACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	8880
Db	9638	CACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	9697
Qy	8881	CACGACCAACCAACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	8940
Db	9698	CACGACCAACCAACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9757
Qy	8941	CACCACTTCTGGTCTGAAAGCAACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9000
Db	9758	CACCACTTCTGGTCTGAAAGCAACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9817
Qy	9001	GACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9060
Db	9818	GACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	9877
Qy	9061	CTTCTTTCAGGGCGGCTTGTCTTTGAGGTCTGCTCTCTGAGGTCTGCTGAGGTCTGAGC	9120





Qy 2521 GTCAATCAAGATGGTGAATGGCGTTGCGGAGGGGGTGTTCGCCCGAGACGTTTCATGTGGAT 2580  
Db GTCAATCAAGATGGTGAATGGCGTTGCGGAGGGGGTGTTCGCCCGAGACGTTTCATGTGGAT 3397  
Qy 2581 AAGCCGTCGCCGACGAGTGGATGCTCCGCGGGGGCGGTGCGGCTGCTACAGGAGCGGTG 2640  
Db GAGCCGTGCCGCGAGTGGATGCTCCGCGGGGGCGGTGCGGCTGCTACAGGAGCGGTG 3457  
Qy 2641 CCGTGGCCGGGGAGCCGCGAGGGCGGTTCGGCGGGGGCGGAGTGTCTGCTGTTGCGGATC 2700  
Db CCGTGGCCGGGGAGCCGCGAGGGCGGTTCGGCGGGGGCGGAGTGTCTGCTGTTGCGGATC 3517  
Qy 2701 GCGGCAACGAATGCGCATGTGATTTTGAGAGGCGCGCGGGGGGGGCTGTGTTGCC 2760  
Db GCGGCAACGAATGCGCATGTGATTTTGAGAGGCGCGCGGGGGGGGCTGTGTTGCC 3577  
Qy 2761 GGGGGTGGGGTGTGGAGGGTCTCCGGGTCTTCGCATTTTCGTTGCTGAGTCCGTTGCC 2820  
Db GGGGGTGGGGTGTGGAGGGTCTCCGGGTCTTCGCATTTTCGTTGCTGAGTCCGTTGCC 3637  
Qy 2821 GCTCCAGTGGCTGTGTCGCCCGGTGCTGAGTCCGTTGCGGGTCCGTTGCCGCTGCC 2880  
Db GCTCCAGTGGCTGTGTCGCCCGGTGCTGAGTCCGTTGCGGGTCCGTTGCCGCTGCC 3697  
Qy 2881 GTTCTGTGCCGCTGTCCGGCTAGGTCTGAGGCTGCGGTTGCGGGGCGAGCGGAGCGTTG 2940  
Db GTTCTGTGCCGCTGTCCGGCTAGGTCTGAGGCTGCGGTTGCGGGGCGAGCGGAGCGTTG 3757  
Qy 2941 CGTCAGTACGTGGCAGTCCCGCGCGAAGTTCGCTTTCGCTTTCGCGATGTGGGTGCGGGTCCG 3000  
Db CGTCAGTACGTGGCAGTCCCGCGCGAAGTTCGCTTTCGCTTTCGCGATGTGGGTGCGGGTCCG 3817  
Qy 3001 TGTGGGGGGCTGTGTCGAGCATGTCGCGTCTGCTGCGCGCGGAGCCGTTGAGGAGCTG 3060  
Db TGTGGGGGGCTGTGTCGAGCATGTCGCGTCTGCTGCGCGCGGAGCCGTTGAGGAGCTG 3877  
Qy 3061 GTCAAGAGGTTGGGGGGCTCGCGCGCGGTGAGCGGATCGCGGGGTGACCAACGGGTCTAT 3120  
Db GTCAAGAGGTTGGGGGGCTCGCGCGCGGTGAGCGGATCGCGGGGTGACCAACGGGTCTAT 3937  
Qy 3121 CGCGCGGTGTGACCGGGGGCTGTGCTCTGCTGTTTCCCGACAGGTTGGGAGTGG 3180  
Db CGCGCGGTGTGACCGGGGGCTGTGCTCTGCTGTTTCCCGACAGGTTGGGAGTGG 3997  
Qy 3181 GCCGGGATGGGTGCGTCTGCTCGCTCTCTCGGGTTCGCGCGCGGATCGAGCG 3240  
Db GCCGGGATGGGTGCGTCTGCTCGCTCTCTCGGGTTCGCGCGCGGATCGAGCG 4057  
Qy 3241 TGCAGGAGGCTCGCGCGCGGTGAGCTGGTCTGTGTGGACATCTCTCGCGCGGGAC 3300  
Db TGCAGGAGGCTCGCGCGCGGTGAGCTGGTCTGTGTGGACATCTCTCGCGCGGGAC 4117  
Qy 3301 GCGGGGATGCGGTGTGGAGCGGGCGAATGTGTTCAGGCTGTGTTTTCAGGCTCATG 3360  
Db GCGGGGATGCGGTGTGGAGCGGGCGAATGTGTTCAGGCTGTGTTTTCAGGCTCATG 4177  
Qy 3361 GTGCTTTGGCTGCTGTGGCGTTCTACGGTATCGAATCCCGAGCGGTCTTGGCCAT 3420  
Db GTGCTTTGGCTGCTGTGGCGTTCTACGGTATCGAATCCCGAGCGGTCTTGGCCAT 4237  
Qy 3421 TCCAGGCGGAGATCGCGCGCGGTGATGTGTGGGGCGGTGAGCTCTGAAGGAGCGGGCG 3480  
Db TCCAGGCGGAGATCGCGCGCGGTGATGTGTGGGGCGGTGAGCTCTGAAGGAGCGGGCG 4297  
Qy 3481 AAGCTGTGCTGTGCGAGCGGGCGTGGCTGTGCGGGGCGGGGCGGATGGCC 3540  
Db AAGCTGTGCTGTGCGAGCGGGCGTGGCTGTGCGGGGCGGGGCGGATGGCC 4357  
Qy 3541 TCAGTCCGCTGCTGCGAGGAGTGGAGAGTCTATTGTTGAGCGGTGGGGGGGGCG 3600  
Db TCAGTCCGCTGCTGCGAGGAGTGGAGAGTCTATTGTTGAGCGGTGGGGGGGGCG 4417

Qy 3601 TTGTGGGTGGCGCGGTCAACCGGCCCCCGCTTCCACCGCCGCTCTCGGGGAGTGCAGAGCG 3660  
Db TTGTGGGTGGCGCGGTCAACCGGCCCCCGCTTCCACCGCCGCTCTCGGGGAGTGCAGAGCG 4477  
Qy 3661 GTGACGAGGTGTGGCGTACTGTGCGGCGACCGGGGTGCGGGCCCGCGGATCCCGGTG 3720  
Db GTGACGAGGTGTGGCGTACTGTGCGGCGACCGGGGTGCGGGCCCGCGGATCCCGGTG 4537  
Qy 3721 GACTATGCTCGCACTGCCCCCATGTGACGCCCTCGCGGAGAGAGTTCGTGGAGCTGCTG 3780  
Db GACTATGCTCGCACTGCCCCCATGTGACGCCCTCGCGGAGAGAGTTCGTGGAGCTGCTG 4597  
Qy 3781 GGGGACATCAGCCCGCAGCCGTCGCGGTCTTCTTCTCCAGCGTGGAGGCACTGTG 3840  
Db GGGGACATCAGCCCGCAGCCGTCGCGGTCTTCTTCTCCAGCGTGGAGGCACTGTG 4657  
Qy 3841 CTGGACACCAACCCCTGGAGCGGCTTACTGTGTACCGCAACTGTGACCGCGGTCCGT 3900  
Db CTGGACACCAACCCCTGGAGCGGCTTACTGTGTACCGCAACTGTGACCGCGGTCCGT 4717  
Qy 3901 TTGAGCGATGCGGTCCAGGCGCTTGGCGGATGACGAGCACCGCGTCTTCTGGAAGTCAAG 3960  
Db TTGAGCGATGCGGTCCAGGCGCTTGGCGGATGACGAGCACCGCGTCTTCTGGAAGTCAAG 4777  
Qy 3961 CCCCACCCACCTCGTCCCGCCCATCGAAGACACACCGAAGACACCGCGGAGAGCTC 4020  
Db CCCCACCCACCTCGTCCCGCCCATCGAAGACACACCGAAGACACCGCGGAGAGCTC 4837  
Qy 4021 ACCGCGATCGGAGCTTCCCGCGGGGCAACAGACACCGCGCGCTTCTTCCACCGCGCTC 4080  
Db ACCGCGATCGGAGCTTCCCGCGGGGCAACAGACACCGCGCGCTTCTTCCACCGCGCTC 4897  
Qy 4081 GCCACACCATATACCCCGCATCGGCACACCCACACCTGGCACACCACTACACCCAC 4140  
Db GCCACACCATATACCCCGCATCGGCACACCCACACCTGGCACACCACTACACCCAC 4957  
Qy 4141 CACCACACCCACCCACCCACACCGACCTCGACCTGCGCCCTTCCACAC 4200  
Db CACCACACCCACCCACCCACACCGACCTCGACCTGCGCCCTTCCACAC 5017  
Qy 4201 CAGGACTATGCGTTCGAGACTCAGACCGGGTTCGCGATTCGCGTTCGCGTTCGCGTGC 4260  
Db CAGGACTATGCGTTCGAGACTCAGACCGGGTTCGCGATTCGCGTTCGCGTTCGCGTGC 5077  
Qy 4261 GGTTCGGGTGCGGTTCGCGCGGGGAGGACTGCGGGCGGGAGCGGAGAGTGGAGTGC 4320  
Db GGTTCGGGTGCGGTTCGCGCGGGGAGGACTGCGGGCGGGAGCGGAGAGTGGAGTGC 5137  
Qy 4321 CGGTTCGGGACCGGTGGCCCGCCAGGACCTTGGAAACCGTTCGACACACTCGCGCTG 4380  
Db CGGTTCGGGACCGGTGGCCCGCCAGGACCTTGGAAACCGTTCGACACACTCGCGCTG 5197  
Qy 4381 CCCCCCTCGCGCGCTGAGACCGGTGTCGCGCATCTTCCGCTTGGCAACCGGCAACAA 4440  
Db CCCCCCTCGCGCGCTGAGACCGGTGTCGCGCATCTTCCGCTTGGCAACCGGCAACAA 5257  
Qy 4441 CAGGACCAAGCCGCTACACCTGAGCCTTACAGGAACTTGGAAACCTTCCACCTC 4500  
Db CAGGACCAAGCCGCTACACCTGAGCCTTACAGGAACTTGGAAACCTTCCACCTC 5317  
Qy 4501 CCCCACCCACCAACCCACCAACCTTGGCTCATCGCATCCCGGAAACCCAGAGCCAC 4560  
Db CCCCACCCACCAACCCACCAACCTTGGCTCATCGCATCCCGGAAACCCAGAGCCAC 5377  
Qy 4561 CACCCCAATACCAACATCTTCAACCTTCAACCAACCGGCTTCAACCGGCTTCAACCGG 4620  
Db CACCCCAATACCAACATCTTCAACCTTCAACCAACCGGCTTCAACCGGCTTCAACCGG 5437  
Qy 4621 CTACCCCTCAACCAACCCACCAACCTTCAACCTTCAACCAACCTTCAACCTTCAACCA 4680  
Db CTACCCCTCAACCAACCCACCAACCTTCAACCTTCAACCAACCTTCAACCTTCAACCA 5497  
Qy 4681 CGACAAAGCCCAACCAACCAACCGGAGCCATCACCGGCTGCTCTCTCTCTCTCTCT 4740

Db	1118	TCCCTGGCGCCCTCTGGCGCTCGCAAGGGTCGAGCGTCTGGGACACAGC	1177
Qy	361	CTGGCGAGATCGCGGACGCCAGTCTCGGGAGCCCTGCTCCCGCGACGCCGCGACGC	420
Db	1178	CTGGCGAGATCGCGGACGCCAGTCTCGGGAGCCCTGCTCCCGCGACGCCGCGACGC	1237
Qy	421	GTGGTGACGCTTTGGAGCCAGGACACAGACCACTTGGCCGGAGCCGGCGCGCTGCTCC	480
Db	1238	GTGGTGACGCTTTGGAGCCAGGACACAGACCACTTGGCCGGAGCCGGCGCGCTGCTCC	1297
Qy	481	GTGGCCGCCACGCCCGGATGAGTCTCTGCCCGAATCGCTCCGTGAGACCGAGGACAAACCCG	540
Db	1298	GTGGCCGCCACGCCCGGATGAGTCTCTGCCCGAATCGCTCCGTGAGACCGAGGACAAACCCG	1357
Qy	541	GCGGGCTCGCGCTCGAGCGCTCAACCGACCCCGGAGCACAGTCTGCTCCGCTGCCGC	600
Db	1358	GCGGGCTCGCGCTCGAGCGCTCAACCGACCCCGGAGCACAGTCTGCTCCGCTGCCGC	1417
Qy	601	GAGGCGTTCGGGACCTTGGTGGCCGACCTCACCGCGCGAGGTGCGCACGCGCATGATC	660
Db	1418	GAGGCGTTCGGGACCTTGGTGGCCGACCTCACCGCGCGAGGTGCGCACGCGCATGATC	1477
Qy	661	CGGTGAGAGTTCGCCGCCCATCTCCGCCCTGATGATAGCCCATCGAGGAACGGGTGCTCAGC	720
Db	1478	CGGTGAGAGTTCGCCGCCCATCTCCGCCCTGATGATAGCCCATCGAGGAACGGGTGCTCAGC	1537
Qy	721	GCCCTGCTGCCCATCACCCACCGCCCTCCCGCATCCCTTCCACTCTCGGTGACCGGC	780
Db	1538	GCCCTGCTGCCCATCACCCACCGCCCTCCCGCATCCCTTCCACTCTCGGTGACCGGC	1597
Qy	781	GCCGCCCTCGACACCCCGGAGTACAGCGCGGCTACTGGTACCGCAACATGTGAGACACG	840
Db	1598	GCCGCCCTCGACACCCCGGAGTACAGCGCGGCTACTGGTACCGCAACATGTGAGACACG	1657
Qy	841	GTCCGGTTCGAGCCCGCCCGCGCTGCTTCTGACAGAGGGGCCCAAGAGTTCGTTCGAG	900
Db	1658	GTCCGGTTCGAGCCCGCCCGCGCTGCTTCTGACAGAGGGGCCCAAGAGTTCGTTCGAG	1717
Qy	901	ATGAGCCCGACCCGGTCTGACCATGAGCCCTCCAGGAGCTCGCCCGGACCTGGGCGAC	960
Db	1718	ATGAGCCCGACCCGGTCTGACCATGAGCCCTCCAGGAGCTCGCCCGGACCTGGGCGAC	1777
Qy	961	ACCACCGGACCGCGACACCGTATCATGGGACGCTCGCGCGCGGACAGGACCCCTG	1020
Db	1778	ACCACCGGACCGCGACACCGTATCATGGGACGCTCGCGCGCGGACAGGACCCCTG	1837
Qy	1021	GACCACTTCGTGACGTCTCTGCCCAACTACGGGGGACATGGTGAGACGTGCGGACAC	1080
Db	1838	GACCACTTCGTGACGTCTCTGCCCAACTACGGGGGACATGGTGAGACGTGCGGACAC	1897
Qy	1081	GTCTCTCGGACGCTGACACGCGCTGTCGCCACGACGACGACGTCTGCTCTGGAC	1140
Db	1898	GTCTCTCGGACGCTGACACGCGCTGTCGCCACGACGACGACGTCTGCTCTGGAC	1957
Qy	1141	CTGGTGCGCCCCACACCATGCGGTGTGTAACGACGACGAGAAACGAGCGACCGCGTCG	1200
Db	1958	CTGGTGCGCCCCACACCATGCGGTGTGTAACGACGACGAGAAACGAGCGACCGCGTCG	2017
Qy	1201	GATGCGGCGCATCGGCGAGTTTCGCCCATCTCGCTTCGACTCCGTCAATGGGTGCGAA	1260
Db	2018	GATGCGGCGCATCGGCGAGTTTCGCCCATCTCGCTTCGACTCCGTCAATGGGTGCGAA	2077
Qy	1261	CTGGCGAACCGCTCAGCAAGGCCACGGGCTCGCGTTGCCGTGACGCTCATCTTCGAC	1320
Db	2078	CTGGCGAACCGCTCAGCAAGGCCACGGGCTCGCGTTGCCGTGACGCTCATCTTCGAC	2137
Qy	1321	CACACACCGCGCGGCTCGCGCGGCTTCGGAGACGGGCGCTCGGCGACCTCGAC	1380
Db	2138	CACACACCGCGCGGCTCGCGCGGCTTCGGAGACGGGCGCTCGGCGACCTCGAC	2197
Qy	1381	GAGGACACCGCGCGGCTCAGGACCTCACCGCGGACCGAGGACCGGCGGAC	1440

Db	2198	GAGGACACCGCGCGGCTACCGGACTCACCCAGCGGCAACGAGGACAGGAGCGGCGAC	2257
Qy	1441	GACCCGATCCCATCATCGGCATGGCATGCGCTTCCCGGGCGAGTCCGGTCCCCGAG	1500
Db	2258	GACCCGATCCCATCATCGGCATGGCATGCGCTTCCCGGGCGAGTCCGGTCCCCGAG	2317
Qy	1501	GACTGTGGAGTGGCGGCTCGGGCGGAGACGCCATCGGGCGGCTTCCCGACGACCGC	1560
Db	2318	GACTGTGGAGTGGCGGCTCGGGCGGAGACGCCATCGGGCGGCTTCCCGACGACCGC	2377
Qy	1561	GGATGGCCACGGAACAGCGTACGCCAGGACCCACAGCGCCCGGACGCTTCTATCCG	1620
Db	2378	GGATGGCCACGGAACAGCGTACGCCAGGACCCACAGCGCCCGGACGCTTCTATCCG	2437
Qy	1621	CAGGGAGCGGGTCTTTCACGACGCGGCGCATCTCGACCCCGGCTTCTTCGGAATCAGT	1680
Db	2438	CAGGGAGCGGGTCTTTCACGACGCGGCGCATCTCGACCCCGGCTTCTTCGGAATCAGT	2497
Qy	1681	CCACGTGAGGACATGGCGATGGATTCGCGACGAGCGGCTGCTGTGGAGAGCGTCTGGAG	1740
Db	2498	CCACGTGAGGACATGGCGATGGATTCGCGACGAGCGGCTGCTGTGGAGAGCGTCTGGAG	2557
Qy	1741	GCGTTCGAGCGGGCGGGAATCGATCCGCTGCTGGTACCGGGTCCCGTACGGGCGTCTTC	1800
Db	2558	GCGTTCGAGCGGGCGGGAATCGATCCGCTGCTGGTACCGGGTCCCGTACGGGCGTCTTC	2617
Qy	1801	GCGGGCGCCCTCTCTTCGACTACGGCCCGCGTATGGACACCGCGTCTCGGAGGGCGCC	1860
Db	2618	GCGGGCGCCCTCTCTTCGACTACGGCCCGCGTATGGACACCGCGTCTCGGAGGGCGCC	2677
Qy	1861	GCGBACGTGAGGGCCACATCTCACCGGTACACGGGACAGCGTCTGTGGGCGGTATC	1920
Db	2678	GCGBACGTGAGGGCCACATCTCACCGGTACACGGGACAGCGTCTGTGGGCGGTATC	2737
Qy	1921	GCCTACAGCTTCGGGCTGGAGGGCGCGCATCACCGTGACACGGGGTCTCGGACATCG	1980
Db	2738	GCCTACAGCTTCGGGCTGGAGGGCGCGCATCACCGTGACACGGGGTCTCGGACATCG	2797
Qy	1981	CTGTGACGCTGACATCTGGGCTGCGAGTCTGCGGTGAGTGACAGCTCGCGCTG	2040
Db	2798	CTGTGACGCTGACATCTGGGCTGCGAGTCTGCGGTGAGTGACAGCTCGCGCTG	2857
Qy	2041	GCGGCGGCTCTCGGTCTATGTCACCCCTCGGATGTTATCGAGTTCCTCCGCGACGCG	2100
Db	2858	GCGGCGGCTCTCGGTCTATGTCACCCCTCGGATGTTATCGAGTTCCTCCGCGACGCG	2917
Qy	2101	GCGGCTGCGGTGGACGCGAGTGCAGGCGTACTCGGCTGACCGCGGACGCGCGCTGG	2160
Db	2918	GCGGCTGCGGTGGACGCGAGTGCAGGCGTACTCGGCTGACCGCGGACGCGCGCTGG	2977
Qy	2161	GGCGAGGGCGTTCGGGATGCTGTTGGTGGAGCGGTTGTTCGGATGCGGTGCGGCGAT	2220
Db	2978	GGCGAGGGCGTTCGGGATGCTGTTGGTGGAGCGGTTGTTCGGATGCGGTGCGGCGAT	3037
Qy	2221	CGGGTGTGCGGTGTGTACCGCGCAGTTCGCGTCAACGAGACGCGTGTGTAATGGGCTG	2280
Db	3038	CGGGTGTGCGGTGTGTACCGCGCAGTTCGCGTCAACGAGACGCGTGTGTAATGGGCTG	3097
Qy	2281	ACGGCGCGAACGGTTCGGGCTCAGGAGCGGTTGATCCGGCAGCGGTTGGCGAACCGCGGG	2340
Db	3098	ACGGCGCGAACGGTTCGGGCTCAGGAGCGGTTGATCCGGCAGCGGTTGGCGAACCGCGGG	3157
Qy	2341	TTGTCCGTGCGGATGTGGATGTGGTGGAGGGGCAACGGGACGGGACGACGCTGGGTGAT	2400
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DEFINITION Sequence 1 from Patent WO0001827.  
ACCESSION AX006889  
VERSION AX006889.1 GI:9994904  
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SOURCE Streptomyces avermitilis.  
ORGANISM Streptomyces avermitilis  
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.  
REFERENCE 1 (bases 1 to 12381)  
AUTHORS Kellenberger, J.I., Leadlay, P.F., Staunton, J., Mearthur, H.A. and  
Stutzman-Engwall, K.J.  
TITLE Polyketides, their preparation, and materials for use therein  
JOURNAL Patent: WO 0001827-A 1 13-JAN-2000;  
KELLENBERGER JOHANNES LAURENZ (CH); LEADLAY PETER FRANCIS (GB);  
STAUNTON JAMES (GB); BIOTICA TECH LTD (GB); PFIZER (US); Mearthur  
HAMISH ALASTAIR IRVIN (US); STUTZMAN ENGWALL KIM JONELLE (US)  
  
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Qy 61 GCGCAGAGCGGACCGCGCGCTGCTGCTGTTTCCCGGCGAGGCGCCGATGCGCG 120  
Db 878 GCGCAGAGCGGACCGCGCGCTGCTGCTGTTTCCCGGCGAGGCGCCGATGCGCG 937  
Qy 121 GGCATGGGAGGAGAACTTCTCGACGCTTCCGAGAGCGTCCGCGAGAGCGTCCGCGCTGC 180  
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Qy 241 GACGCTCCCGGCTGACCGGCTGAGCTGCTCAGCGGACCGCTTCCGCGCTCATGATC 300  
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15161 AATCGACTGCTTGTGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15120  
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Db 11021 CTGGGACGGTGTTCGGGCGCAAGTGGATGCGCTCTTTCGTTGATGAGCTGACCGG 11080  
Qy 10981 GGTATGAGCTGTTCGGGCTGCTGCTCTCTCGGCGGGGATTCCTGGGCTCGGCC 11040  
Db 11081 GGTATGAGCTGTTCGGGCTGCTGCTCTCTCGGCGGGGATTCCTGGGCTCGGCC 11140  
Qy 11041 GGGGAGGCGCAATACGCGCGGCGCAATGCGCTCTGGAACGGCTGGGTCGCGG 11100  
Db 11141 GGGGAGGCGCAATACGCGCGGCGCAATGCGCTCTGGAACGGCTGGGTCGCGG 11200  
Qy 11101 GCGGCGGCTGTCGGGCGGCTGCGCTGCGGCTGGGGCTGGGAAGAGGCGAGCGGATG 11160  
Db 11201 GCGGCGGCTGTCGGGCGGCTGCGCTGCGGCTGGGGCTGGGAAGAGGCGAGCGGATG 11260  
Qy 11161 ACCGGGACCTTCGGCGGCGACCGACCGCGGATCATTCGGTTCGGCTGCTGCTGCCC 11220  
Db 11261 ACCGGGACCTTCGGCGGCGACCGACCGCGGATCATTCGGTTCGGCTGCTGCTGCCC 11320  
Qy 11221 TCGACCCCGGACGCACTGGGCGCTTTCGATGCGGCTGCTGCTGGAACGGCTGGTCTG 11280  
Db 11321 TCGACCCCGGACGCACTGGGCGCTTTCGATGCGGCTGCTGCTGGAACGGCTGGTCTG 11380  
Qy 11281 CTGGCGCGGACCTTCGGCGGCGGCGGCTGCGGCGGCTGCTGCTGGAAGAGGCGAGCTG 11340  
Db 11381 CTGGCGCGGACCTTCGGCGGCGGCGGCTGCGGCGGCTGCTGCTGGAAGAGGCGAGCTG 11440  
Qy 11341 GCGACCCCGGCGGCGACCGACCGGCGGCTGCGGCGGCTGCGGCGGCGGCGGCGG 11400  
Db 11441 GCGACCCCGGCGGCGGCGGCGGCGGCGGCTGCGGCGGCTGCGGCGGCGGCGGCGG 11500  
Qy 11401 CTGCAACCGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11460  
Db 11501 CTGCAACCGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11560  
Qy 11461 GTCCGCTCCACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11520  
Db 11561 GTCCGCTCCACATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11620  
Qy 11521 CGGCGGTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11580  
Db 11621 CGGCGGTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11680  
Qy 11581 TCCGCGACCGGAGCTTCGCGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11640  
Db 11681 TCCGCGACCGGAGCTTCGCGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11740  
Qy 11641 ACCCTCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11700  
Db 11741 ACCCTCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11800  
Qy 11701 GTGTTGGCGGAGCTTCGACAACTCGGCGGCTTCGCGGCGGCTTCGACAAACCGGAGCG 11760  
Db 11801 GTGTTGGCGGAGCTTCGACAACTCGGCGGCTTCGCGGCGGCTTCGACAAACCGGAGCG 11860  
Qy 11761 GCCAGCGGAGGTCACCTTCGGGCTGAGTCACTCATGTTGAGGTGGAACCGGAGCGG 11820

Db 7481 GTGGATGAGCCGTGCGCCGATGTGGAATGGTCCGGGGTGGCGATGCTGTCGAGCGAG 7540  
Qy 7441 ACGGTGCCCTGCGCGGGGAGGGGGCTTACGCGGGGACAGGAGTGTATCATTCGGC 7500  
Db 7541 ACGGTGCCCTGCGCGGGGAGGGGGCTTACGCGGGGACAGGAGTGTATCATTCGGC 7600  
Qy 7501 GTACGGGACAAAGCCCACTCATCTCTGGAAGAACACCGCCGACGACGTTCCGGGG 7560  
Db 7601 GTACGGGACAAAGCCCACTCATCTCTGGAAGAACACCGCCGACGACGTTCCGGGG 7660  
Qy 7561 GGACACCGCGGGGAGGGTGAACGGGGACGACGATGAGGCTGTCGGGAGTCTT 7620  
Db 7661 GGACACCGCGGGGAGGGTGAACGGGGACGACGATGAGGCTGTCGGGAGTCTT 7720  
Qy 7621 GGGGTGTGGCTGGCTGTGTGCGCAAGTCCAGCGCGGCGCTCGCGGCCAGGCCAG 7680  
Db 7721 GGGGTGTGGCTGGCTGTGTGCGCAAGTCCAGCGCGGCGCTCGCGGCCAGGCCAG 7780  
Qy 7681 GCCCTGACGGCCACTCAACGACACACCGGCGCTCGACCTGCGGATGTGGAATACAC 7740  
Db 7781 GCCCTGACGGCCACTCAACGACACACCGGCGCTCGACCTGCGGATGTGGAATACAC 7840  
Qy 7741 CTCGCCACGGCGCGCGCTGTGTGACACACCGCGCACCTCATCGCGCGGACCGGAC 7800  
Db 7841 CTCGCCACGGCGCGCGCTGTGTGACACACCGCGCACCTCATCGCGCGGACCGGAC 7900  
Qy 7801 ACGTTCCTGCAAGCACTCAGGCACTCGCGGAGCGGCGGCGGCGGCGGCGGCGGCG 7860  
Db 7901 ACGTTCCTGCAAGCACTCAGGCACTCGCGGAGCGGCGGCGGCGGCGGCGGCGGCG 7960  
Qy 7861 AGCAGCGCGCGGGGAGCGGAGACCGGGAGCGCGGAGGCGGAGGAGGCGGAGGCGGAG 7920  
Db 7961 AGCAGCGCGCGGGGAGCGGAGACCGGGAGCGCGGAGGCGGAGGAGGCGGAGGCGGAG 8020  
Qy 7921 TCGGAGAGGGACACCAAGCGCGCGGATGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7980  
Db 8021 TCGGAGAGGGACACCAAGCGCGCGGATGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8080  
Qy 7981 TTGCGCGCGGCACTCAAGCAATCTGCAACCACTCGACCGCGGCGGCGGCGGCGGCGG 8040  
Db 8081 TTGCGCGCGGCACTCAAGCAATCTGCAACCACTCGACCGCGGCGGCGGCGGCGGCGG 8140  
Qy 8041 CTCGCCCTCTCAACCAAAAGCAACGACGAGGAGCGGCGGCGGCGGCGGCGGCGGCGG 8100  
Db 8141 CTCGCCCTCTCAACCAAAAGCAACGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8200  
Qy 8101 ACCGCTACGCGCGGCGGCGGCTCTTGGCTTCAGGTCGCGGCGGCGGCGGCGGCGG 8160  
Db 8201 ACCGCTACGCGCGGCGGCGGCTCTTGGCTTCAGGTCGCGGCGGCGGCGGCGGCGG 8260  
Qy 8161 GACGGCTACCACTCACCGCGGCACTTACGCGGAGCACTCCCTCGGCGGAAATCACGCG 8220  
Db 8261 GACGGCTACCACTCACCGCGGCACTTACGCGGAGCACTCCCTCGGCGGAAATCACGCG 8320  
Qy 8221 GCCCACTTCGCGGCACTCAACCTTCAACGAGCGGCGGCGGCGGCGGCGGCGGCGG 8280  
Db 8321 GCCCACTTCGCGGCACTCAACCTTCAACGAGCGGCGGCGGCGGCGGCGGCGGCGG 8380  
Qy 8281 ACCCTATGCAACGATGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8340  
Db 8381 ACCCTATGCAACGATGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8440  
Qy 8341 ATCAACCACTCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8400  
Db 8441 ATCAACCACTCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8500  
Qy 8401 ACCTCCCTCTGATCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8460  
Db 8501 ACCTCCCTCTGATCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8560  
Qy 8461 CAAAGGCGATCAAAACCAACCGCTCCCGACCAACCGGCTTCCACTCCCCCGACAC 8520  
Db 8561 CAAAGGCGATCAAAACCAACCGCTCCCGACCAACCGGCTTCCACTCCCCCGACAC 8620

Qy 8521 AACCCCATCTCTAAACCACTCCACGACACACCAAAACCTTCACTACCCACCCAC 8580  
Db 8621 AACCCCATCTCTAAACCACTCCACGACACACCAAAACCTTCACTACCCACCCAC 8680  
Qy 8581 ACCCCCTCTATCAGCGGCAACACCCGACCCGACCAATCTCTTCAACCCGCTACTAGGAC 8640  
Db 8681 ACCCCCTCTATCAGCGGCAACACCCGACCCGACCAATCTCTTCAACCCGCTACTAGGAC 8740  
Qy 8641 CAAAGCGCGGCAACACCGCTGAGTACGCGACACACCAACCAACCAACCTTCAACCAACGCG 8700  
Db 8741 CAAAGCGCGGCAACACCGCTGAGTACGCGACACACCAACCAACCAACCTTCAACCAACGCG 8800  
Qy 8701 GTCAACCACTTATCTGAACCTCGGACCGGACCAACCAACCTTCAACCAACCAAC 8760  
Db 8801 GTCAACCACTTATCTGAACCTCGGACCGGACCAACCAACCTTCAACCAACCAAC 8860  
Qy 8761 CTCCCAACCCGCGGACCAACCACTCTCAACCAACCAACCAACCAACCAACCAAC 8820  
Db 8861 CTCCCAACCCGCGGACCAACCACTCTCAACCAACCAACCAACCAACCAACCAAC 8920  
Qy 8821 CACCTCTCAACCAACCTTGGGCAACCAACCAACCAACCAACCAACCAACCAACCAAC 8880  
Db 8921 CACCTCTCAACCAACCTTGGGCAACCAACCAACCAACCAACCAACCAACCAACCAAC 8980  
Qy 8881 CACGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 8940  
Db 8981 CACGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 9040  
Qy 8941 CACCACTACTGGCTGGAAGACACAGCCGGTCCCGGCAACGTTGACGAGCGGACTC 9000  
Db 9041 CACCACTACTGGCTGGAAGACACAGCCGGTCCCGGCAACGTTGACGAGCGGACTC 9100  
Qy 9001 GACCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 9060  
Db 9101 GACCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 9160  
Qy 9061 CTTCTTCAGGGCGCTTGTCTTTGAGTTCGATCCGCTGGCTGGCTGACCATGCGGCTGGC 9120  
Db 9161 CTTCTTCAGGGCGCTTGTCTTTGAGTTCGATCCGCTGGCTGGCTGACCATGCGGCTGGC 9220  
Qy 9121 GGCAAGTGTCTGTCTGGGCGGCACTTCTCTGAACTCGCCCTTCAATGCGGGGACATAC 9180  
Db 9221 GGCAAGTGTCTGTCTGGGCGGCACTTCTCTGAACTCGCCCTTCAATGCGGGGACATAC 9280  
Qy 9181 GTGGGCTGCAACCGGAGTGGATGAGCTACCGTTCATCGGCGGCTGGTTCCTGTGGAT 9240  
Db 9281 GTGGGCTGCAACCGGAGTGGATGAGCTACCGTTCATCGGCGGCTGGTTCCTGTGGAT 9340  
Qy 9241 GGGGCTGTGAGTGTGAGGTTGGGTTGGCTGGCTGGGAGGGGCGGCGGCTTGGTG 9300  
Db 9341 GGGGCTGTGAGTGTGAGGTTGGGTTGGCTGGCTGGGAGGGGCGGCGGCTTGGTG 9400  
Qy 9301 AGTGTATATCGCGGGTGGGAGTGTCTTGTGGGGGCTGGCTGGGCTGGGCTGGG 9360  
Db 9401 AGTGTATATCGCGGGTGGGAGTGTCTTGTGGGGGCTGGCTGGGCTGGGCTGGG 9460  
Qy 9361 ACGTGTATCGCTCGGGGCTGGTGGTGGGCTGGCTGGTGGTGGTGGTGGTGGTGGT 9420  
Db 9461 ACGTGTATCGCTCGGGGCTGGTGGTGGGCTGGCTGGTGGTGGTGGTGGTGGTGGT 9520  
Qy 9421 CTGCGGGGCTGTGGCGCGCGGGGCTGGCTGGGCTGGATGTCTGATGTCTCCGTGAC 9480  
Db 9521 CTGCGGGGCTGTGGCGCGCGGGGCTGGCTGGGCTGGATGTCTGATGTCTCCGTGAC 9580  
Qy 9481 CGTTTGGCTGGGCTGGTGTGTGTGTGGGGCGGCTGTGTGTGGGGCTGGCTGGGCTGG 9540  
Db 9581 CGTTTGGCTGGGCTGGTGTGTGTGTGGGGCGGCTGTGTGTGGGGCTGGCTGGGCTGG 9640  
Qy 9541 CGTGTATGGGGGATTTGCTGGCTGAGTGTGTCTGCGGAGGAGGCGTGGGCTGATGCG 9600  
Db 9641 CGTGTATGGGGGATTTGCTGGCTGAGTGTGTCTGCGGAGGAGGCGTGGGCTGATGCG 9700

Qy	5221	CAACACTCTCTCTCTCA	CAGCCGAAACGGGCCCC	CACACCCCCCA	CAGCAACACCTTCA	CC	5280
Db	5321	CAACACCTCTCTCTCTCA	CAGCCGAAACGGGCCCC	CACACCCCCCA	CCCGCCCA	CAGCAACACCTTCA	5380
Qy	5381	ACCCAACTCTCAAA	AAAAAGGATCCACT	CACACATAC	CACCTTCCGACAC	CCAGCAACCCCA	5340
Db	5381	ACCCAACTCTCAAA	AAAAAGGATCCACT	CACACATAC	CACCTTCCGACAC	CCAGCAACCCCA	5440
Qy	5341	GACCACTCTCAAA	CAACTCTCTCA	ACACCATCTCC	CCCCCA	CAACACCCCTTCA	5400
Db	5441	GACCACTCTCAAA	CAACTCTCTCA	ACACCATCTCC	CCCCCA	CAACACCCCTTCA	5500
Qy	5401	CACACCGAGGATCT	CTGACGACGCGAC	CGCTTAC	ACAACTCTAC	CCCCCA	5460
Db	5501	CACACCGAGGATCT	CTGACGACGCGAC	CGCTTAC	ACAACTCTAC	CCCCCA	5560
Qy	5461	AAGCTCTCTCGG	CGCAAGGCCACAG	CGCCACCTCT	CCACAACTTCA	CCCCCA	5520
Db	5561	AAGCTCTCTCGG	CGCAAGGCCACAG	CGCCACCTCT	CCACAACTTCA	CCCCCA	5620
Qy	5521	CCCCTACCGCTT	CTGTCTTACTCT	CTCGCGCGCC	CCACTTTCGGCG	CACACCCGCGCA	5580
Db	5621	CCCCTACCGCTT	CTGTCTTACTCT	CTCGCGCGCC	CCACTTTCGGCG	CACACCCGCGCA	5680
Qy	5581	GCCAACTAGCG	CGCAGCAACGCT	ACTCTGACG	CGCTTCCGCG	CACACCCGCGCA	5640
Db	5681	GCCAACTAGCG	CGCAGCAACGCT	ACTCTGACG	CGCTTCCGCG	CACACCCGCGCA	5740
Qy	5641	CACCTCCCGC	CACAGCATCGCT	CTGGGACCTT	GGCAAGAA	CGGACCTGGCTGATTCG	5700
Db	5741	CACCTCCCGC	CACAGCATCGCT	CTGGGACCTT	GGCAAGAA	CGGACCTGGCTGATTCG	5800
Qy	5701	GACAAAGCCCG	CGCATATCTCG	ACCGCGCGGGTTC	CGACCATGT	CACCCGAGTTCGCC	5760
Db	5801	GACAAAGCCCG	CGCATATCTCG	ACCGCGCGGGTTC	CGACCATGT	CACCCGAGTTCGCC	5860
Qy	5761	ACGCGACGGT	TACGACGAGGAT	TCGCGGACAC	CGAAACGGCG	CGTATGTCATCGCGAC	5820
Db	5861	ACGCGACGGT	TACGACGAGGAT	TCGCGGACAC	CGAAACGGCG	CGTATGTCATCGCGAC	5920
Qy	5821	ATCGACTTGG	ACAGATCGAAC	ACACTCTC	AGACGACCTT	GGTGGCGCGCGCGG	5880
Db	5921	ATCGACTTGG	ACAGATCGAAC	ACACTCTC	AGACGACCTT	GGTGGCGCGCGCGG	5980
Qy	5881	GAAGGAGAC	CAGCTGTTC	AGCGGCCCACT	CCACCGCG	GAGTTCACAAAACCTTCGCC	5940
Db	5981	GAAGGAGAC	CAGCTGTTC	AGCGGCCCACT	CCACCGCG	GAGTTCACAAAACCTTCGCC	6040
Qy	5941	CATCAGACGT	CGCGGACCAAC	CGGCGCGCAT	TGCTCGAGCT	TCGTACGAGACCATGTGCGG	6000
Db	6041	CATCAGACGT	CGCGGACCAAC	CGGCGCGCAT	TGCTCGAGCT	TCGTACGAGACCATGTGCGG	6100
Qy	6001	GCAGTGTCTCG	GACGCGGAC	CCGAAAGCCAT	TCGCGCGG	ACGACGATGTTCCGTGCACTC	6060
Db	6101	GCAGTGTCTCG	GACGCGGAC	CCGAAAGCCAT	TCGCGCGG	ACGACGATGTTCCGTGCACTC	6160
Qy	6061	GGCTTCGATT	CACATCAG	CGGCGCTG	AGTTCGGA	AACTGCTGATCAAGGCAACAGGACTC	6120
Db	6161	GGCTTCGATT	CACATCAG	CGGCGCTG	AGTTCGGA	AACTGCTGATCAAGGCAACAGGACTC	6220
Qy	6121	CGCCTTCTGT	CTCGCTGGTCTT	CGACAC	CCCGACCCCT	CGCAAACTCGCGCTACACCTG	6180
Db	6221	CGCCTTCTGT	CTCGCTGGTCTT	CGACAC	CCCGACCCCT	CGCAAACTCGCGCTACACCTG	6280
Qy	6181	CAGAACCAACT	CGCGGGGAC	CAGACGCG	GATCGGCTCTT	CAGCGGACGCGCTTACCGCC	6240
Db	6281	CAGAACCAACT	CGCGGGGAC	CAGACGCG	GATCGGCTCTT	CAGCGGACGCGCTTACCGCC	6340
Qy	6241	GAGGCTTCTGT	CACCGAGCCGAT	CGCATCGT	TGGCATGGCT	CTGCTCTGTTTCCCGCGGGA	6300
Db	6341	GAGGCTTCTGT	CACCGAGCCGAT	CGCATCGT	TGGCATGGCT	CTGCTCTGTTTCCCGCGGGA	6400
Qy	6301	GTGACCTCG	CGCGGACGACTT	CTCGGGATCT	GTATCTCT	CCGACGAGGACGCGATCGCGGGA	6360

Db	6401	GTGACCTCGCGGAGCACTTCTGGGATCTGATCTCTCTCCAGCAGGACGGATCTCGCGGA	6460
Qy	6361	TTCCCCACGACCGCGGCTGGGACCTTGGACA CGCTCTTACGACCCCGACCCGACCAACCCCC	6420
Db	6461	TTCCCCACGACCGCGGCTGGGACCTTGGACA CGCTCTTACGACCCCGACCCGACCAACCCCC	6520
Qy	6421	GGCACTGTCTACACCCGAAACGGCGGATTCCTCTTAGACGACGAGCCACTTTCGACGCGGAA	6480
Db	6521	GGCACTGTCTACACCCGAAACGGCGGATTCCTCTTAGACGACGAGCCACTTTCGACGCGGAA	6580
Qy	6481	TTCTTTGGGATCAGCCCCCGGGAAGCCCTCGCCATAGAACCCCGACGACGACGCTCTCTC	6540
Db	6581	TTCTTTGGGATCAGCCCCCGGGAAGCCCTCGCCATAGAACCCCGACGACGACGCTCTCTC	6640
Qy	6541	GAACCCGCTTGGGAACCATCGAACCGCGGATCAACCCCGACACCCCTCCACGGCACC	6600
Db	6641	GAACCCGCTTGGGAACCATCGAACCGCGGATCAACCCCGACACCCCTCCACGGCACC	6700
Qy	6601	CCCAACGGAGTCTTACCGGACCAACCGGACGAGACTACGACCTTCGCTGCAACACGCG	6660
Db	6701	CCCAACGGAGTCTTACCGGACCAACCGGACGAGACTACGACCTTCGCTGCAACACGCG	6760
Qy	6661	GGCCAGTCAACCGATGTTTTGCACTGACCGGAACCGCCCGGACGCTCATCTCCGTCGT	6720
Db	6761	GGCCAGTCAACCGATGTTTTGCACTGACCGGAACCGCCCGGACGCTCATCTCCGTCGT	6820
Qy	6721	ATCTCGTACAGTTTGGTTTTGAGGTCCTCGCGTTCGGTGGACACGGCTTGTTCCTCG	6780
Db	6821	ATCTCGTACAGTTTGGTTTTGAGGTCCTCGCGTTCGGTGGACACGGCTTGTTCCTCG	6880
Qy	6781	TCGTTGTGTGCTTTGCACTCTGGCCTCTCAGCGCTTCGGTCCGGTGGAGTCTCGATGGCG	6840
Db	6881	TCGTTGTGTGCTTTGCACTCTGGCCTCTCAGCGCTTCGGTCCGGTGGAGTCTCGATGGCG	6940
Qy	6841	CTTCCCGGGGTGACCGGTGATGTCTCTCCGGTGCCTTCGTGAGTGTTCGCGGCAG	6900
Db	6941	CTTCCCGGGGTGACCGGTGATGTCTCTCCGGTGCCTTCGTGAGTGTTCGCGGCAG	7000
Qy	6901	CGGGCTCTGCGCGGACGGGCAATTGCAAGCGTTCTCGCGCGCGGACGGGACCGGC	6960
Db	7001	CGGGGTCTGCGCGGACGGGCAATTGCAAGCGTTCTCGCGCGCGGACGGGACCGGC	7060
Qy	6961	TGGGGTGAGGGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCCCATCGCAACGGT	7020
Db	7061	TGGGGTGAGGGTGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGCCCATCGCAACGGT	7120
Qy	7021	CACCGTGTCTGCGCGTGTGGTGGCGAGTTCGGGTCAACGAGACGGTGGAGCAACGGT	7080
Db	7121	CACCGTGTCTGCGCGTGTGGTGGCGAGTTCGGGTCAACGAGACGGTGGAGCAACGGT	7180
Qy	7081	CTGACCGGCGCCACGGGCGTCCACGACGGGTGTCATCCGACGGGCCCTCGCCACGCC	7140
Db	7181	CTGACCGGCGCCACGGGCGTCCACGACGGGTGTCATCCGACGGGCCCTCGCCACGCC	7240
Qy	7141	GGCTTGTGCGCGGTGATGTGACGCGGGTGGAGGCCCAACGAGACGGTGGAGCAACGGT	7200
Db	7241	GGCTTGTGCGCGGTGATGTGACGCGGGTGGAGGCCCAACGAGACGGTGGAGCAACGGT	7300
Qy	7201	GACCCGATCAGAGGCCACAGGCCCTCTTCGCACTTACGGAACGACCTGTCGCGGAGGGG	7260
Db	7301	GACCCGATCAGAGGCCACAGGCCCTCTTCGCACTTACGGAACGACCTGTCGCGGAGGGG	7360
Qy	7261	CCGCTGTGGCTGGGCTCGGTCAGTCAAGTGTGCGGTACACACAGGCTCGCGGGGGTCT	7320
Db	7361	CCGCTGTGGCTGGGCTCGGTCAGTCAAGTGTGCGGTACACACAGGCTCGCGGGGGTCT	7420
Qy	7321	GCCGGGTGATCAAGATGAGTGGCGCTCGGGCATGCTCTGCTGCGCGGACGTTTCAT	7380
Db	7421	GCCGGGTGATCAAGATGAGTGGCGCTCGGGCATGCTCTGCTGCGCGGACGTTTCAT	7480
Qy	7381	GTGGATGAGCCGTCGCCGCATGTGGACTGTGTCGCGGGTCCGGTGCAGCTGCTGCAGGAG	7440





Qy	841	GTCCGGTTTCAGACCCGCCCGCTGCTTCTGACGAGGGGCCCAAGACGTTTCGTTCGAG	900
Db	941	GTCCGGTTTCAGACCCGCCCGCTGCTTCTGACGAGGGGCCCAAGACGTTTCGTTCGAG	1000
Qy	901	ATGAGCCCGACCCCGGTCTGACCATGCGGCTTCAGGAGCTTCGCCCGGACCTTCGGCGAC	960
Db	1001	ATGAGCCCGACCCCGGTCTGACCATGCGGCTTCAGGAGCTTCGCCCGGACCTTCGGCGAC	1060
Qy	961	ACCACCGGACCGCGACACCGTGTATGATGGGACGCTCGCGCGGGCCAGGGACACCGTG	1020
Db	1061	ACCACCGGACCGCGACACCGTGTATGATGGGACGCTCGCGCGGGCCAGGGACACCGTG	1120
Qy	1021	GACCACTTCCTGACGCTCTCTGCCCACTACGCGGGCATGTGAGACGTCCGGCAACACC	1080
Db	1121	GACCACTTCCTGACGCTCTCTGCCCACTACGCGGGCATGTGAGACGTCCGGCAACACC	1180
Qy	1081	GTCTCTTCGGACCGCTTACCGCGTGTCCCGGACGCTCGCGCGGGCCAGGACGCTTCCTGGAC	1140
Db	1181	GTCTCTTCGGACCGCTTACCGCGTGTCCCGGACGCTCGCGCGGGCCAGGACGCTTCCTGGAC	1240
Qy	1141	CTGGTGCAGCGCCACACCATGCGGCTGTGAACGACGACGGAACGAGCGCACCGCGTCG	1200
Db	1241	CTGGTGCAGCGCCACACCATGCGGCTGTGAACGACGACGGAACGAGCGCACCGCGTCG	1300
Qy	1201	GATGCGGCGCCATCGGCGAGTTTCGCCACCTCGGCTTCGACTCCGTCATCGGTTTCGAA	1260
Db	1301	GATGCGGCGCCATCGGCGAGTTTCGCCACCTCGGCTTCGACTCCGTCATCGGTTTCGAA	1360
Qy	1261	CTGGCAACCGGCTCAGCAAGGCCACGCGGCTCGGGTTGCCGCTGACGCTCATCTTCGAC	1320
Db	1361	CTGGCAACCGGCTCAGCAAGGCCACGCGGCTCGGGTTGCCGCTGACGCTCATCTTCGAC	1420
Qy	1321	CACACACCGCGCGGCTCGCGCGCTTCGGACCGCGGCTCGGCGCACCTCGAC	1380
Db	1421	CACACACCGCGCGGCTCGCGCGCTTCGGACCGCGGCTCGGCGCACCTCGAC	1480
Qy	1381	GAGGACACCGCGCGGCTACCGGACTCACCCAGCGGCCACGAGGACGCGCGGAC	1440
Db	1481	GAGGACACCGCGCGGCTACCGGACTCACCCAGCGGCCACGAGGACGCGCGGAC	1540
Qy	1441	GACCGATCGGCATCATCGGATGCGATGCGGTTTCGCCGGGCGGAGTCCGTTCCCGGAG	1500
Db	1541	GACCGATCGGCATCATCGGATGCGATGCGGTTTCGCCGGGCGGAGTCCGTTCCCGGAG	1600
Qy	1501	GACTGTGGGAGCTGGCGCTTCGGCGGAGAGCGCATTCGGCGCTTCGCCACCGACCGC	1560
Db	1601	GACTGTGGGAGCTGGCGCTTCGGCGGAGAGCGCATTCGGCGCTTCGCCACCGACCGC	1660
Qy	1561	GGATGGCCCAACGAGCGTCAAGCCAGGACCCACGAGCCCGGACGTTCTATCCG	1620
Db	1661	GGATGGCCCAACGAGCGTCAAGCCAGGACCCACGAGCCCGGACGTTCTATCCG	1720
Qy	1621	CAGGAGCGGGTTCCTTTCAGACCGCGGCGCATTCGAGCGCGGCTTCCTCGGAATCAGT	1680
Db	1721	CAGGAGCGGGTTCCTTTCAGACCGCGGCGCATTCGAGCGCGGCTTCCTCGGAATCAGT	1780
Qy	1681	CCACTGAGGACACTGGCGATGATCCGAGCAGCGGCTGCTGCGAGACGCTTCCTGGAG	1740
Db	1781	CCACTGAGGACACTGGCGATGATCCGAGCAGCGGCTGCTGCGAGACGCTTCCTGGAG	1840
Qy	1741	CGTTTCGAGCGGGGGAATCGATCCGCTGTGCGTACGCGGCTCCCGTACGCGGCTTC	1800
Db	1841	CGTTTCGAGCGGGGGAATCGATCCGCTGTGCGTACGCGGCTCCCGTACGCGGCTTC	1900
Qy	1801	CGGGCGGCTTCCTTCGATACGGGCGCGTATGAGACACCGCGCTTCCTCGAGGGCGCC	1860
Db	1901	CGGGCGGCTTCCTTCGATACGGGCGCGTATGAGACACCGCGCTTCCTCGAGGGCGCC	1960
Qy	1861	CGGACGCTGAGGGGCCACATCCTCACCGTACACGGGACGCGTCTCTCGGCGGCTATC	1920
Db	1961	CGGACGCTGAGGGGCCACATCCTCACCGTACACGGGACGCGTCTCTCGGCGGCTATC	2020
Qy	1921	GCCTACAGCTTCGGGCTGGAGGGCGCGCGATCACCGTGGACACGCGGCTGCTCGGACATC	1980

Db	2021	GCCTACAGCTTCGGGCTGGAAAGGCGCGCGCATCACCGTGACACGGGCTCTCGGACATCG	2080
Qy	1981	CTCGTGACGCTGATCTGGCGTCCAGTCCGCTCGGTCGGGTGAGTGCACGCTCGCGCTG	2040
Db	2081	CTCGTGACGCTGATCTGGCGTCCAGTCCGCTCGGTCGGGTGAGTGCACGCTCGCGCTG	2140
Qy	2041	GCGGCGGCTCTCGGTCATGTCACCCCTCGGATGTTCAATGAGTTCTCCCGGACGCGC	2100
Db	2141	GCGGCGGCTCTCGGTCATGTCACCCCTCGGATGTTCAATGAGTTCTCCCGGACGCGC	2200
Qy	2101	GGGCTGTCGTGAGACGGCAGGTGCAAGCGTACTCGGCTCGACCGGACGCGGCTGG	2160
Db	2201	GGGCTGTCGTGAGACGGCAGGTGCAAGCGTACTCGGCTCGACCGGACGCGGCTGG	2260
Qy	2161	GGGAGGGCTCGGATGCTGTTGGTGGAGCGGTTGTCGATGCGGTCGCGCTGGGCGAT	2220
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DEFINITION	Streptomyces avermitilis polyketide synthase gene cluster (aveA1, aveA2, aveA3, aveA4) and aveC, aveE genes, complete cds.		
ACCESSION	AB032367		
VERSION	AB032367.1	GI:5902890	
KEYWORDS	AB032367		
SOURCE	AB032367		
ORGANISM	Streptomyces avermitilis		
REFERENCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.		
AUTHORS	Ikeda, H., Nonomiya, T., Usami, M., Ohta, T. and Omura, S.		
TITLE	Organization of the biosynthetic gene cluster for the polyketide anthelmintic macroide avermectin in Streptomyces avermitilis		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9509-9514 (1999)		
MEDLINE	99380548		
REFERENCE	1 (bases 1 to 64957)		
AUTHORS	Ikeda, H., Nonomiya, T., Usami, M., Ohta, T. and Omura, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-SEP-1999) Haruo Ikeda, School of Pharmaceutical Sciences, Kitasato University, Microbial Chemistry; 5-9-1 Shirokane, Minato-ku, Tokyo 108-8641, Japan		
FEATURES	(E-mail: ikeda@mc.pharm.kitasato-u.ac.jp, Tel: +81-3-5791-6242, Fax: +81-3-3444-6197)		
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Qy 24661 CCCACCCGAGGAATGTGCTCCCATCTGGGACACAACTCGTGCAGCTTAGACGAGAA 24720  
Db 24661 CCCACCCGAGGAATGTGCTCCCATCTGGGACACAACTCGTGCAGCTTAGACGAGAA 24720  
Qy 24721 GAGACGCGGCACTGTGGAATGCTCTCCGCAAGTGCCCATCGCGTACCGTTCGAGGAC 24780  
Db 24721 GAGACGCGGCACTGTGGAATGCTCTCCGCAAGTGCCCATCGCGTACCGTTCGAGGAC 24780  
Qy 24781 GAACCGATCGGCATCATCGGATGCGATGTCGCTTCCCGCGGCGGATCGTTCGCGGAC 24840  
Db 24781 GAACCGATCGGCATCATCGGATGCGATGTCGCTTCCCGCGGCGGATCGTTCGCGGAC 24840

Qy 24841 GACCTGTGGAAATGCTCGCTTCGGGTAAAGACGCTATCGCGCTTTCOCGACCGACGC 24900  
Db 24841 GACCTGTGGAAATGCTCGCTTCGGGTAAAGACGCTATCGCGCTTTCOCGACCGACGC 24900  
Qy 24901 GGCTGGGACCTGGACACGCTCTACGACCCCGACCCGACACCCCGGACCTGTACACC 24960  
Db 24901 GGCTGGGACCTGGACACGCTCTACGACCCCGACCCGACACCCCGGACCTGTACACC 24960  
Qy 24961 CGAAACGGCGATTTCTTACGGCGAGGCGACCTTTCGACGCGCAATTTCTTCGGCATCAGC 25020  
Db 24961 CGAAACGGCGATTTCTTACGGCGAGGCGACCTTTCGACGCGCAATTTCTTCGGCATCAGC 25020  
Qy 25021 CCCCGGAAGCCTTCGCTATGGAACCCCGACGACTCTCTCTCGAAACCGCTCGGAA 25080  
Db 25021 CCCCGGAAGCCTTCGCTATGGAACCCCGACGACTCTCTCTCGAAACCGCTCGGAA 25080  
Qy 25081 ACATCGAAACGACGCGGCTCAACCCCGACACCTTCCGACGAGCTCTCTCGAAACCGCTCGGAA 25140  
Db 25081 ACATCGAAACGACGCGGCTCAACCCCGACACCTTCCGACGAGCTCTCTCGAAACCGCTCGGAA 25140  
Qy 25141 GCGGAATCAAGCTCAAGACGCGCGCATATCCGCAAGCGCTGATGTGGAGACC 25200  
Db 25141 GCGGAATCAAGCTCAAGACGCGCGCATATCCGCAAGCGCTGATGTGGAGACC 25200  
Qy 25201 ATCGAGGCTACGCGCTTGAACCGGAGTTCGGGAGTGTGGCGTCCGGCGGCTGCTTAC 25260  
Db 25201 ATCGAGGCTACGCGCTTGAACCGGAGTTCGGGAGTGTGGCGTCCGGCGGCTGCTTAC 25260  
Qy 25261 ACCTCGGGCTCGAAGCGCGCGGTTCGGTGGATACGCGGTTCGTCGTCGTCGTTGGTG 25320  
Db 25261 ACCTCGGGCTCGAAGCGCGCGGTTCGGTGGATACGCGGTTCGTCGTCGTCGTTGGTG 25320  
Qy 25321 GCGTTCATTTGGGCGGCGAGGCGTTCGCTGGGAGTGTGGCGTTCGATGGCGCTTTCGCGG 25380  
Db 25321 GCGTTCATTTGGGCGGCGAGGCGTTCGCTGGGAGTGTGGCGTTCGATGGCGCTTTCGCGG 25380  
Qy 25381 GGTGTGACGCTGATGTCTCGGCTACGCTTGTGGAGTTCACCTCAGCGGGGCTG 25440  
Db 25381 GGTGTGACGCTGATGTCTCGGCTACGCTTGTGGAGTTCACCTCAGCGGGGCTG 25440  
Qy 25441 GCGCGGACGGGCGGTGCAAGGCTTATTCGGCGGCTGCTGACGGTACCGGCTGGGCGGAG 25500  
Db 25441 GCGCGGACGGGCGGTGCAAGGCTTATTCGGCGGCTGCTGACGGTACCGGCTGGGCGGAG 25500  
Qy 25501 GGTGTGGGATGCTGCTGGTGGAGCGGCTTCCGACGCGGCTTCGCAACCGGTCACCGGTGTC 25560  
Db 25501 GGTGTGGGATGCTGCTGGTGGAGCGGCTTCCGACGCGGCTTCGCAACCGGTCACCGGTGTC 25560  
Qy 25561 CTGGCGCTGCTGGTGGGCTCAACAGGAGCGGTTCGAGCAACCGGCTTCGACCGGCTG 25620  
Db 25561 CTGGCGCTGCTGGTGGGCTCAACAGGAGCGGTTCGAGCAACCGGCTTCGACCGGCTG 25620  
Qy 25621 CCCAAGGGGCTTCCGACGAGCGTTCATCCGCTCAGGCGCTTCGCAATCGGGGAGTCAACC 25680  
Db 25621 CCCAAGGGGCTTCCGACGAGCGTTCATCCGCTCAGGCGCTTCGCAATCGGGGAGTCAACC 25680  
Qy 25681 CCGGCGGATGTCGACGAGTGGGCGGCGACGCGACCGGAGCACTCTGGGCGGAGCGGATC 25740  
Db 25681 CCGGCGGATGTCGACGAGTGGGCGGCGACGCGACCGGAGCACTCTGGGCGGAGCGGATC 25740  
Qy 25741 GAGGCGGAGGCTCTCTGGGCGGCTTACGGAACACACCGCGCCCAACCGGCTTCGTTGG 25800  
Db 25741 GAGGCGGAGGCTCTCTGGGCGGCTTACGGAACACACCGCGCCCAACCGGCTTCGTTGG 25800  
Qy 25801 CTGGGATCCCTCAAAATCCAAATCGGCGACGACGCGCGCGGCGGAGTGC 25860  
Db 25801 CTGGGATCCCTCAAAATCCAAATCGGCGACGACGCGCGCGGCGGAGTGC 25860  
Qy 25861 ATCAAGATGATGCGGCTTGGCGAAGCGGCTCTGCCACAGACCCCTTCCAGTGGAGCGAG 25920  
Db 25861 ATCAAGATGATGCGGCTTGGCGAAGCGGCTCTGCCACAGACCCCTTCCAGTGGAGCGAG 25920



Db 19321 CAGGCCAATAGCCGCGAGCCAAACGCCCTACCTCGAGCCGCTCGCCCAACACCGCCACACC 19380  
Qy 19381 CACCACTCCCGCCACCAAGCATCGCTGGGCACTCTGCAAGGAACCGACTGCGCACT 19440  
Db 19381 CACCACTCCCGCCACCAAGCATCGCTGGGCACTCTGCAAGGAACCGACTGCGCACT 19440  
Qy 19441 GGTCAAGTCAGGAAACATCTCCGCGCGCGGAGATGTTGCGCATGCCGCCGAGTTGGCG 19500  
Db 19441 GGTCAAGTCAGGAAACATCTCCGCGCGCGGAGATGTTGCGCATGCCGCCGAGTTGGCG 19500  
Qy 19501 GTCCAGCTGTTAGCGCGCATCGGAGCGGCGCGGAGTCTCTCGTCCCGCATATC 19560  
Db 19501 GTCCAGCTGTTAGCGCGCATCGGAGCGGCGCGGAGTCTCTCGTCCCGCATATC 19560  
Qy 19561 GACTCGAAGAAATTCGGACCGGTTCTCTCCAGCAAGTCGTCCGTTCTGCTCGAGACCTT 19620  
Db 19561 GACTCGAAGAAATTCGGACCGGTTCTCTCCAGCAAGTCGTCCGTTCTGCTCGAGACCTT 19620  
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Db 19621 CCCAGGCAACAGGGAACCTGAGAGCGCGCAGTACCGTTGAGCAGAGAGGACAAAC 19680  
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Db 19681 CTCGGCAACTCTCATGGTTCGTCTCCAGCAAGTCGTCCGTTCTGCTCGAGACCTT 19740  
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Db 19741 GTCCGATCCTACTCCGCGGAGTGTCTCGGCGCGACGACTCCGAGGCCATCCCGCCGCT 19800  
Qy 19801 CGGCTGTTCAGGATCTAGGTTGACTCGCTTTCGCGCGTGGAGCTTCGCAACCAACCTC 19860  
Db 19801 CGGCTGTTCAGGATCTAGGTTGACTCGCTTTCGCGCGTGGAGCTTCGCAACCAACCTC 19860  
Qy 19861 GCAGCAGACGAGCTGGCTCTGCGGACGACTCTCGTCTTCGATTAACCCAGCCAC 19920  
Db 19861 GCAGCAGACGAGCTGGCTCTGCGGACGACTCTCGTCTTCGATTAACCCAGCCAC 19920  
Qy 19921 AAGCTCGCCCAATTTCTCTCTCGAGATCGGAGTTCAGCCGCAACCTCAACTCCG 19980  
Db 19921 AAGCTCGCCCAATTTCTCTCTCGAGATCGGAGTTCAGCCGCAACCTCAACTCCG 19980  
Qy 19981 CTTCCGACACCCCGGCGAGCTCGATGAGCCGATCGCCATCGTTGGCATGGCTGTGCG 20040  
Db 19981 CTTCCGACACCCCGGCGAGCTCGATGAGCCGATCGCCATCGTTGGCATGGCTGTGCG 20040  
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Db 20041 TCCCGCGCGAGTGAACCTCGGCGAGCTCTGCGGACGACTCTGGGATCTGATCTCTCCGAGCAGGAC 20100  
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Db 20101 GCGATCGGCGATTTCCCAACGACCGCGGCTGGGACCTGGACACGCTTACGACCCGAC 20160  
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Db 20161 CCCGACACCCCGGCACTCTACACCGAAGCGCGGATTCCTCTACGACGAGGCCAC 20220  
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Db 20221 TTGAGCCGGAATTTCTCGGATACGCCCCCGGAGGCCCTTCGCGATGGACCCCGAGAA 20280  
Qy 20281 CGACTCTCTCGAAACCGCTGGGAACCATCGAACACGCGGCATCAACCCCGACAC 20340  
Db 20281 CGACTCTCTCGAAACCGCTGGGAACCATCGAACACGCGGCATCAACCCCGACAC 20340  
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Db 20341 CTCACGSCACCCCGGAGTCTTACCGGCAACCAACGAGACGAGCCAGCGGCACAC 20400  
Qy 20401 ATCCGTACGCGCCGAGCGGTACGAGGATTCGTCTGACCGGGGAGCCACGAGATC 20460  
Db 20401 ATCCGTACGCGCCGAGCGGTACGAGGATTCGTCTGACCGGGGAGCCACGAGATC 20460

Qy 20461 GCCTCCGCGCGAATCTCTTAATCTCGGTTGGAAGGCCCTGCGGTACCTTCGACACA 20520  
Db 20461 GCCTCCGCGCGAATCTCTTAATCTCGGTTGGAAGGCCCTGCGGTACCTTCGACACA 20520  
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Db 20581 TGACCATGGCTTGGCGCGGCGGCGACGAGTATGACACCCGATCACCCTTCACCGAA 20640  
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Qy 20701 GACGTTACCGGCTGGGCTGAGGCTGCGGCGTCCGCGAGCGGCTCTCCGACGCC 20760  
Db 20701 GACGTTACCGGCTGGGCTGAGGCTGCGGCGTCCGCGAGCGGCTCTCCGACGCC 20760  
Qy 20761 CGCGCAACGCTCACCGTCTGCGGCGTGGTGGCGAGTGGTCAACAGGACGCT 20820  
Db 20761 CGCGCAACGCTCACCGTCTGCGGCGTGGTGGCGAGTGGTCAACAGGACGCT 20820  
Qy 20821 GCGAGCAACGCTCTGACCGCGCGCAACCGGCGCTCCGAGAGCGGCTCATCCGCGAGGCC 20880  
Db 20821 GCGAGCAACGCTCTGACCGCGCGCAACCGGCGCTCCGAGAGCGGCTCATCCGCGAGGCC 20880  
Qy 20881 CTGCGCAACCGGACTGACCGCGCGCTCGATCGGTTGAGGCGCCACCGGACCGGC 20940  
Db 20881 CTGCGCAACCGGACTGACCGCGCGCTCGATCGGTTGAGGCGCCACCGGACCGGC 20940  
Qy 20941 ACCACTTTGGCGCGACCGATCGAGGCGCGGCGCTCCGCGACTACGAGACGAGCCGT 21000  
Db 20941 ACCACTTTGGCGCGACCGATCGAGGCGCGGCGCTCCGCGACTACGAGACGAGCCGT 21000  
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Db 21001 CCCGCGCAACCGGCGCTGTTGGCTCGTCAAGTCCAACTCGGAGCGGCGCCACCGGACCGGC 21060  
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Db 21181 CTGCTGACGAGACGCTGCTGCGCGGAGGCGGCGGCGGCGGCGGCGGAGGAGTG 21240  
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Db 21241 TCATCATTCGCGCTGAGCGGCGCAACCGCGCGGCGGCGGCGGCGGCGGAGGAGTG 21300  
Qy 21301 GAGTTCGCGGCGGAGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGGAGTG 21360  
Db 21301 GAGTTCGCGGCGGAGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGAGGAGTG 21360  
Qy 21361 GGCAGTCTCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGGAGTG 21420  
Db 21361 GGCAGTCTCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGGAGTG 21420  
Qy 21421 CAGGCCAGGCGCTTCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGGAGTG 21480  
Db 21421 CAGGCCAGGCGCTTCGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGGAGTG 21480  
Qy 21481 GGATACACCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGGAGTG 21540  
Db 21481 GGATACACCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGGAGTG 21540

Qy	17161	GCCTTCAGGTGGCTCCACGGCTCTCTCACCGGCTACCGAGGTACCATCACCCCCCACTAC	17220
Db	17161	GCCTTCAGGTGGCTCCACGGCTCTCTCACCGGCTACCGAGGTACCATCACCCCCCACTAC	17220
Qy	17221	TACGGCGGACACTCCCTCGGGGAATACACGGCGGCACTCGCGGGATCTTACCCCTC	17280
Db	17221	TACGGCGGACACTCCCTCGGGGAATACACGGCGGCACTCGCGGGATCTTACCCCTC	17280
Qy	17281	ACCGAGCGCACACCCCTCATACCCCAACGGCGCACCTCATGCAAAACCATGCCCCCGGC	17340
Db	17281	ACCGAGCGCACACCCCTCATACCCCAACGGCGCACCTCATGCAAAACCATGCCCCCGGC	17340
Qy	17341	ACCATGACACACCTCCACACACCCCCCAACATACCCACCACTCACCGCGCACGAA	17400
Db	17341	ACCATGACACACCTCCACACACCCCCCAACATACCCACCACTCACCGCGCACGAA	17400
Qy	17401	AACGACCTCGGCATCGCGGCATCAACACCCCGCACCTCGCTGTCATCAGGGGCACCCC	17460
Db	17401	AACGACCTCGGCATCGCGGCATCAACACCCCGCACCTCGCTGTCATCAGGGGCACCCC	17460
Qy	17461	CACACCGTCCAAACATCACACCCCTCTGCCAAACAAAGGATCAAAACCAAAACCCCTC	17520
Db	17461	CACACCGTCCAAACATCACACCCCTCTGCCAAACAAAGGATCAAAACCAAAACCCCTC	17520
Qy	17521	CCCAACAAAAGCGCTTCCACTCCCGCCACACCAACCCCATCTCTCAACCAACTCCACCG	17580
Db	17521	CCCAACAAAAGCGCTTCCACTCCCGCCACACCAACCCCATCTCTCAACCAACTCCACCG	17580
Qy	17581	CACACCGAAGCTTACCTACACCCCGCCACACCCCGCTCATCAGCGGCACACCCCA	17640
Db	17581	CACACCGAAGCTTACCTACACCCCGCCACACCCCGCTCATCAGCGGCACACCCCA	17640
Qy	17641	CCGACCAACTCTTCAACCCCGCTTGGACCCCAAGCGCGCAACACCGTGGACTAC	17700
Db	17641	CCGACCAACTCTTCAACCCCGCTTGGACCCCAAGCGCGCAACACCGTGGACTAC	17700
Qy	17701	GCCACCAACCCAAACCTTCCACCAACACCGCGGTACCACTATCGAACTCGGACCC	17760
Db	17701	GCCACCAACCCAAACCTTCCACCAACACCGCGGTACCACTATCGAACTCGGACCC	17760
Qy	17761	GACACACCTTACACCTTACCCACACCAACCTTCCCAACACCCCGCACACCCCTC	17820
Db	17761	GACACACCTTACACCTTACCCACACCAACCTTCCCAACACCCCGCACACCCCTC	17820
Qy	17821	ACCTTACACCCCGCCACACCCCGCTTCCACCAACCTTCCCAACCTTCCCAACCTC	17880
Db	17821	ACCTTACACCCCGCCACACCCCGCTTCCACCAACCTTCCCAACCTTCCCAACCTC	17880
Qy	17881	ACCAACCTTGGCACCCCGCTTACCAACCAACCAACCAACCAACCAACCAACCAAC	17940
Db	17881	ACCAACCTTGGCACCCCGCTTACCAACCAACCAACCAACCAACCAACCAACCAAC	17940
Qy	17941	CACCTGACCTTCCACCTTACCCCTTCAACACGAGCACTACTGCTCGAAGCAACAG	18000
Db	17941	CACCTGACCTTCCACCTTACCCCTTCAACACGAGCACTACTGCTCGAAGCAACAG	18000
Qy	18001	CGGGTGGCGGATCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTC	18060
Db	18001	CGGGTGGCGGATCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTC	18060
Qy	18061	GCAGAGTGGAGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTC	18120
Db	18061	GCAGAGTGGAGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTC	18120
Qy	18121	ACCAGCTTGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTC	18180
Db	18121	ACCAGCTTGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTCGGGTTC	18180
Qy	18181	TGGACACCGCACCAACAGCGCATCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18240
Db	18181	TGGACACCGCACCAACAGCGCATCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18240
Qy	18241	AAACCCCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18300

Db	18241	AAACCCCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18300
Qy	18301	GAACCCAGACCCACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18360
Db	18301	GAACCCAGACCCACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18360
Qy	18361	ATCACCCCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18420
Db	18361	ATCACCCCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18420
Qy	18421	ACCGACCAACAGCCCAAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCTC	18480
Db	18421	ACCGACCAACAGCCCAAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCTC	18480
Qy	18481	GCCCTCGACGAAACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18540
Db	18481	GCCCTCGACGAAACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18540
Qy	18541	CTCACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18600
Db	18541	CTCACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18600
Qy	18601	ACCAACCGCACCAACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18660
Db	18601	ACCAACCGCACCAACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18660
Qy	18661	TGGGACTTGGCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18720
Db	18661	TGGGACTTGGCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18720
Qy	18721	CTCCCCACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18780
Db	18721	CTCCCCACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT	18780
Qy	18781	CACCAACCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTT	18840
Db	18781	CACCAACCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTT	18840
Qy	18841	ACCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18900
Db	18841	ACCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	18900
Qy	18901	ACCGGCGGAAACCGGCGCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTT	18960
Db	18901	ACCGGCGGAAACCGGCGCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTT	18960
Qy	18961	ACCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	19020
Db	18961	ACCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	19020
Qy	19021	ACCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	19080
Db	19021	ACCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	19080
Qy	19081	CCAGACCAACTTCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTT	19140
Db	19081	CCAGACCAACTTCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTT	19140
Qy	19141	ATCCACACCGGATCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTT	19200
Db	19141	ATCCACACCGGATCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTT	19200
Qy	19201	AACACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	19260
Db	19201	AACACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTTCAACCTT	19260
Qy	19261	ACCCCTTCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTT	19320
Db	19261	ACCCCTTCAACCTTGGCGATCGGACACCCCGCATACCAATCTCTCAACCTTCAACCTTCAACCTT	19320
Qy	19321	CAAGCCAACTAGCGCGGACGCAACCGCTTCAACCTTGGCGATCGGACACCCCGCATACCTTCAACCTT	19380

Db 14941 TTGGCCCTGTTGGCACCACCATCGCGCGCTGTGCTGGGCCATGCCACTCCCGAAGTGATC 15000  
Qy 15001 GTTCCGAACAAGCCCTTCAAAGAGAGCTGGGTTTTGATTTCTCTCGCGCAATTCAGCTTCGT 15060  
Db 15001 GTTCCGAACAAGCCCTTCAAAGAGAGCTGGGTTTTGATTTCTCTCGCGCAATTCAGCTTCGT 15060  
Qy 15061 AATCGAGTGTCTGTGAGCTTGACCTGCGGCTTCCGGCCACGCTGATCTTCGATTACCCC 15120  
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Db 15121 ACTCGAGTGGCGCTTTGCGAGTTCTCTCGGGCGGCGATCTCGAGCGGACACAGGACG 15180  
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Db 15181 ACCACTCGTCTCGCGCTAACTCGGTTCCCGCCGACGAGCCGATCGCCATCGTCGGCATG 15240  
Qy 15241 GCCTGTGGTACCCCGGTGATGTACGACGGTTCGATGATCTCTGGCAGGTGGTCAGTGGT 15300  
Db 15241 GCCTGTGGTACCCCGGTGATGTACGACGGTTCGATGATCTCTGGCAGGTGGTCAGTGGT 15300  
Qy 15301 GGCATGACGGATCGGCGGATTCGCGACGAACCGTGGGTGGGACCTCGACACGCTGTAC 15360  
Db 15301 GGCATGACGGATCGGCGGATTCGCGACGAACCGTGGGTGGGACCTCGACACGCTGTAC 15360  
Qy 15361 AACCCGACCCGGACCAACGAGAACAGCTACACCCGAGCGGCGGATTCCTTTACGAC 15420  
Db 15361 AACCCGACCCGGACCAACGAGAACAGCTACACCCGAGCGGCGGATTCCTTTACGAC 15420  
Qy 15421 GCAGCAATTTGATTCGCACTTCTTCGGTATCAGTCCGCTGAGGCACTGGCGATGGAC 15480  
Db 15421 GCAGCAATTTGATTCGCACTTCTTCGGTATCAGTCCGCTGAGGCACTGGCGATGGAC 15480  
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Qy 15721 GTCGACACTGCTGCTCTTCGCTGCTGCTCTGACACTGGGCTGTTCAGGCGCTGCGG 15780  
Db 15721 GTCGACACTGCTGCTCTTCGCTGCTGCTCTGACACTGGGCTGTTCAGGCGCTGCGG 15780  
Qy 15781 TCCGGCAGTGTTCATGGCCCTCGCGGTGGGCTCAAGTGATGTCAACCCCGGCGGG 15840  
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THE KITASATO INSTITUTE
OS Streptomyces avermitilis
PN JP 200245457-A/1
PD 12-SEP-2000
PF 24-FEB-1999 JP 1999046961
PR
PI SATOSHI OMURA, HARUO IKEDA
PC C12N15/00, A61K31/70, C12N1/15, C12N9/88, C12P19/62, PC
C12Q1/68/CO7D493/22,
PC (C12N1/15, C12R1:465), (C12N9/88 C12R1:465), C12N15/00 CC
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    /db_xref="taxon:33903"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 30690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 GCCGACGAGCGGACGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 61 GCCGACGAGCGGACGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Qy 121 GGCATGGGAAGGAATCTCTCGACCTTCCGACGCTTCCGAGAGAGGTCCGCGCCCTGC 180
Db 121 GGCATGGGAAGGAATCTCTCGACGCTTCCGACGCTTCCGAGAGAGGTCCGCGCCCTGC 180
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 22:17:14 ; Search time 49787 Seconds  
(without alignments)  
17939.725 Million cell updates/sec

Title: US-09-914-286-1  
Perfect score: 30690  
Sequence: 1 gtcagaggatgacgcg.....acgaagtgagacagcgtga 30690

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_ets:\*

12: gb\_ey:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_ets:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rod:\*

36: em\_htg\_mam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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3	11548	37.6	12381	6	AX006889	AX006889 Sequence	
4	10078	32.8	11096	1	AF275943	AF275943 Streptomy	
5	6437.2	21.0	31422	6	E38021	E38021 Avermectin	
C	7	4852.2	15.8	113193	1	AB032367	AB032367 Streptomy
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16	3399.8	11.1	53784	1	AMM223012	AJ223012 Amycolato	
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20	3194.8	10.4	49377	6	I88042	I88042 Sequence 1	
21	3142	10.2	50000	6	AX089417	AX089417 Sequence	
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24	3142	10.2	80161	6	AR165018	AR165018 Sequence	
25	3140.6	10.2	28958	6	AR044578	AR044578 Sequence	
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ALIGNMENTS

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LOCUS E38020 30690 bp DNA linear PAT 31-JAN-2002  
DEFINITION Avermectin aglycon synthase gene.  
ACCESSION E38020  
VERSION E38020.1 GI:18626909  
KEYWORDS JP 2000245457-A/1.  
SOURCE Streptomyces avermitilis.  
ORGANISM Streptomyces avermitilis  
Bacteria; Actinobacteria; Actinomycetales; Streptomyces.  
REFERENCE 1 (bases 1 to 30690)  
AUTHORS Omura, S. and Ikeda, H.  
TITLE Avermectin aglycon synthase gene  
JOURNAL Patent: JP 2000245457-A 1 12-SEP-2000;

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RESULT 12  
SNA278573/c

LOCUS SNA278573 84985 bp DNA linear BCT 17-MAY-2001  
DEFINITION Streptomyces natalensis pimarin biosynthetic gene cluster.  
ACCESSION AJ278573  
VERSION AJ278573.1 GI:12055067  
KEYWORDS ABC transporter; cholesterol oxidase; cytochrome P450 monooxygenase; ferredoxin; glucosyl transferase; macrolide efflux pump; mycosamine dehydratase; orfx; pimA gene; pimB gene; pimC gene; pimD gene; pimE gene; pimF gene; pimG gene; pimH gene; pimI gene; pimJ gene; pimK gene; pimS gene; pimS1 gene; pimS2 gene; pimS3 gene; pimS4 gene; polyketide synthase; sensory transduction protein; thioesterase.  
SOURCE Streptomyces natalensis.  
ORGANISM Streptomyces natalensis  
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces, 1 (bases 1 to 84985)  
REFERENCE Aparicio J.F., Foces, R., Mendes, M.V., Olivera, N. and Martin, J.F. A complex multienzyme system encoded by five polyketide synthase genes is involved in the biosynthesis of the 26-membered polyene macrolide pimarin in Streptomyces natalensis Chem. Biol. 7 (11), 895-905 (2000)  
JOURNAL 20547809  
MEDLINE 11094342  
PUBMED 11094342  
REFERENCE 2 (bases 1 to 84985)  
AUTHORS Aparicio, J.F.  
TITLE Direct Submision  
JOURNAL Submitted (27-JUN-2000) Aparicio J.F., Molecular Genetics, Institute Of Biotechnology - Inbiotec, AV. REAL 1 - LEON, 24006, SPAIN  
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Qy 26645 GCGCTCTTACGGCATCGAACCAGACCGGCTCTTCGGGACATTCACAGGAGAAATTCGCG 26704  
Db 23640 TGAAGCCTTGGGCGCATCACCGAGCTTCGTGGCGGCGACTTCCATCGCGAGATCGCG 23699  
Qy 26705 CGGCCACATCTGGCGGCGACTCAGCTCAAGAGCGCGCCAAACCGTTGCATCGCA 26764  
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Qy 22854 TCTGACACGGTGGTGGCGGCTCTCGCGCTGGGACCGCGCAACCAACCAACCGCGCG 22913  
Db 19834 ACTGACCGCGGCTCTGGAGCGCGGCAACAACCGCGCGCTTACGCGGCTCGGCGC 19893  
Qy 22914 CATCAACCTGGACTTACAGGAACCTGGAACCTTCAACCTTCCCTCCACCAACCAACA 22973  
Db 19894 CATAGCGCGCGCGCTCGCGTTCGCTGGAGGCGCTCTCGCTCGCGCGCGCGCGCG 19953  
Qy 22974 ACCCAACAACTGGCTATGCGCATCC-----GAAACCGAGACCAACCAACCA 23027  
Db 19954 CACCACCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCA 20013  
Qy 23028 CATCAACCACTCTCAGCAACCTCCACACCGGATCAACCGCATCCCGCTCCCTCAGTGT 23087  
Db 20014 CGACCGCGCGGCGCACCGTGTCTCGTGAATCTTCTTCTTCTTCTTCTTCTTCTTCT 20073  
Qy 23088 CAACACACCAACCAACCAACCAACCAACCTTCAACCAACCTTCAACCAACCAACCAACA 23147  
Db 20074 CGAGCACCGCGCGCGCGCGCACCGCTCCACCGGACTTCTTCTTCTTCTTCTTCTTCT 20133  
Qy 23148 AGCCCAACACACCAACCAACCAACCAACCAACCGGCTCTCTCTCTCTCTCTCTCT 23207  
Db 20134 CCGCTCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 20193  
Qy 23208 AACACCCACCCCAACCAACCAACCAACCAACCGGACCTCTCAACCTCAACCTCC 23267  
Db 20194 GGACGCTCTCGCGACACCTCTCGGCGCACCGGATCGGACCGGCGCGCGCGCGGACT 20253  
Qy 23268 CCAACCAACCAACCAACCAACCAACCAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 23327  
Db 20254 GCGCGCTCTCGCGACCGCGGAGGCGCGTCCCGGACCTGTCTGTCTGTCTGTCTGTCT 20313  
Qy 23328 CACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 23348  
Db 20314 CACCCCGGCGCGCGCGCTTCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 20373

Qy 23349 ----- 23348  
Db 20374 GCCTCAACAGTGGCTCGCGGACCGCTTTCGCGACCGCGCGCTTGTCTGTCTGTCTGTCT 20433  
Qy 23349 ---CCTCAACACACCCCAACCAAGCCCAAACTGGGGAGCTGCGCGCGACCAACCTCTCTGTGA 23405  
Db 20434 CCGCGCACCGGACCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTATCCGACCGC 20493  
Qy 23406 ACACCCACACACCGCGGGAATCATGACCTCCCGACACCGCGCGCGCGCGCGCGCGCT 23465  
Db 20494 CCGCACGAGAACCCCGCGCGCTTTCGCGCTCTCGACCTCGCGCGCGCGCGCGCGCG 20553  
Qy 23466 CCACACCTCAACCAACCACTTCAACCAACCCCAACCAACCAACCAACCAACCTTCCGCTTCCGAC 23525  
Db 20554 CGACCGGAGACCTTGGCGACCGCGCTTGGCGCGCGCGCGCGCGCGCGCTCGCGCT 20613  
Qy 23526 CACCGGACCAACACCGCGCGCTTACCCCGACACCGCTTCAACCGCGCGCGCGCGCGCGCT 23585  
Db 20614 CCGCGGACCGGACCGCGCGCGCGCTTGGCGCGCGCTTGGCGCGCGCGCGCGCGCGCT 20673  
Qy 23586 CACCCCGACCCCGGACCGGACCGCTTCAACCAACCGCGCGGACCGCGCGCGCGCGCGCT 23645  
Db 20674 CACCTGGAACCGGACCGGACCGCTTCAACCAACCGCGCGGACCGCGCGCGCGCGCT 20733  
Qy 23646 CCTCACCGACCTTCAACCAACCGCGCGGACCGCGCGCGCGCGCGCGCGCGCGCT 23705  
Db 20734 CCGCGCGGACCTTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 20793  
Qy 23706 GCGCGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23765  
Db 20794 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 20853  
Qy 23766 CTTACCATCACCTTGGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCG 23825  
Db 20854 GGTCCAATCGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 20913  
Qy 23826 CATCCCGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23885  
Db 20914 GGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 20973  
Qy 23886 CCGCGTCTCGGAAACCGATCGCGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 23945  
Db 20974 CTTCTCGGCTCTCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21033  
Qy 23946 CCGCGCGGATCTGATGATGCTGCTGCGGACCGGACCGGACCGGACCGGACCGGACCG 24005  
Db 21034 CCGCTGGCACCTGCAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21090  
Qy 24006 CTGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24065  
Db 21091 CTGCTCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21150  
Qy 24066 ATACTGGACCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24125  
Db 21151 CTTCTGGACCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21210  
Qy 24126 CTGGGCGCGCTGGCGCGGAAAGGCGATGTGCGCGGATGCGCGCTCATGTTTACCTTGA 24185  
Db 21211 CTGGGCGCGCTGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGAC 21270  
Qy 24186 AAAGCGGCGATCTCGCGGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24245  
Db 21271 G-----CGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21300  
Qy 24246 GCGCGACCGCGCGGAAATCCAACTGATCATCGCGGACATCGACTGGGAGCGCTTGTCCC 24305  
Db 21301 GACCTGGAACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21360  
Qy 24306 CCGCTTACCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24365  
Db 21361 CGCG-----CGGCTCGCGCTCGACCTGCGCGCTTCTGCGCGCGCGCGCGCGCG 21416

Qy	20451	CACCAGCATCGCTCCCGCCGAATCTCTCATCTCGGGTTGAAGGCGCTCGGTGTCAC	20510	18157	CGCGCGAGAGGCGCTCGCGCGTCTTCTCCGCGCAGGGCTCCAGCGCCCGGCGCAT	18216	
Db	17086	GGCAGCGTCATCTTCGGCGCGCTCTCTACACCTTCGGCGCGAGGGCCCGGCGTCAC	17145	Qy	21543	-----CGCGACACCTTCTGCAAGCACTCCAGGCACTCGCGCAGGCGGCAACC	21590
Qy	20511	CCTCGACACAGCGTGTCTCTCTCGTGTGCGCTCGACCTCGCGTGCAGTCCCTCAG	20570	Db	18217	GGACCGGAACCTCCAGCGCGCTTCGCGGTGTTCCGCGCGGCTTCGACGAGATCAGCG	18276
Db	17146	CGTCGACACCGCGTGTCTCTCGTCTCTGTCGCTGCACTGCGGCGCTCCAGGCGCTGCG	17205	Qy	21591	CAACCCCGCGCTCATCACAGCAGCGCCCGAGCGGACCGGAGCAGGAGGCGCGCAGG	21650
Qy	20571	GTCGGGTGAATGACACCATGGCTTTGGCGGGGGCGGCACCGGTATGACCCCGCATCAC	20630	Db	18277	GCTCTCGACACCACTCGACCGCGCTGCGGAGGTGCTCTGGGGCACCGACGCCGA	18336
Db	17206	CGGCGCGAGTGTCTCATGCGCTTGGCGGGCGCGGTCTCATATGCGCACCCCGGGGCC	17265	Qy	21651	AAAGACCGCATTCATCTGCTTCGGACAGGGCACCAAGCGCCCGGACATGCGCCACCGGCT	21710
Qy	20631	CTTCACCGAATTCGCCCGCCAAACCGGACTCGCCCGCGACGGGGTTGCAAGGGTTCTC	20690	Db	18337	CCTGCTGAAGACACCGGGTGGGCCCAACCGCGCTGTTTCGCGGTGAGG-...TCGCGCT	18393
Db	17266	GTTCTCGCTTACCGCGCAGAGCGGCTTGGCGCGCGCGCGCTGCAAGCGCTTCTC	17325	Qy	21711	CTACACACACCCCGCTTTCGCGCGCACCTCAACGACATCTGACACCCACCTCGACCC	21770
Qy	20691	GGCGCGCGCTGACGGTACCGCTGGGTGAGGTGTGGGGATGCTGTGTGAGAGCGGCT	20750	Db	18394	CTACCGCTGCTGTCGCTCCCGCGTCAACCGGAGTTCCTGTCGCGGCGCATCTCCATCGG	18453
Db	17326	CGACCGGGCCGACGGCACCGGCTGGGCGAGGGCGCGGCATGCTGTCTGTATGCGGCT	17385	Qy	21771	CCACCTCGACACACCCCTCTCTCCCGCTCTCACCCAAAGACAGACAGACACACAGCA	21830
Qy	20751	CTCGAGCGCCCGCGCAACGGTCAACGGTCTCTCGCGTGTGTGTCAGTGGGTCAA	20810	Db	18454	CGAGCTCGCGCGCGCGACGTCGCGGGTCTCTCCCTCGAAGACGCTTGACCTCGT	18513
Db	17386	CTCGAGCGCCGAGCGCGAGGGCGCGCGTCTCTCGCGTGTGCGGGCTCCGCCATCAA	17445	Qy	21831	GGACGGGCGCGACTGCTCTCAGCAGACCCCG-...TACGCCAGCGCCGCTCTT	21881
Qy	20811	CCAGGACGGTGCAGACAAAGTCTGACCGCGCCCAACGGGCGCTCCAGCAGCGCGTAT	20870	Db	18514	CGCGCGCGCGCGCTCATGCGGCGCTTGCAGGCGCTGCGCGCGCGGATGCTCGGATCGG	18573
Db	17446	CCAGGACGGCGCTCCAAAGCGCTGACCGCTCCCAACGGCGCTCCAGCAGCGCGTAT	17505	Qy	21882	CGCTTTCAGGTGCGCTTCCACCGCTCTCACCGAGGCTACACATCCCGCCCACTA	21941
Qy	20871	CGCGAGCGCTCGCGCAACGGGAGCTGACCGCGCGCGACGTCGATGGGTGAGGGCCA	20930	Db	18574	CGCCACCGAGGAGGAGTCAACCCCGCGCTCAACCGAGCGTCTCGATCGCGCGCTCAA	18633
Db	17506	CGCGCGCGCTGAGAGCGCGCCACTCACCGCGCGCGACATCGACGCGCTCGAGGGCCA	17565	Qy	21942	CTACGGCGGACACTCTCTCGCGGAAATCACCGCGCGCTCTCGCGCGGCTCTCTCACCT	22001
Qy	20931	CGGACCGGACCACTTTGGCGGACCGCATCGAGCGCCAGCGCATCTCGCGACTACGG	20990	Db	18634	CGGGCCACCTCGTCTGTCGCGGCAACGAGAGCGCTCGCGCGATCGGGGCGG	18693
Db	17566	CGGACCGGACCACTTTGGCGGACCGCATCGAGCGCCAGCGCTCTCGCGACTACGG	17625	Qy	22002	CACGAGCGCACCGCTCATACCAACCGCGCACCTCATGCAAAACCATGCCCCCGG	22061
Qy	20991	ACAGGACCGTCCCGGCAACGGGCGCTTGTGCTGGGCTCGTCAAGTCCAACTCGGACA	21050	Db	18694	CTTACCGCGCAGGACCGCAAGACCAACCGCGCTCGCGGTGAGCACGCTTTCACCTCGCC	18753
Db	17626	ACAGGACCGGC-----GCGGCGCTGTGCTCGGCTCGGTGAAGTCCAACTCGGCA	17679	Qy	22062	CACATGACCACTCTCACACCAACCCACACACATCACCCACCATCTACCGCGCCACGA	22121
Qy	21051	CACAGCGCGGGGGCGTGGCGGAGTATCAAGATGTGTATGGCCCTCGCGACCG	21110	Db	18754	GCTATGACCCGATGCTGGGGAATTCGCGCGCTGCGCGCGGCGCTGACCTACCAAGA	18813
Db	17680	CACCGAGCGCGCTCGGTGCGCGCGGTGATCAAAATGATATGCGGTTCGAGCGCGG	17739	Qy	22122	AAAGGACTCGCCCATCGCGCCATCAACACCCCGC-----	22157
Qy	21111	GACACTCCACCGACTCTCCAGCGGATGACCGCTCGCGCATGTGAGTCTGTCGCGGG	21170	Db	18814	GCAGCGATCCCGTCTCTCTCAACCTCACCGGACCGCTCGCGCGCGTTCGCGCGCTG	18873
Db	17740	CGTGTGCGCGAGCTGTGACGCGCACCAGAACCCACACAGGACGTGTGACTGACCGCGG	17799	Qy	22158	-----CTCCCTGCTCATCAGCGGCGAC	22178
Qy	21171	TGCGGTGAGTGTGACGAGACGGTGCCTGCGCGCGGGAGGGGCGCGCGCGCGGCGG	21230	Db	18874	CTCGCGGACTACTGGGTGCGCGCATCGTCCGAGGCGGTCTCGGTTCCGCGCGCGTAC	18933
Db	17800	CTCGGTGACCTCTCGACGAGACGGTGCCTTGCGC-----CGAGACCGGACGCGCGCGG	17856	Qy	22179	CCCCCACACCGTCCAAACATCACCAACCG-...TC	22209
Qy	21231	GGCAGGAGTGTATCATTTTCGGGGTTCAGGGGACCAACCGCCACGTCATCTCGAAGAGC	21290	Db	18934	CGCGCTCACCGACCGCGCGGTGACCGCTGTCGAACTCGCGCGGCGCGCGCGGTGCTGTC	18993
Db	17857	CGCGGGGTCTCTCTTCGCGCATCAGCGGACCAACCGCCACGTCATCTCGAACAGCG	17916	Qy	22210	TGCCAAACAAAGGACATCAAAACCAAAACCTCTCCCG-...AC	22247
Qy	21291	ACCGCGCGAC-----GAGTTTCGGGGGAGCACCGCCCGCGACGAGG	21331	Db	18994	CGCATGGCCAGGAATCCCTGCGGAGCGGCGCGCGCGCTGCGGTGCTGCGCAAGGA	19053
Db	17917	CCCCACCGCCCCGAGAGCCACACCGAACCACACCGTCTCGCGCGCGCGCTGTCGCGGTG	17976	Qy	22248	CAACACCGCTTCACCTCCCGCCACACCAACCGCATCTCTCAACCTCACCAACGACAC	22307
Qy	21332	ATGCGGTGAGTGGGAGGAGGTGTGTCGCGGAGTCTCTGGGGTGTGGCGGTGGGTGTG	21391	Db	19054	CGCGCGCGGAGGTCTCTCGCGCTGACCGGCTGGCGCGCGCGCGCGCGCGGTGCTGTC	19113
Db	17977	GGCGTCTCCGCGCGACGCGCGCGCTTCGACGCGCCAGCGCGCGCGCGCTCACCGGCA	18036	Qy	22308	CCAAACCTCACCTACACACCCACACCGCTCATCACCGCGGACCGCGCGCGCGCGCGG	22367
Qy	21392	CGGCAAGTTCGAGCGCGCGCTTCGCGCGCCAGGCGCGAGCGCGCTGCG-...ACGCGCA	21443	Db	19114	GGTCCGTGGCGCGCGCTCTTTCGAGCGGCAACCGCGCGCGCGCGCGCGCGCGCGCGG	19173
Db	18037	CCTCGCGACACCGCGACCGCGACCGCGCTCTCGAGCTCGGCTACCGGCTTCGCGGAGCG	18096	Qy	22368	CCAACTCTCACCGCGCGCTTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22427
Qy	21444	CCTACCGACACCGCGCGCTTCGCTCGCGAGTTCGCGATACCTCTCGCGCGCGCGCGG	21503	Db	19174	CCCTTTCAGGACCGAGGGTCTTGGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG	19233
Db	18097	CGCCACCTTTCGAAACACCGCGCGCTCTGCTCCCGAGCGGACCGGACTCTGACCTCGG	18156	Qy	22428	CAC-----CACCAGAACCTCTCCACCAACGCGGCTCACCACTTACATCGAACTCGG	22478
Qy	21504	CGCGGTGTTGACACCGCGCGCACCTCTCATCGCGCGCGA-----	21542				



Db 14878 GCCGCGCTGACCGCGCCCTGTGTGGTCTGTGACCCCGGGCGCGTCCGCCACCGCGCGCGAC 14937  
Qy 18628 GACCCCTCTCACACACCCCAAGCCCAAACTTGGGGACTCGCCCGGACCACTCTCTC 18687  
Db 14938 GAGCCCTCGACAGCCCGGCGCCCTGTGGGCTCGCGGGTGTGGCCCTG 14997  
Qy 18688 GAAACCCGACCCACCGCGCGGAATCATGTGACTCTCCGACACACCCCGGCGCGGCGG 18747  
Db 14998 GAAACCCCGGACCGGTGGGCGCGGCTGTGACTCTCGCGCGGCGGCGGCGGCGGCGG 15057  
Qy 18748 CTCACACCTTACCCAAACCTTACCCAAACCCCAACCCCAACCCCAACCTTCCGCTCCG 18807  
Db 15058 GGGGCGCGCTTACCGCGCTGTCTCGCGACCCCGCGGTGAGGAACTCTCGCGTCCG 15117  
Qy 18808 ACCACGGGACCCACACCGCGCGCTTACCCCGGACCCCGGCGGCGGCGGCGGCGG 18867  
Db 15118 GCCACGGGCTGTCTCGCGCGGCGATGTGTGACGCGCGCGGCTCGCGCGCGGCGG 15177  
Qy 18868 CCCACCCCGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18927  
Db 15178 GCGCGTGGCGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15237  
Qy 18928 CACTTACCCGACCTTACCAACCCACCAACCCACCCGCGGCGGCGGCGGCGGCGG 18987  
Db 15238 GGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15294  
Qy 18988 ACCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19047  
Db 15295 CGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15354  
Qy 19048 CACTTACCTTACCACTTGGGACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19107  
Db 15355 CGGTCACCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15414  
Qy 19108 ACCATCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19164  
Db 15415 GACTTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15474  
Qy 19165 GAGCGCACTTACCACTTACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19224  
Db 15475 GAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15534  
Qy 19225 CACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19284  
Db 15535 ACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15594  
Qy 19285 TACTTCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19344  
Db 15595 TTCTCTCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15654  
Qy 19345 GCCTACTCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19404  
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Qy 19405 GCCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19461  
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Qy 19462 CGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19521  
Db 15775 CACCGCAAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15834  
Qy 19522 ATCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19581  
Db 15835 CTGAGAGACGACGACACCCCTCGCGGTGACCTTCTGAGCTGGGAGGCGGCGGCGGCGG 15894  
Qy 19582 GTTCTCTCC-----AGCAAGTCTGTGGTCTGTGCGGAGGCGGCGGCGGCGGCGGCGG 19633  
Db 15895 AGCTTACCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15954  
Qy 19634 GAA-----CTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19683  
Db 15955 GTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 16014

Qy 19684 CGGCAACTCTCTCATGGTCTGCTACGTTTCGAGCAGGAAGAAGAGCTGCTCAGCCTCGTC 19743  
Db 16015 CGCGCCACCTTGGAGGAGCTGTCTCGCGCGCGAGCGCGCGCGGCGCTTGGTCGAGCGGCTC 16074  
Qy 19744 CGCATTCATCTCGCGGCGGAGTCTCGGGGCGGAGCACTTCGAGGGGCGATCCCGCGCGGTCGG 19803  
Db 16075 CGCGCGGAGGCGTCCGGGACCTTCGGCGACACACCCCGCGAGCGCATCCCGCGCGCGCT 16134  
Qy 19804 CTGTTTCAAGGATCTAGGTTTCGACTCTGCTTTCGCGGCTGGAGCTTCGCAACCACTCGCA 19863  
Db 16135 GCCTTTCGCGAGCTCGGCTTCGACTCTGCTTACCCTGCGTTCGAACTGCGAACCGGCTGCGC 16194  
Qy 19864 GCACAGAGGAGCTGGCTTCTCGCGACGACTCTCGTCTTCGATTATCCCGAGCGCCACCAAG 19923  
Db 16195 ACCGCGCTCGGCTCGGCTCGCGCGCGGCTCTCTTCGACACACCCCGCGCGCGGCGG 16254  
Qy 19924 CTGCGCCAAATTTCTGCTCTCGGAGATCGCGAGTTCGAGCGCGGCAACTC----- 19973  
Db 16255 CTGCGCGGCGGCGGCGGCGGCTCTCTTCGCGACCGCGCGCGGAGCGCGGCGGCGGCGG 16314  
Qy 19974 -----AATCTCGGCTTCGCGA----- 19989  
Db 16315 CGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 16374  
Qy 19990 ----- 19989  
Db 16375 CTGCGCAAGGCGGCGGCTCTCTCGACATGGTGTGAACTCTCGCGGAGGAGCGCGGCGG 16434  
Qy 19990 ----- 19989  
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Qy 19990 ----- 19989  
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Qy 19990 ----- 19989  
Db 16555 CACGAAACCGGCAAGTAAGTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 16614  
Qy 19990 -----CGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 20030  
Db 16615 GCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 16674  
Qy 20031 GGCTGTGCTTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 20090  
Db 16675 CGGCTGCGGCTTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 16734  
Qy 20091 CGAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 20150  
Db 16735 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 16794  
Qy 20151 CGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 20210  
Db 16795 CGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 16845  
Qy 20211 CGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 20270  
Db 16846 CGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 16905  
Qy 20271 CCGCGCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 20330  
Db 16906 CCGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 16965  
Qy 20331 CCGCGCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 20390  
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Qy 20391 CGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 20450  
Db 17026 CGCGGAGGCTCATCAAGCGGCTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 17085

QY 16420 GGGAGGGGGCGCTCGCGGGGAGAGGTGTATGTTTCGGGTTCAGCGGCACCAACGCC 16479  
DB 12886 GAGAGCGGGCGCCCCCGCGGGCGGTGTCTCTCTGTTTCGGATCAGCGGCACCAACGCC 12945  
QY 16480 CAGGTATCTCTGGAAGAGCACCAGCCGACCAACATCTCCGTGAGACACACCAGCGGAGAC 16539  
DB 12946 CACCTGATCTCTGGAAGAGCGCCCGGCCACCAAGCGCC----- 12982  
QY 16540 GCGCGGAGAGAGCGCGCGAGCATGTTTCGGGGGAGCGCGCGGAGCGAGCGCGGT 16599  
DB 12983 -----CAGCGAGACCGCGCGCTTCGGGGACACCGCGACCGAGCATCGTTCG-- 13027  
QY 16600 ACCGCGGGGAGGAGTGTCTCTCTCGCGGAGTCCAGGGGTGTGCGCGGTGCTGTG 16659  
DB 13028 -----TCCCTTGGCGGCTC 13041  
QY 16660 TCGGCAAGTTCGAGCGCGCTTCGCGCGCCAGGCGCCAGGCGCTTCGACGCGCACTTACC 16719  
DB 13042 GCGGCAAGTTCGCGCGCGCTTCGCGCGCCAGGCGCGCGCGCTCTCTCGCGACCGTTCGAG 13101  
QY 16720 GACCAACCGGCGCTGACCTTCGCGAGCGTTCGGGTACACCTTCGCGCACCGCGCGCGGTG 16779  
DB 13102 CACGACCGCGGAGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13161  
QY 16780 TTGCAACCGCGCGCGCTTCATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16839  
DB 13162 CTCGGAACCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13221  
QY 16840 GCATCTCGCGGAGGAGAACCCACACCCCGCGGTTCATCCAGAGCGCGCGCGCGCGCGCG 16899  
DB 13222 GCGCTGTCCACCGCGCGCGCTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13281  
QY 16900 GGGACCGGGAGGCGCGAGGAAGACCATTCATCTGCTTCGCGAGCGGCGCGCGCGCG 16959  
DB 13282 GAGGAG-----CGGTCTTCGCTTCCTCCCGCGCGCGCGCGCGCGCGCGCGCG 13323  
QY 16960 CCGCGCATGGCGCGCTTCACACACACCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCG 17019  
DB 13324 TGGGAATGGCGCGCGCTTCCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13383  
QY 17020 ATCTGCAACCGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17079  
DB 13384 TCGCGAGCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13433  
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DB 13434 -----GGCGCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13473  
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QY 17260 CTCGCGCGCGCGCTTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17316  
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QY 17317 CTCATGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17376  
DB 13651 CTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13710  
QY 17377 ACCCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17436  
DB 13711 ACCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13770  
QY 17437 TCCCTGCTATCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17496  
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DB 13831 CAGGCGGTTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13890  
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DB 13951 CCGTTCTACTCTGAGGTTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14010  
QY 17677 CAAGCGCGCAACCGGTTCGACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17736  
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DB 14071 GCGGACACCGCGCTTCATTCGAGGTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 14130  
QY 17797 CCAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17856  
DB 14131 GAGACGAGGAGCGCGGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14190  
QY 17857 CTCTTCAACCACTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17916  
DB 14191 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14250  
QY 17917 CACAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17976  
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Qy 14326 CAGGCGATCAAAACAAACCTCCCGACCAACCGCTTCCATCCCGCCCGACCAAC 14385  
Db 10789 CGCACCTCGCGACCGCTATCCACCGCGCGCATCGAGCTGTCGCGCTCCCGAC 10848  
Qy 14386 CCCATCTCAACCACTCCACAGACACACCAACCTCTCCTACCAACCCACCCACAC 14445  
Db 10849 ACCACGCGGAGGTTCCGCGAGCTGTGACGCAAGGTACCGGCGACGATCTC 10908  
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Db 10909 GACGAACTGCTCGACGACGCGAACTTGACGACTTGTCTGTACTCTCACCGCGC 10968  
Qy 14506 CAGCGCGGAACACCGTGCATAGCGCACACCAACCGCTTCCACCAACAGGCGTC 14565  
Db 10969 ATGTGGGCGAGCGGCTGACCGCGCTACGTGCGCGCAACGCTATCTGTCCGCGTC 11028  
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Qy 14863 GAGCAAGCCACGACCCCATCAACCCCGCTGCGTATGTCCTGTGGGCAAGTCTCCGAC 14922  
Db 11329 GACCCCGGCGCGCGCGACGCGCTGCGCGCGCTGCGCGCTCGCGCGCGCC 11388  
Qy 14923 GAGCGAGACGAGAGTGTGGCGCTGTGGCGACCAATGGCGCGCTGTGCTGGCGCAT 14982  
Db 11389 GAAACGAGACCGGCTGCTCTACCTTGTGCGCACCGAGGCGCGCGCTCTCGGCGAC 11448  
Qy 14983 GCCACTCCCGAAGTATCGTTCCGAAACAGGCTTCAAGAGCTGGGTTTTGATTCTCTC 15042  
Db 11449 GCCTCGGCGAGTCTTCCCGAGGCGCGCGCTTCCGTGACCTCGGCTTCGATCGGTG 11508  
Qy 15043 GCGCAATTCAGCTTCTGPAATCGACTGTCTGCTGACGTTGACCTCGCGCTTCCGCGCACG 15102  
Db 11509 ACCCGGTGGACCTTGGCAACCGGCTGTGCGCGCACCGGACTCGGCTGCTCGACG 11568  
Qy 15103 CTGATCTCGATTACCCACTCGATGGCGCTTTGCGATGTTCTTCGCGGCGCGATCGTC 15162  
Db 11569 ATGCTTTCGACCAACCCCACTGCGCGCGCTGCGCGCGCTTCTTGAAGACACGCGCGTC 11628  
Qy 15163 GGAGCGGACACGACGACGAC---CACTCTGCTCCGCTACTCGGCTCC---CCGCGACGAG 15219  
Db 11629 GCGTCCCGGCGCGGACCGGAGGACGACCGCGCTACCGGCAACCGCGCGGACGAGAC 11688  
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Db 11749 CTGTGCGGCTCGCCCTCGACGGGCGGACGATCATCTCGGAGTTCCCGCGGACCGCGGC 11808

Qy 15340 TGGACCTCGACACGCTGTACAACCCGGAACCCGGAACCAACCGAACCAGCTACACCCGG 15399  
Db 11809 TGGACGCGCGGCGCTGTACGACCGCGGACCCGACCGCGCCGCGCACACCTACTCCGTC 11868  
Qy 15400 AGCGCGGATTCCTTTAGGACGAGGCAATTTGATCCGACTTCTTCGATCAGTCCG 15459  
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Qy 15460 GTCGAGCACTGGCGATGGAGCCCGACGAGCGGCTGTCTGGAAACAGCGTGGAGAGC 15519  
Db 11929 GCGAGGCGGTTCGCATGAGACCGCGAGCGGCTCTCTGTGGAGACCTCTGGAGGCG 11988  
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Qy 15700 CTGGAAGGTCCGCGCTTACAGTGCACACTGCTCTCTCTGCTCTCTGCTCTCTGAC 15759  
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Qy 15820 GTGATGTCAACCCCGCGGCTGCTGAGTGTTCGCGGCGAGCGGCGCTGCGCGTGGAC 15879  
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Qy 16180 GCGCTCTCGGCACTACGAGAGGAGCGCGCGCGCGCAACGAAACGCTGTGCTGGGTGCG 16239  
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Qy 16240 ATGAAGTCAACATCGGCGACGCGAGGCTGCGCGAGGTGTGGCGGGGTCTCATCAAGATG 16299  
Db 12709 GTGAGTCAACATCGGCGCACACCGAGCGCGCGCGGTCTGCGCGCGCTCATCAAGATG 12768  
Qy 16300 GTGATGCGGTGCGGAATGCTCTGCTCGCGGAGCTGTGATGTGATGAGCGGTCTCGCG 16359  
Db 12769 GTGCTGCGCATGAGCGCGCGGAACTGCGCGGACCTGCGGACCTCGACGCGCGCTCCAGC 12828  
Qy 16360 CATGTGAGTGTGCTCGGCGGCGGTGAGCTGCTGAGGAGAGGCTGCGCTGCGCGCGCG 16419  
Db 12829 CACGTGAGTGGACCGCGCGCGGTGGAATCTGCTGCGCGGCGCACCCCGGTGCGC---C 12885







Qy	7756	GCCGTGTTTGAACACACGCGGCCACCTTCATCGCCGCGGACCGCGACAGTTCCTGCAAGCA	7811
Db	4279	GCCGCGCTCGCCACACGCGGCGGTCTCTCTGCCGCGCGCGACCGCGCGGACGCG	4338
Qy	7816	CTCCAGGCACTCGCCGAGCGAGCCACCCCGCGGTTCATCCACAGCAGCGCCCGGGC	7875
Db	4339	GTGAG-----CAGCGCCGCGGTGGGCGCCACAGCGCGCG-----	4374
Qy	7876	GGGACCGGGACCGGGGAGCGCAGGAAAGACCGGCATTTCATCTGTCTCCGACAGGGCAC	7935
Db	4375	-----ACCGCGCTCTCTCTTCGCGCCAGGCGAGC	4404
Qy	7936	CAAGCCCCGGCATGGCCACGGGCTCTACACACCGACCCCGTCTTTCGCGCGCGCACTC	7995
Db	4405	CAGCGCCGGGCATGGGCGCGAACTCGCGCGCGGTCTCCCGTGTTCGCCGACGCACTG	4464
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Qy	8056	CAAAAAGCAAAAGCAACGAGGACGGCGCGCGCACTGTCTCAGCAGACCGCGTACGCCAG	8115
Db	4525	GGCACCGAC-----GCCGCGCTCTTGACCGGACCGGCTGGACCCAG	4566
Qy	8116	CCGCGCTCTTTCGCTTCGAGTGCGCCCTCCACGCGCTCTCTACCGAGCGGTACCAACATC	8175
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Db	4624	ACCCCGCACTTCGTTCGCGCGCACTCCGTTCGCGGAGATCGCGCGCGCCACGTCGCGCGC	4683
Qy	8236	ATCTCACCTCTACCGACGCGCACACCCCTCATCACCAAGCGCGCCACCTTCATGCAAAAC	8294
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Qy	8413	ATCAGGGCACCCCGCACACGCTCCAAACATACACCACTCTGCGCAACAAAGGCATC	8472
Db	4855	GTCCCGGAGCGGAGACGCGTTCGGCACTGACCGCGCTTCGCCGACCGGCGCGG	4914
Qy	8473	AAACCAAAACCTTCGCCACACACGCTTCATCTCCCGCCACACCAACCCCATCTCTC	8532
Db	4915	CGCACGCGGCTGGCGCTCTCGACGCTTTCACCTCGCGCTGATGGAGCCCATGCTC	4974
Qy	8533	AACCACTCCACGACACACCAAAACCTTACCTTACCAACCCACCCACACCCCGCT---	8588
Db	4975	GAGCGCTTCGGGAGCTGCTGAGCCGACTGACCTTCCACGAGCGGTGATTCGCGCTGTC	5034
Qy	8589	-----CATCACCGCAACACCCACCGGACCAACTCTCTCAACCCCGCACTACTGGACCCAA	8643
Db	5035	TCCNACTTCAGGTGAACCTTCGCGGAGTGAATACAGCGCGGAGTACTGGGTCCGG	5094
Qy	8644	CAAGCCCGCAACCGCTGCACTACGCCACCAACCAACCCCTTCCACCAACGCGGCTC	8703
Db	5095	CAGTCCGCGACACCGTCCGCTTCGCGGACGGCATACCGACTGGCCAAAGGCGGCGCC	5154
Qy	8704	ACCACTTACATCGAACTTCGAGCCGACAAACCTTACACCTTACACCTTACCCACCAACCTC	8763
Db	5155	GAGTCTCTGATCGAACTTCGCGCCCGGCGGCTGTGTTCGCGATGGCCCGCGACACCTC	5214
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Db	5275	GCCTTCGCGCGGCCCTTCGCGCGCGCTGCGACACCCCTCGGCGGTCCCGGTGCACTGGCGCGCC	5334
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Db	5335	TTCTACGCGGCAACCGCGCGCGTGAACCTGCCACCTACGCTTCCAGCAGCTG	5394
Qy	8944	CATCTGCGTGAAGCAACACACCGCGGTGCGGCAACGTGTAGACGCGGACCTGAC	9003
Db	5395	CGCACTG-----GCCACCCCGCGCCGCAACCGCGCGCGCGCGCG	5439
Qy	9004	CCACCGAACACCCCTACTCGGCGGCAATTCGAACCTGCGACTGACGCTGAGCGCTT	9063
Db	5440	GCCTTCGCGCACCCCTGCTCGCGTCCGCGTGAACCTCGCCAGCGCGCGGACCGCTC	5499
Qy	9064	CTTGACAGGCGCTTGCTTTGAGGTGCATCCGTTGGCTGGCTGACCATGCGCTCGCGCGC	9123
Db	5500	TGCTCCGCGCCTCTCCCTCGCACCCACCCCTGGCTCGCCAGCGCGCGGACCGCTCGCGG	5559
Qy	9124	ACGGTGTGTGTGCGGCGCACTTCTCTCGAACTTGCCCTTCATGCGGCGCATACGCTG	9183
Db	5560	CGGTCGTGTGCGCGCAACCGCGCTGCTGGAACCTGCGCGTGGCGCGCGGACGAGCGC	5619
Qy	9184	GGCTGCGACCGAGTGAATGAGCTGACGCTGCATGCGCGCTGTGTGTTCTGTGTGATGGG	9243
Db	5620	GGCTGCGACGTCCTGCGACGAACCTCCACCTCACACCCCGCGCGCTGCCCCAGACGCC	5679
Qy	9244	GGTGTGAGTGTGCAGGTTGGGGTTGCGGCTGCGGATGGGAGGGCGCGCTTTTGGTGAGT	9303
Db	5680	GCCTTGACGTCAGGTGACGTCGCGCCCGCGACACACCGGCGCGCGCGCTCACC	5739
Qy	9304	GTGTATGCGCGGGTGGAGTGCTTGTGTGGGGTGTGCTGCGGTGGGTGTGTGACG	9363
Db	5740	GTCCACACCCGCCCGACACCAACCGCGCGCGGACTGGAGCCGATGCGGCACCGGCAAC	5799
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Db	5800	CTCGGACGAC-----CCGCGCTGTCGACGCCAAGCCGCCACCGGCGCGCAC	5847
Qy	9424	GCGGGGTGTGCGCGCGCGGGTGGCGGTGGATGCGATGGTGTCCGTGACCGT	9483
Db	5848	CGGCGCCCTGCGCGCCCGCGACGCGAACCCCTCGACCTCGCCGACCACTACGACCG	5907
Qy	9484	TTGCTCGGGCTGCTGTGTGTTTTGGGCCCGGTGTTTTCGGGGTGTGCGGTGTGCGGT	9543
Db	5908	CTGCGGACCGCGGCTTCGACTACGGGCCGACCTTCGCGGCTGCGGGCGCGCTGCGCA	5967
Qy	9544	GATGGGGGATTTGCTGGCTGAGGTGTGCTGCGGAGAGGCGGTGGGTGTATGCGGCT	9603
Db	5968	CGCGCGCGGAGATCTTCGCGGACGTGGAAATGCCCGCCCGGCAACCGCGGACGCGCCC	6037
Qy	9604	GGTTTTGGGTGCAATCGCGGCTTGTGCGATGGTGTGTGCA-GCGCTGTGCGGTGTGCT	9662
Db	6028	GACACGGACTGCAACCCCGCTCTCTCGACGCGGCCGCGACGCGGCCATGGCGGTGAC	6087
Qy	9663	TCCGGTGGGACGCGGTTTGGGAGGGGCGGGTTTCGGGAGAGGTGTTGCGGTGCCGCG	9722
Db	6088	GGCACCGTGCCGTCGCTGGCACGGGTCGCGCTGACCGGTGCGCGCCACCGCGCTG	6147
Qy	9723	TGTGTGGGTGTGTGTGCTTACCGGGCGGGTG-----TGACCGGTGTGCGGGTGGT	9777
Db	6148	CGGTCGCGCATTCGCGCCACCAACACCGGACGCTGACCTCATCCGCGGTGACGCTGCAC	6207
Qy	9778	GTGTGCGCTGTGCGGCGGGCGGCGGCGGTGAGCGGTGTGCGTGTGTTGCGGGATGAG	9837
Db	6208	GGCGCGCGGTGTGTCACCGTGAAGCCCTCACCCCGCGCGCTGACCGAGAGAACGC	6267
Qy	9838	GCGGGTGTGCGGTGGGTGCGTGCATGCTGCTTGTGAGTTGCGGCTGTGGATATGGGTG	9897
Db	6268	GCCGCCCGGACGCGCGGACGCGCGGAGCGCGCGGAGACGCCCGCGACGCCCGCGGCC	6327
Qy	9898	TTGCGTGTGTCTCGGTTTCGCGGGGCGCGGGGTTGCGTGTATGCGGTGCACTGGGCT	9957

Qy	29831	GGCCGCTCCGCACTGCCGAGCTCTGGCGCTGTTCGACGCGGCTTTGGCCGACGCGCGAGC	29899
Db	39737	GGTTCCTGGAGATGGGCAAGACCGACATCCGGCGCGCGGACTCCGTTCCCGACGCGCTCT	39796
Qy	29891	CGTTC 29896	
Db	39797	CCTACC 39802	
RESULT 11			
AX211705			
LOCUS	AX211705	65140 bp	DNA linear PAT 06-SEP-2001
DEFINITION	Sequence 1 from Patent WO0159126.		
ACCESSION	AX211705		
VERSION	AX211705.1	GI:15523937	
KEYWORDS			
SOURCE	Streptomyces noursei.		
ORGANISM	Streptomyces noursei		
	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;		
	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.		
REFERENCE	1 (bases 1 to 65140)		
AUTHORS	Zotchev, S.B., Sekurova, O.N., Fjaervik, E., Brataset, T., Stroom, A.R., Valla, S., Ellingse, T.E., Sletta, H.V. and Gulliksen, O.M.		
TITLE	Gene cluster encoding a nystatin polyketide synthase and its manipulation and utility		
JOURNAL	Patent: WO 0159126-A 1 16-AUG-2001; Norges Teknisk Naturvitenskapelige Universitet (NO); STIFTELSEN IND OG TEKNISK FORSKNING VED NORGES TEKNISKE HOGSKOLE (NO); ALPHARMA AS (NO); Sinvent AS (NO); Zotchev, Sergey Borisovich (NO); Sekurova, Olga Nikolayivna (NO); Fjaervik, Espen (NO); Brataset, Trygve (NO); Stroom, Arne Reidar (NO); Valla, Svein (NO)		
FEATURES		Location/Qualifiers	
source	1. .65140	/organism="Streptomyces noursei"	
	/db_xref="taxon:1971"		
	/notes="ATCC 11455"		
BASE COUNT	8270 a 25171 c 22273 g	9426 t	
ORIGIN			
Query Match	12.3%;	Score 3777;	DB 6; Length 65140;
Best Local Similarity	51.4%;	Pred.No. 2.6e-307;	
Matches 12853;	Conservative	0; Mismatches 10415;	Indels 1737; Gaps 109;
Qy	6256	GAGCCGATGCCATCGTTGGCATGGCTGTCTGTTTCCCGCGGAGTGACCTCGGCGGAC	6315
Db	2827	GACCGGTGTGTCTGTCGGAATGACCTGCGTTATCCGGTGGGTGCGCGGCCGAG	2886
Qy	6316	GACTTCGGGATCTGATCTCTCCGAGCAGGACGCGATCGGGGATTCCTCCACCGACCGC	6375
Db	2887	GACTCTGGGAACTGTGTCGACACCGCGCGGACGACACCGCTTCCCGGACGACCGC	2946
Qy	6376	GGCTGGGACCTGGACAGCTCTACGACCCCGACCCCGACACCCCGGACCTGTCTACAC	6435
Db	2947	GGCTGGGACCTGGCGCACT-----GGCGCGGACGACCCCGCGCGCGGACCC	2997
Qy	6436	CGAAACGGCGGATTCCTCTACGACGACGCGCACTTCGACGCGCGAATCTTCGCGCATCAGC	6495
Db	2998	CGCGAGGCGGATTCCTCACCGCGCGCGCGGACCTTCGACGCGCGCTTCTTCGCGATGTCG	3057
Qy	6496	CCCCGGGAAGCCCTCGCCATGACCCCGACGMA CGACTCTCTCTCGAAAACCGCTGGGAA	6555
Db	3058	CCCCGGGAGGCCGTCTCCACCGACCGCAACAGCGCTCTGCTCTGGAGACCGCTGGGAA	3117
Qy	6556	ACCATCGAACACCGCGGATCAACCCACACCTTCACGCGACCCCGACCGAGTCTTC	6615
Db	3118	GCCTGGAGCGCGCGGATCGACCCGCACTCTCTCGCGGACCGGACCGGACCGGCTTTC	3177
Qy	6616	ACCGGACCAACGGACAGGACTACGCACTTCGCGTGACAAACCGGGGCGAGTCAACCGAT	6675
Db	3178	GTCCGGCGGACGCGGCGAGACTACCGCGCGGTACACACCGCTTCGCCGACGACTTGGAC	3237

QY	6676	GGTTTGCAC	TGAC	CCGAA	CCCGCG	CAGCG	TCA	CTCCGG	TCTG	TACTCG	TACACG	TTT	6737
DB	3238	GGACACG	CCCTCA	CCGCG	CTGG	CCCGCG	TGCG	CTCCGG	TCTGCG	CTCG	CTGCG	TACG	3297
QY	6736	GGTTTTG	AGGGT	CCTG	CGGT	TGTG	GTGGA	CACGG	CTTGT	TCTCTG	TCTG	TGTG	6795
DB	3298	GGCCTCG	AAAGG	CCCGCG	CTC	ACG	GTG	CACAC	CGTCT	CTCTG	TCTG	TGTG	3357
QY	6796	CATCTGC	CTG	TACAG	GCTT	CGT	TGGG	TGAG	TGCT	CGAT	GCCT	TG	6855
DB	3358	CATCTGG	CGGT	TCG	CGC	CTT	CGCG	TGGG	TGAG	TGAC	CCG	CTT	3417
QY	6856	ACGCTGA	TGTG	CTC	CGGT	TGCT	TG	TGAG	TTTTT	TCG	CGC	AGGGG	6915
DB	3418	ACGCTGA	TG	CCAC	CCCG	CGCT	TG	TGCG	CCAC	CCG	CAG	GGG	3477
QY	6916	GACGGG	CATT	GC	AAAGG	GT	TCT	CGCG	CGCG	GGA	CGG	GA	6975
DB	3478	GACGGC	CGCT	GC	AAAG	CGT	TCT	CGC	GA	CGCG	GA	CGG	3537
QY	6976	GGGATG	CTG	TGTG	TGAG	CGGT	CT	CGA	CGCC	AT	CGA	CGG	7035
DB	3538	GGCATG	CTG	TCTG	TGAG	CA	CTT	GC	CGC	CGCG	CGC	CG	3597
QY	7036	GTGTG	CGT	GGC	AGT	GC	CGT	CAAC	CAG	GA	CGGT	TC	7095
DB	3598	GTGCTG	CG	CGCT	CG	CGCT	CAAC	CAG	GA	CGG	CGCT	TC	3657
QY	7096	GGGCG	CTC	CAG	CAG	CGT	GT	CAT	CGC	GA	GGC	CT	7155
DB	3658	GGTCCC	CC	CGAA	CG	CGT	CAT	CGC	CGC	CGC	CT	CG	3717
QY	7156	GATGT	CGA	CGG	TG	GAG	GC	CA	CGG	CA	CGG	CA	7215
DB	3718	GACATG	AT	CTG	T	GAG	GG	CG	CA	CGG	CA	CGG	3777
QY	7216	CAGGCC	CT	CT	CG	CA	CT	AC	CGA	CAG	GA	CGG	7275
DB	3778	CGGGCG	TG	T	CGCG	CT	AC	GGC	CA	GGG	CA	CGG	3837
QY	7276	TCGGT	CAAG	TCC	AA	TG	TC	GT	CA	CA	CAG	GGT	7335
DB	3838	TCCCTG	AA	TG	CC	CA	CT	CG	CC	CA	CG	CA	3897
QY	7336	ATGGT	GAT	G	CGG	CT	CGG	CA	CGT	TG	CGA	TG	7395
DB	3898	ACCGT	CT	G	AC	CT	G	CGG	CA	CGG	CA	CGG	3957
QY	7396	CCGATG	TG	CA	TG	CT	CGG	TG	CGG	TG	CA	TG	7455
DB	3958	CGCCAG	TG	CA	TG	CT	CGG	TG	CGG	TG	CA	TG	4016
QY	7456	GGCGGG	AG	GGG	CGG	TCA	CGG	CGG	CGG	AG	TG	CA	7515
DB	4017	--	AC	CG	CG	CA	CGG	CG	CGG	CGT	CT	CT	4074
QY	7516	GCCCA	GT	CA	TCT	CGA	GA	GA	CA	CCG	CG	GA	7575
DB	4075	GCCCAT	G	TG	T	CT	CGA	GA	GG	CGG	CGG	CG	4132
QY	7576	GAGGGT	G	A	CG	GG	CAG	CGA	CGA	TG	AGG	TG	7635
DB	4133	-----	CC	CT	CG	CC	CG	CA	CGG	T	CGG	CGG	4158
QY	7636	CTGGT	TG	CG	CC	CA	AGT	CG	CAG	CG	CGG	CT	7695
DB	4159	CCGGT	CT	CG	CG	CA	CG	CCG	CA	AG	CC	CT	4218
QY	7696	CTC	AC	CGA	CCA	CC	CGG	CT	CGA	CT	CGG	AG	7755
DB	4219	CTCG	CA	CA	CC	CA	CT	CGA	CT	CGG	AG	CT	4278



Qy 25496 CCGAGGGTGTGGGATGCTGCTGTGGAGCGGCTCTCCGACCGCCGTCGCAACCGGTACCC 25555  
Db |||||  
Qy 35621 CCGAGGGCGCGCGGTGCTGCTGTGGAAAGGCTCTCCGACCGCCAGCGCAACGGCCACC 35680  
Db |||||  
Qy 25556 GTGTCTTGGCGGTGGTGGCGTGGAGTGGTCAACAGGACGGTGGAGCAACGGTCTGA 25615  
Db |||||  
Qy 35681 CGGTGCTCGCGGTGGTGGCGGTCTCGCGCTCAACAGGACGGCGCTCCAAACGGCTTCA 35740  
Db |||||  
Qy 25616 CCGCGCCCAAAGGGCCCTCCAGACAGGTGTATCCGTGAGGCCCTGGCCCAATGGCGAC 25675  
Db |||||  
Qy 35741 CCGCCCCAAAGGCCCTCTCCAGACAGCGGTATCCGCGAGGCCCTCGCCAAAGCGCGCC 35800  
Db |||||  
Qy 25676 TGACCCCGGCGATGTGACACAGTGGAGGGCCACGGCACCGGGACCACTCTGGGGGACC 25735  
Db |||||  
Qy 35801 TGGCCACCGCGACATCGACCGGTTCGAGGCGCACGGACCGGACCGCGCTCGCGGACC 35860  
Db |||||  
Qy 25736 CGATGAGGCCAGGCACTCTTGGCGGCTTAGGACAAACACGGCCCCACACCGCCCT 25795  
Db |||||  
Qy 35861 CCATCGAGGCGCAGAGCATCTCGCCACTTAGGCGCAGGACCGCGCCCA-----CCGG 35914  
Db |||||  
Qy 25796 TGTGCTGGGATCCCTCAAATCCAAATCGGGCAGCACAGCGCGCGCGGCGTGGGCG 25855  
Db |||||  
Qy 35915 TGTGCTCGGCTCGATCAAGTGAACATGGGCCACACCGAGCGCGTCCGGCGTGGCG 35974  
Db |||||  
Qy 25856 GAGTCATCAAGATGGTGTATGGCCCTGCGCAACGGGCTGCTGCCACAGACCCTCCACGTTG 25915  
Db |||||  
Qy 35975 GCGTATCAAGATGATATGGGATGCGGACGGCGTCTCCCGCGGACCTCGACGTG 36034  
Db |||||  
Qy 25916 ACGAGCCACCCCGCAGTGCATGCTGCTCCAGGGCGAGTGAACACTCTGACACAAACGG 25975  
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Qy 36035 ACCGGCCCTCCACCCACGCTGACTGGACACCGGCGAGTGGAACTCTCACCGACGCC 36094  
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Qy 25976 TGCCCTGGCGCGCGACCCCGCGCGCGCGCACCGCGCGGTGTCATCATTTGGGCG 26035  
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Qy 36095 ACCGTGGCCCG-----AGACTGGAGCGCGCGCGCACCGGATCTCTCTTGGCG 36148  
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Qy 26036 TCAGCGGCACCAAGCCCGCACATCTCTCGAAGAGACACCCACTCCCGAGGACAGCGATA 26095  
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Qy 36149 TCAGCGGCACCAAGCCCGCATCTGTCGAACAGGCGCCCGGACACCGCCCGGAGGG 36208  
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Qy 26096 CCGAGCAGAACCGGCTCGCAACGCAACAGCGCTTGGCCCATCCCTCTCTTCCGTTG 26155  
Db |||||  
Qy 36209 CTGACGACACTCCGCGCGCGCACCGCGCGGACCTGCGTGGTGTCTCTCCCGCGCAC 36268  
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Qy 26156 CGGTGTCGAGGTCTGAGCGCGGTGTCGCGCGCAGGACAGCGTTGCGCAGTACG 26215  
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Qy 36269 GCGCGCCCTGCGGACACAGGCGCACCGGCTGTCTGACCACTCGACCGCCCGACGGCG 36328  
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Qy 26216 TGGCAGCCCGCGGACATGTACCTGCGGACATTTGGTGGCGGTCTGGCCCGCGCGCGG 26275  
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Qy 36329 ACCGCGGCCCAACCGCCCTG-----GACACCGGCTTCTCCTCGCCACACCGCG 36379  
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Qy 26276 CCGTACTGGAAACACG-----CGCGGTCTCTTGGCGCGGACCGGAGGAACTGGCGAGG 26332  
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Qy 36380 CCGCCCTGGAAACACCGGCTCGCGGTCTGTCACCGGACCGGACCGGACCGCGGACG 36439  
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Qy 26333 CACTGACAGCCCTGACGCGCGGAAACCCACCGCCACATCACAGGCGCACACCGCGG 26392  
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Qy 36440 CCCTGACCGCTTGGTGGCAGCGCACCGCCCGCGGACCGCCACAGAAAGACACGCGCG 36499  
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Qy 26393 GCGGTGACCGGGGGGCGTCTTCTTTCCTCCCGGACAGGGGGCGGCGTGGGCGGGGA 26452  
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Qy 36500 GACGACCCGCTGGCGG-----CCCTCTTCTCGGCGAGGCGCCAGCGCTGGGCA 36553  
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Qy 26453 TGGGCTGACCCCTGTCTACTCTCTCAACCGGTGTCGCGGAACATCGACGACGATGCGAGA 26512  
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Qy 36554 TGGGCGCGGAATCCACCGCGGTTTCCCGGTGTTTCGACAGGCGGCTCGACACCGCGGTG 36613  
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Qy 26513 AAGCCCTCACCCCTGGGTGCTGCTGCTGACCGGACATCTGACCGCGACCGCGACG 26572  
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Qy 36614 ACCTGCTCGACGCGAACTGGGCGGCGCACCTCTCGGGAAGGTGAT---CTGGGCGCACCG 36670  
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Qy 26573 ACCCGCATGGCAACAAGCCGACGTGTCCAGCCCGTGTCTTTCAGCATCATGTCTCTCC 26632  
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Qy 36671 ACGCGCGCTCAACAGACCGGCTTACCCAGCCCGCTTACCCAGCGCTGTCGCGCTCGCC 36730  
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Qy 26633 TCGCGCGCTGTGGCGTCTCTAGCGATCGAAACCGGACGGGTCTCTGGCCACTCCGAGG 26692  
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Qy 36731 TCTAACCGCTGATCGAATCTTGGGCGTTCGCCCGGACTTCTCGCGCCACTTCCATCG 36790  
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Qy 26693 GAGAAATCGCGCGCCACATCTGCGCGGCACTTCAGCTCTGAAAGACCGCCCAAAACCG 26752  
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Qy 36791 GCGAGATCGCGCGCGACGTGCGCGGGTGTCTTCTCCCTGGAGGACGCTGACGCTGG 36850  
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Qy 26753 TTGCACTTGGCAGCGCGGCACTGCGCGCGGTGACGAGCGCGGGCGCATGCGCTCACTGC 26812  
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Qy 36851 TGGCGCGCGCGCGCGGCTGATGACGCGGTGCGCGCGCGGGCGATGCTGCGCGCTCG 36910  
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Qy 26813 CCCTGCGCGCGCAGGACGTGCGAGCTCAATTTCCGAAACGCTGGGAGGCGAGTTGTGG 26872  
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Qy 36911 AGGCCACGAGGACGAGGTGAGCCGCTGTCTACCGAGCG-----CGTCCGGA 36958  
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Qy 26873 TGGCAGCCCTCAACGGCGCCCACTTCCACACCGTCTCCGGCGACACCAAGCGGTGGATG 26932  
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Qy 36959 TCGCGCGGATCAACGGCGCCCACTCGCTCGTCTCTCGGCGACGAGACCGCCACTCG 37018  
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Qy 26933 AGGTGCTGGCGCACTGACGACACCGGCTTACGGGCGAAACGCAATCCCGCTGACATAG 26992  
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Qy 37019 CCGTGGCGCGCGACTCGCGGAAACAGGGCGCGCGCACACCGGCTGCGGGTACGCCACG 37078  
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Qy 26993 CCTCCACTGCCCCACGCTCCAAACCTCCACGACGAACTCTCTGCACTGTGTGGAGACA 27052  
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Qy 37079 CTTTCCACTCGCGCTGATGGACCCGATGCTCGCGGAGTTCCGCGCGGTGCGCGAGGCC 37138  
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Qy 27053 TCACCCCGCAGCGCTCCACCGTTCCTTCTCCACCGTGGAAAGGACCTTGGCTGGACA 27112  
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Qy 37139 TGTCTAGGCGGACCGCAGATCCCGGTGTCTTCAACTCTACCGCGCGGTGCGCGAGC 37198  
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Qy 27113 CCACAAACCTTGGAC---GCGCGCTACTGTGACCGAACTTCCACAGCGCGCTCGCTTCA 27169  
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Qy 37199 GCACCTGTCTCGGCACTGCGGACTACTGTGGTTCGCGCACGTCGCGAGCGGTGCGCTTCG 37258  
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Qy 27170 GCACGCGCATCCAGACCTGACGACGAGACACCGGCTTCTCATGMAATACGCCCC 27229  
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Qy 37259 CCGACGCGCATCCGCGCTTCAACGACCGCGGTGCGGCGCTTCTGAACTCGGCGCGG 37318  
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Qy 27230 ACCCACCTCTGTCCTCCCGCATCGAAGACACACCGGAAACACCAACGAAACATCACCG 27289  
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Qy 37319 ACGGCACTGCGC-----GCCCTGGCGCGAGCTGCGCCCGCGACCGCTCT 37366  
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Qy 27290 CGACCGGAGCTTCGCGCGGGGACAAACGACACCGCTTCTTCTACCGCGCTTGGCGCC 27349  
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Qy 37367 CCGTCCCGCTCTCGCGCAAGGACCGGAGACGAGGAGCGCGCGGTGCGGCACTGGCGCC 37426  
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Qy 27350 ACACCGACACCGGATCGGACACCGACCTGCGACCACTGCGACCACTACACCCAAACCC 27409  
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Qy 37427 GGTGTGACACCGCGCGGTCCCGGTGAGTGGACGCGGTCTTACGCGCGGACCGCGCGCC 37486  
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Qy 27410 ACCCCCAACCCCAACCGACCTCGACCTGCGCCACTTACCTTCTTCCAAACACCAAGC 27469  
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Qy 37487 ACCGAC-----CGACCTGCGGACCTTACGCTTCCAGTACGAGC 37525  
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Qy 27470 ACTACTGGCTCAACACCGGACCAACAAACCGGACCTTCAACACCGCGCTCAACCCCA 27529  
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Qy 37526 GCTACTGGCCCAAGGCCACCTACCGGCGCGCGACGACCGGCTGCGGCTGACCGCGC 37585  
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Qy 27530 CCACAGACCGCTCTTCAACCGGCACTTCACTCCCTGCGGACAAACACCACTACTCA 27589  
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Qy 37586 CCGACCAACCGGCTGCTCGGCGCGGCTGCTGCTGCGCGGCTCGGACGAGCTCTGTGCTCA 37645  
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Qy 27590 CCGGCGCGCTCTCTTCTAGCAGCCACCGCTTGGGTTCACGACACACCGCTCGCGCATGG 27649  
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Qy 37646 CCGGACCGCTGTGCTGCTGCGCACCCACCTTGGCTGCGGACCACTGCTGCGCGCATGG 37705  
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Qy 27650 TCCTCTTGGCGGACCGCGCTCTCGAACTCGCCCTTCCAAAGCGCGGGAACGGGTGGACT 27709  
Db |||||

Db	33449	CCGGCGCGC-----AAGCCGTCCTCGGCGCCTTGGCACCCGCTCGGCACCGTCTCTGGTCAACC	33503
Qy	23620	GGGGAAACCGGCGCCTTCGCGACCCACCTCACCCACCACTCACCCACCCACCAACCCACCC	23679
Db	33503	GGGGACACCGGCGCCTTCGGCGCGCAGTGCGCCCGCGCTGGCCA---AGGACGGCGCC	33559
Qy	23680	CAACACCTCTCTCAACAGCCGAACCGGCCCCACACACCCCCACGCAACAACCTCAACC	23739
Db	33560	CAGCACCTGCTCTGTCTAGCGCCGCGGCGCGGACGCTCCCGGTGCGGCGAACTGCGC	33619
Qy	23740	ACCCAACTCCAAACAAAAGCATCCACTCACCATCACCACTGGCACACAGCAACCAACCA	23799
Db	33620	GCGGAATGACGCGTTGGGACACCGACGTCACGGTGCGCGCTGCGAGCTGCGCGACCGC	33679
Qy	23800	GACCAACTCCAAACAACTCTCTCAACACATCCCGCCCAACACCCCTCTACCAACCGTCAATC	23859
Db	33680	GACCAGTACGGCGCTCTTGAGCGCGCTGCCCGCGACCGGCGCTGACCGGTGGTG	33739
Qy	23860	CACACGCGGCGTCAATCTCTTGGCCCCGTGTGCGAAACCGATGCGGAATCTCTTCTCT	23919
Db	33740	CACACCGCGCGCTCTCGACGACGCGTACTGACCGGCTCACCCCGAGCGGTTCAG	33799
Qy	23920	TCCGTTACGCGAGGAAGCAACGGGCGCGGCGATTCTGTCATGAGTTGCTGTGACCAAT	23979
Db	33800	GAGGTGTTCCGCGCCAAAGGTCACTCGCGCCCTGCTGTGACGAGCTGACCCGCGACCGC	33859
Qy	23980	GAACCGCTTGAAACACTTCTATCTCTCTGTCGGGCGCGGCGCTTGGGCGAGCGGAAT	24039
Db	33860	GA---GCTGCGCGGTTCGTCTCTTCTCTCGCTCCGCGCGGTGCGGAAACCGGGC	33916
Qy	24040	CAGTGCATATCTCGGCGGCAACGATACCTGGACGCGCTCGGACGCGATCGTCAGACA	24099
Db	33917	CAGGCCAACTACGCGCTGCAACGCGCTCTGGACGCGCTCGCGAAACGCGCGGTG	33976
Qy	24100	CATGGACTTCCGGGGCATGATCGCTGGGGCCCCCTGGGCGGAAAGGCGATGTCGGCC	24159
Db	33977	CTGGCGTGGCGCCCACTCGGTCTCTCTGGGTGCTCTGGGAGGCGGCGCATGCGCCAC	34036
Qy	24160	GGTGATCGGCTCATGTTACTTGGAAGAGCGGGCATTTCTGCGATGAGGACGCGATG	24219
Db	34037	GCGACGGCGGACGAGGCGCGCGCGCGCGCGCTCGGGCGCATGACCCGCACTC	34096
Qy	24220	GCGCTCGGCGATTCCATCGTGGCGGGCGACGCGCCGAATTTCAACCTGATCATCGCG	24279
Db	34097	GCGTGGAAGCCCTGTGTCGCTTGGTGCAG---GAAGGACCGACCGCGGTGCTGCC	34153
Qy	24280	GACATCACTGGGAGCGCTTGTCTCCGCGCTTACCGCTCGACGCAAGCGCGTCAATC	24339
Db	34154	GAGTGGCCCTGGAACGCGTTTCGCGCGCGCTTCGGCGGCGAGCCGACCCAGCGCCCTGCTG	34213
Qy	24340	GAGGACATTCGGAGGTTTCGGAAGCGGCTCAGGAGCTTGAAGCAGCTGCGTCGACGGCA	24399
Db	34214	CGGGATTTCCCGGCTACCCGAGGCGC-----TCGCGCGCC	34250
Qy	24400	AAGACGACACAGCTCAGCCGATTGGGACGTCTCTCCGTGAGCGATTGGCGCGACTGACG	24459
Db	34251	AGGCGGACGAGCGCGGACGCGCGCG---GGCTGGCGCGCGACTGCGCGCTGCGG	34306
Qy	24460	TCCTCAAGCAGAACAGGTGCTGTCGGCGTATTTCGGACAGGCATCTGACACGTTCTC	24519
Db	34307	CCGCGCCCGCGCTGGACACCGTTGTGGACCTGTGCGCACCGCGCGCGCAGGTTGCTC	34366
Qy	24520	GGCTTCGTAATTCGGGAAGCATCGAGGACCAACGAGCTTCCGCGGACCTCGGCTTCGAC	24579
Db	34367	GGCTACCCCGACACCGAAGCGGTTCGCGCGCGAAGCGTCTCTTCGCGACCTGGGTGTCAC	34426
Qy	24580	TCGCTACGCTCGGCTCAGATTTCAGCAAGGAACCTCGCCAAAGGAAACCGGACTGCCACTCCC	24639
Db	34427	TCGCTCGGCGCGTTCGAGCTGCGCAACCAACTGAGCGCGGCGACCGGCTGAACTTGGCG	34486
Qy	24640	CCGTCCCTGCTTTCGACTATATCCACCCCGCAGGAATGTGCTGCCA-----TCGCCA	24686

Db	34487	GCACGCTGGTGTTCGACCAACCGACCCCTCTGGTCTCTGGGGGAGACACATCTCTCGGCGGG	34544
Qy	24687	-----	24686
Db	34547	CTTTCCCGACGAGCCCGCGGTCCGAGACGAGACGGAGATCCGGGCCCTGCTGGCC	34606
Qy	24687	-----TCTGGGCACA	24696
Db	34607	TGGTCCCGCTCGACCAACTGGGGAGATCGGGTCTCTGGAGCCCTGCTCCAGCTCGCC	34666
Qy	24697	CAACTCGTGCACCTAGACGACGAGAGGACGGCAGCTGTTCGAATGCTCTCCCGCAAGTG	24756
Db	34667	GGACGGCGCGCGCGCGCGGACGCGGACGCGGAGTCCGTGCAGCTCATGACAGTG	34726
Qy	24757	GCCCATCGGCGTACCGTCTGAGG-----	24778
Db	34727	GCAGACCTGGTGGCGGCGCGCTCAACGGCCAGTCCGACCTGTAGCGGATTTGATGGAGC	34786
Qy	24779	-----	24778
Db	34787	AGACGATGAACGCGCCCGAGAACCCCGAGACCCCGAGAACAAAGTAGTCGCGCAGCTCC	34846
Qy	24779	-----	24778
Db	34847	GGCGCGGTCGAAAGGAGACCGACCGGCTCGCGCGGAGAACCGGATGCTGGTCCGGCGG	34906
Qy	24779	---ACGAAACCGATCGGCATCATCGGTATGGCATGTGCTTCCCGCGCGCGTACGTTCTG	24835
Db	34907	CCAAGNACCGATCGCGTGGTGGCATGGCTGCGCTTCCC CGCGCGCTCGACATCCC	34966
Qy	24836	CCGACGACTGTGGGAATTGCTCGCTTCGGGTAAAGACGCTATCGGCGTCTTCCGACCG	24895
Db	34967	CGGAAGCGCTGTGGGAGATGGTCGCACCGCACCGACGTGATCTCCGGATTTCCCGGACG	35026
Qy	24896	ACCGCGCTGGGACCTGGACAGCTCTAGACCCCGACCCCGACACCCCGGCACTGCT	24955
Db	35027	ACCGCGCTGGGACCTGGAGGCGCTGCGCAACAGCGGACCGACGCCCGGACACCGAGC	35086
Qy	24956	ACACCGGAAACGCGGATTCCTCTACGGCGGAGGCACTTCGACGCCGAAATTTCTCGGCA	25015
Db	35087	TCAGCCAGCGCGGANTTCTTGGACTGATCGCCGACTTCGACCCCGGCTTCTTCGGGA	35146
Qy	25016	TCAGCCCCCGGAAGCCCTGGCATGGAACCCCGAGAACGACTCTCTCTCGAAACCGGCT	25075
Db	35147	TCTCACCGCGGAGGCGGTCAACATGGACCCGCAACAGCGCTCTCTGTGTACACCGGCT	35206
Qy	25076	GGGNAACCATCGAACACGCGGCGCATCAACCCCAACCTCTCACGGCACCCCAACCGAG	25135
Db	35207	GGAGGCGGTGAGCGGGCGGGATCGACGCCACACGCTGCGCGCCACCCCGACCGGCG	35266
Qy	25136	TCCTGGCGGAAATCAACGCTCAAGACACGCGCGCATATCGGCCAAAGCGTATGTGG	25195
Db	35267	CGTTATCGGCACCAACGGCCAGGACTAGCCCTA CTTGCTCGTCCGCTCCCTTGGACGAGC	35326
Qy	25196	AGACCATCGAGGCTACGCCCTGACCGGCAGTTTCGGGAAGTGTGGCGTCCGCGCGGGTGG	25255
Db	35327	CCACC-----GGCGCAGTGGGCACCGGCATCGCGCCAGCGCCCTCCGCTCGGCTCT	35380
Qy	25256	CCTACAGCTCGGGCTCGAAGGCCCGCGGTGTTCGGTGGATACGGCGGTTCGTCGTGCT	25315
Db	35381	CCTACACCTTCGGCTCTCGAAGGCCCGCGCTCACCGTGCAGACACCGCTCTGCTCGTCGC	35440
Qy	25316	TGTTGGCGTTGCAATTGGGGGGCGAGCGGTTGCGTGGCGGTGAGTGTTCGATGGGGCTTG	25375
Db	35441	TGTTGGCTTGCACTTGGCCGTGAGCGCTCGGCNAACGGCGAGTTCGGCATTGGCGCTGG	35500
Qy	25376	CCGGGGGTGACGGGTGATGTGCTCTCCGGGTACGTTTGTGGAGTTCTCAGCTCAGCGGG	25435
Db	35501	CCGGCGGCTGACGATGATGGCCACACCGGGCTCGTGGTGGAGTTTCAGCGGCCAGGGCG	35560
Qy	25436	GTCTGGCCCGGAGACGGCGGTGCAAGGCCATATTCGGCGGCTGCTGACGGTACCGGCTGG	25495
Db	35561	GGTTGGCCCGGAGACGCGCTGTCAGAGCGCTTCGCGGAACGCCCGCAGCGCACCGGCTGGT	35620



Qy 21416 GGGCCAGGCGCCAGGCGCTGCAAGCCCACTACGACACACCCCGGCTTGCACCTCGCGC 21475  
Db |||||  
Qy 31395 GGGCCAGGCGCGCGGCTCTCTGGCGCGCTCAGCGCCACCCGACACCCGGGCGCGC 31454  
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Qy 21476 AGCTCGGATACACCTTCGCGCCACGCGCGGCGGTGTTGACACGCGCGCACTCCATCG 21535  
Db |||||  
Qy 31455 ACCTGGCGTACTCTCTGGCGACCAACCCGGGCGCTTCGAGCACCGGCGCGGATCACCG 31514  
Db |||||  
Qy 21536 CGCGGACCGGACACCTTCCTGCAAGCACTCAGGCACTCGCGCAGCGGAACCCAC 21595  
Db |||||  
Qy 31515 CACCGACACAGCGGCTTCGCAACCGGCTTGACCGCGCTCGCGAGGCAACCAACCGGCC 31574  
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Qy 21596 CGCGCGTATCCACAGCAGCGCCAGGCGGACCGGACCGGAGCGCGGAGCGCGAGAAAGA 21655  
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Qy 31575 CGCACCGCGGAACACACCTCC-----AGGCGACCGGAAAGC 31613  
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Qy 21656 CGGATTCATCTGTCGGAAGGCAAGGCAACCAAGCCCGCGGATGCGCAACGGCTCTTACC 21715  
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Qy 31614 GCGCGTGTCTCTCCGCGCAGGCTCCAGCGCTGCGGATGCGGCGCGAACTGACG 31673  
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Qy 21716 ACACCCAGCGCTCTCGCGCGGCACTCAAGGATCTGACCACTCGACCTCGACCCAC 21775  
Db |||||  
Qy 31674 AGCGCAACCGGCTGTCCGCGAGGCTTCGACTCGTACTGCGCGCGCTTCGACGACGCGC 31733  
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Qy 21776 TCGACCAACCGCTCTCCCGCTCTCACCACCAACGACAAACGACAAACGAGGACG 21835  
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Qy 31734 TCGACACCGCTCGGAGCGTGTGCGGCAACGACGAGG-----31776  
Db |||||  
Qy 21836 CGCGCGCACTGTCAGCAGACCGCGTACGCGCGCGCTCTCTGCGCTTCAGGTCG 21895  
Db |||||  
Qy 31777 -----GGCGGTGACGCGCAACCGGAAACACCGCGCGCTGTTCGCGCTGAAAGTCG 31829  
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Qy 21896 CCCTCCAGCGCTCTCAGCAGCGCTACACATCACCCCGCTACTACCGCGGACACT 21955  
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Qy 31830 CGCTCTACCGCTGAT-----CGAATCTGGGGGTGGCGCGGACTTCTGGCGCGGCACT 31886  
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Qy 21956 CCCTCGGCGAATACCGCGCGCCACCTCGCGCGGATCCTCAGCTCCTCAGCGCGCA 22015  
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Qy 31887 CGCTCGGCGAGCTCGCGCGCGGCAACGCTCGCGGGGTCTCTCTCGACGACGCTGCC 31946  
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Qy 22016 CCCTCATCACCGAGCGGCACTCTATGCAAAACAT-----GCCCGCGGCAACATGACCA 22072  
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Qy 31947 GCCTGGTGGCGCGCGCGCTCTATGACAGCGCTCCCGCGCGCGGCGGCGCATGTCG 32006  
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Qy 22073 CCCTCCACACCCCAACACATCACCGACACCTCAGCGCGCAACGAAAGACCTCG 22132  
Db |||||  
Qy 32007 CGCTGAGGCGACGAGGACGAGGTACCCCGCTCTCAGCG-----ACGGCGGT 32057  
Db |||||  
Qy 22133 CCATCGCGCGCATCAACACCGCGCTCTCTCGTATCAGCGGCAACCCCGCACCGGTC 22192  
Db |||||  
Qy 32058 CCCTCGCGCGGTCAACGACGACGCGCGGTGCTCTCGCGCGGCGGCGACGCGGTGA 32117  
Db |||||  
Qy 22193 AACACATCACACCGCTTGCACAAACAGGATCAAAACCAAAACCTCCCGCAACAC 22252  
Db |||||  
Qy 32118 CGCGCTGGGCGAGCGGTGGCGAAACGGGCGCACCGCACCGCGGTGGGTGAGCC 32177  
Db |||||  
Qy 22253 AGCGCTTCACTCCCGCAACACCGACCGCTCTCAACCACTCAACGACACCCCA 22312  
Db |||||  
Qy 32178 AGCGCTTCACTCGCACTCTATGACCGCATGCTGGGGAATTCGCAACGCTCGCGGAGG 32237  
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Qy 22313 CCCTCACCTACACCCACACACCG-----CCTCATACCGCGCAACACCG 22360  
Db |||||  
Qy 32238 GCCTGGATACACCGCGCGGCTATCCCGGTGCTCTCAACTCAGCGGGAAGTGGCG 32297  
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Qy 22361 CACCGACCAACTCTCAACCCCACTACTGGAACCAACAGCGCGCAACCGTGGACT 22420  
Db |||||  
Qy 32298 ACGGGCGGACCTGTGCTCGCGACTACTGGGTGCGGCACTCGCGGCACTCGGT 32357  
Db |||||  
Qy 22421 ACGCCACCAACCAACCTTCCACGACGCGGTCAACCACTTACTGAACTCGGAC 22480  
Db |||||  
Qy 32358 TCGCGGAGCGGTGCGCAACATGGCGGACCGCGGCGGTGACCTCTTCTCTGAACTCGGCG 32417  
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Qy 22481 CCGACAAACACCTTCACACACCTCTCAACCAACCAACCTCTCCCAACACCCCAACCAACC 22540  
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Qy 32418 CCGACGCGGTCTCTCGCGCATGCGCGCGCATGCGCGCACCGGACCGCGCTCG-----32468  
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Qy 32469 TCGTCCGCGCGCTCGCGCGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAAC 32528  
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Qy 22601 CCACACACCTTCGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAAC 22660  
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Qy 32529 GACTGCAAGTTCACCGGCGGCGGTTCGGCTGGGAGCGGTACTTTCGGCGCGCGCGCGC 32588  
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Qy 22661 CCCACCTGACCTCCCAACCTTACCCCTTCCAAACCAACCACTACTGCTGCAACTACCA 22720  
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Qy 22721 GCGCGCAAAACGAGCGCGGTCAAAAGGCTTCTCGCGCTCGGC--TCCAGACACCGCGCAG 22779  
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Qy 32641 --GTCCCTTCGCGCGCGCATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 32698  
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Qy 22780 TCGGAGTTCGGGACGCGGTGAACGAGGAGACCTCCAGAGCGCTCGCGGAAACCTCGAC 22839  
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Qy 32599 GCGGCTTTCGGGAGCGGTTCGACAGAGGACTTACCGGATTTGGAATTCGTAATTCGAC 32758  
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Qy 22840 ATCGACGCTCTGCTCTGGAACGCGGTGCGCGCACTCTCGCGCTGGAACCGGCAACCA 22899  
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Qy 32759 GTGAGAGCGACGCACTGTCCAGGTCTGCGCGCGCTGTGAGTGGGCGAGCGCGCAG 32818  
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Qy 22900 CAGACAGCGCGCATCAACCTGGAACCTTACAGGAAACCTTGGAACCTTACCGCTC 22959  
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Qy 32819 GCGACGAGTCCCACTGGGAGGTGGCGCGCACCGCATCTGCTTGGAAAGCGCTCACCGC 32878  
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Qy 22960 CCACACCGCACCAACCGGCAACCTGCTCATCGCATCCCGGAAACCGGCAACCGCAC 23019  
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Qy 32879 GCGCGCTTGGACACCGGAGCGCTCAGCGGCACTTGGCTGCGGTGGTCCCGAGGCG 32938  
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Qy 23020 CACCGCACATCAACCAATCTCACAAGCTCACAACCAACCGGCACTCACCGCATCCCG 23079  
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Qy 32939 TTGCGCGACGACCTCTGGGTGACCAACCGCTGGAAGCGCTCGGTACCCACTCTGTGAT 32998  
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Qy 23080 CTCACTGTAAACCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAAC 23139  
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Qy 32999 CTGAGGTGCGGAGGCGGCGCGCGCGCGCTGCGCGCGGCTGCGCGCGGCTGCGCG 33046  
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Qy 23140 CGACAAACGCGCAACCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 23199  
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Qy 33047 -----GCGCGCACCGGCGCGCGCTTTCGGCGCGGTAATCTCTCTCTGCGC 33097  
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Qy 23200 CTGACGAAACACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 23259  
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Qy 33098 CTGCGCGAGGAGCTCACCGGCGGTGCGCG-----GGGGAACCGGCTGACCACT 33148  
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Qy 23260 ACCCTCCCGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 23319  
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Qy 33149 ACCCTCTCCAGGCGCTCGGCGACCGCGGCGGTTCAGCGACCGCTGTGTGCTGCTGCGC 33208  
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Qy 23320 AAGCGCACACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAAC 23379  
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Qy 33209 AGCGCGCTCTCGCGCGCGGCAACCGGCGCGGCGGCGCGGCGGCGGCGGCGGCGGCT 33268  
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Qy 23380 GGACTCGCGCGCAACCGCTCTCGAAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCA 23439  
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Qy 33269 GGCTGGCGCGGTTCGGCGCTTGTAGTACCGGAGCGCTGGGCGGCGCTGGTGGACCTG 33328  
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Qy 23440 CCGACCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAAC 23499  
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Qy 33329 CCGGAGGAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAAC 33388  
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Qy 23500 CACCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAAC 23559  
Db |||||  
Qy 33389 GGGAGGAGCGGTTCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 33448  
Db |||||  
Qy 23560 ACCTCACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCG 23619  
Db |||||

Db	29277	CCCTAGGCGCGCCCTCAACGGCGG-----CGCTGGAGC	29312	Db	30318	AGCAGCGGATCTCTCGAACAACGTCCTGGAGGCGCTTGGAGCGCGCGCATCGACCCGG	30377
Qy	19274	CTTCTGCTCTTACTCTCTCCGCGCGCGCACTTCGGCGCAACCGCGGCAAGCAACTACG	19333	Qy	20336	ACACCTCCACGCGACCCCGACCGAGTCTTACCGGCAACAAAGGACAGACACACCGG	20395
Db	29313	CTTCTGCTCTTCTGCGCTCCATCGCGCGGCTCTGGGCGGTGCGCGCGCGCGCGGAGG	29372	Db	30378	CGACGCTGCGCGGAGCGGCAACACCGCGCTTCTGTCGGCGGCGGCTCCGGCA-----	30432
Qy	19334	CGCAGCGCAACGCTTACCTCGACGCGCTCGCCACACCGCGCAACACCACTCCCGG	19393	Qy	20396	CACACATCCGTCAGGCGCGCGAGCGGTACCGAGGATTCGTCTTGAACGGGCGAGCCACCA	20455
Db	29373	CGCGTCCGGGCGCTACTCGACGCTTCGCGCGCGCTTCGCGGACCGCGGCAACCCCGG	29432	Db	30433	-----CTACCGCGCGCGAGGAGGCGCGGCGAGTGG--CAGACCGCGCAGTCCGCCA	30482
Qy	19394	CCACAGCATCGCTTGGGCACTTCGCAAGGAAACGGAATGCGCACTGGTCAAGTACAGC	19453	Qy	20456	GCATCGGCTCGGCGGCAATCTCTACATCTCTGGTTGGAAAGGCGCTTGGTCAACCTCG	20515
Db	29433	CACTGGCGGTGCGCTGGGCGCGCTGG-----GCCGACCTGGTGGCGCGCTCTCGCGG	29486	Db	30483	GCCTGCTCTCGGTCGCTCGCTTACACCTTCGSCATCCAGGCGCCACCGCTGTGCGTGC	30542
Qy	19454	AACATCTCCGCGCGCGCGGATGTTCCGCATGCGCGCGCGCGAGTGGCGGTCAAGTGTG	19513	Qy	20516	ACACAGCGTGTCTCTCTCTCTGTCGCTCGCTCGACCTCGCTGCGAGTCTCTCAGGTCCG	20575
Db	29487	CGCACTCGGGATGAACGGCTTGCCTGATGAGACCGGACACCGCACTGACCGCGCTCA	29546	Db	30543	ACACCGCTGCTCTCTCTCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	30602
Qy	19514	ACGCGCGCATCGCAGCGCGCGCGCGAGTCTCTCTGTCGCGGATATCGACTGGAGAAAT	19573	Qy	20576	GTGAATGCACATGCTTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20635
Db	29547	GCGCGCGCTGCGCGACGGGTCCGCGCGGAGCGGTGCGCGACGTCTGCTGGGAGACT	29606	Db	30603	CGCAATGCTCGATCGCTGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30662
Qy	19574	TGGGACCGGTTCTCTCC---AGCAAGTCTGCTGCTTCTGCTGAGGACCTTCCCGAGCAC	19630	Qy	20636	CGCAATTCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20695
Db	29607	TGCGCGCTTCCACACGAGGCGCGCGCACCGCTGTTGACGCGCTGCGCGAGCGCC	29666	Db	30663	TCGAGTTTCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30722
Qy	19631	AGGGAACGTGAGGAGG-----CGCGAGTACGTTGAGCAGGAGGAGGAGCACAAC	19681	Qy	20696	CGGCTGAGCGGTACCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20755
Db	29667	GCGCGCGCTTCCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG	29726	Db	30723	ACGCAACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30782
Qy	19682	TCGCGCAACTCTCATGCGTCCGTCACGTTCCGAGCAGGAGGAGGAGTGTCTGAGCTCG	19741	Qy	20756	ACGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20815
Db	29727	ACGCGCGGTGGTTCGCCGAGCAGCGCGCGCGGCAACGAGCCATCTGCTGGGACTGG	29786	Db	30783	ACGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30842
Qy	19742	TCGCGCATCACTCCGCGGCGGAGTCTGCGGCGGCGGAGTCTGAGGCGGCGGCGGCGG	19801	Qy	20816	ACGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20875
Db	29787	TCACCGAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	29846	Db	30843	ACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30902
Qy	19802	GCTCTTCAGGATCTAGGTTTCACTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	19861	Qy	20876	AGGCGCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20935
Db	29847	TGCGCTTCGCGCACTTGGGCTTCGATCGCTGACCGCGGCGGCGGCGGCGGCGGCGGCGG	29906	Db	30903	AGGCGCTTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30962
Qy	19862	CAGCACAGAGGAGTGGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	19921	Qy	20936	CGGCGCACCTTTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20995
Db	29907	CGCGGGAACCGGCTTCACTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	29966	Db	30963	CGGCGCACGCGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	31022
Qy	19922	AGCTCGCGCAATTTCTGCTCTCGGAGATCGCGGAGTTCAGCGCGGCGGCGGCGGCGGCGG	19981	Qy	20996	ACGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21055
Db	29967	CCCTCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30026	Db	31023	ACC-----GCGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	31076
Qy	19982	TTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20035	Qy	21056	AGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21115
Db	30027	TGGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30086	Db	31077	AGGCGCGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	31136
Qy	20036	GTGCGTTCCCGCGGCGGAGTCACTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20095	Qy	21116	TCCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21175
Db	30087	GCCTGTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30146	Db	31137	TGCGCGGCTCTCTGTCGCGGAGAACCTCTGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	31196
Qy	20096	AGGACCGCATTCGGGAGTTCCCGACCGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20155	Qy	21176	TGCGAGCTGCTGACCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21235
Db	30147	TCGAGCGGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30198	Db	31197	CCCACCTGCTCACCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	31253
Qy	20156	CGGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20215	Qy	21236	GAGTGTCTATCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21295
Db	30199	-CGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30257	Db	31254	CCGCTCTCTCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	31313
Qy	20216	GCCACTTCGAGCGGAAATTTCTTCGCGCATCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG	20275	Qy	21296	CCGACGAGCTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21355
Db	30258	CGGACTTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	30317	Db	31314	CGGAGGAACTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	31353
Qy	20276	AGCAAGCATCTCTCTCGAAACCGGCTGGGAAACCATCGAAACCGCGGCGGCGGCGGCGGCGGCGG	20335	Qy	21356	CTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21415
				Db	31354	-----GCTGCGGCTTCTTGTCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	31394



Db	25338	AGCAACTCGCGAACTGCGGAGCAGGAGCGCGGAGCGGTCTGAGACCTGCTGGGTA	25397
Qy	14957	CCCATGCGCGCGCTGCTGGGCGCATGCCACTCCGAGTATGATGTTCCGACAGAGCCT	15016
Db	25398	CCCAGGTGCGCGCGCTGCTGGGCGACGCGACCGCGGACCGTCCGAGACACACGCT	25457
Qy	15017	TCAAAGAGCTGGGTTTGAATCTCTCGCGCGCAATTCAGCTTCGTAATCGACTGTGTGTG	15076
Db	25458	TCCGCGACTGGGCTTCGACTCGTGACCATCTCGAATCGGCAAGCCCTCAACGCG	25517
Qy	15077	ACGTTGACCTGCGGCTTCGCGGACAGCTGATCTTCGATACCCACTCCGATGGCGTTT	15136
Db	25518	CCACCGGCTGAGCTGCGCGCATCTCGGCGACCGCTGCTACGACTCCACCGCGCGAGATGG	25577
Qy	15137	GCCAGTTCCTCGGCGCGGATCGTGGG-----ACGGGACA	15172
Db	25578	GGGACTTCCTGTCGCCGAATCTCTCGGCACCTGCGCCACGACACCGCGGACCGTCTG	25637
Qy	15173	CAGGACGACCACTCGTCTGCGGCTAACTGGGT-----CCCGCGGACG	15217
Db	25638	CCAGACGGCTCCCGAAGCTCTCAGCTTCGTTGAGCAGGGCGGTACCCCTTCGAGC	25697
Qy	15218	AGCGATCGCATCTGCGGATGCGCTCTGCTACCGGTGATGTACGACGGTTCGATG	15277
Db	25698	ACCGATCGCGCTCATCGGCATCGGCTGCGCTTCCCGGCGGCGTCAACACCGCGAGG	25757
Qy	15278	ATCTCTGCGAGTGTGATGTTGCCATGAGCGATCGGCGGATTCGCGAGACCGTG	15337
Db	25758	AGCTTGGAGCTCTCGACGAGGGCGCGGATCAGCGCTTCCCGGACGACCGC	25817
Qy	15338	GTTGGGACTCGACACGCTGTACAAACCGGACCGGACCGACGACACCACTACACCC	15397
Db	25818	GCTGGGACTCGCGCGCTGGGGC-----CGCGGCTCCGACACCC	25859
Qy	15398	GGAGCGGCGATTCCTTTACGACGAGGCAATTTTCGATCCGATCTTCTCGGTATCAGTC	15457
Db	25860	TGAGGGCGGCTTCTGACCGCGCTCGCGGCTTCGAGCGCGGTTCTTCTGGCATCTCGC	25919
Qy	15458	CGCGTAGGCACTGGCGATGGAACCGGACGAGCGGCTGCTGTGGAACACGTTGGGAGA	15517
Db	25920	CCCGGAGCGCTGGCGATGGAACCGGACCGGCTGCTGTGGAACACGTTGGGAGG	25979
Qy	15518	GCATCGAACAACGCTTGCTCAACCGCGACAGCTCTCGTGGCACACCAACCGCGCTTCG	15577
Db	25980	CGCTGAGGGGCGGCGATCGACCGACCGCTGCGGCGCTCCACACCGCGGCTTCG	26039
Qy	15578	CCGGCTGACCTACACGACTACGCGCGGCTTTCCACAGCTCCGGGAGGGTTGAGG	15637
Db	26040	TCCGACCAACCGCGCAGGACTACCGGACGCTGTTGCGCGGCTCCGCTCGACGTTGGCG	26099
Qy	15638	GATATCTCGGCAACGAGCGGACGAGCATCGCTCGGCTGCTCGGCTACGCTCTCG	15697
Db	26100	GCTAGTCGCGCACCGGCAACACCGCAGGCTGATGTCGGCGGCTGCTACGCGCTCG	26159
Qy	15698	GCTCGAAGGTCGGGCTTCACAGTCGACCTGCTGCTTCTGCTCGCTGCTGCTGCTG	15757
Db	26160	GCTCGAAGGTCGGGCTTCACATCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	26219
Qy	15758	ACCTGGCTGTCAGGGCTGCGGTCGGGAGTGTTCATGCGCCCTCGCGGGTGGCGTCA	15817
Db	26220	ACTGGCGCGCGGCGCTGCGCGCGGAGTGGGAGCTGCTGTTGGCGCGCGCTCT	26279
Qy	15818	CGGTGATGTAACCCCGCGGTTCTGGAGTTTTCGGCGAGCGGCGCTGGCGGTTG	15877
Db	26280	CGGTATGGCGAGCGCGGACTCTTCTGTCGATCTTCACCCAGGGCGGCTTGGCACCG	26339
Qy	15878	ACGGCGGTCGAAGGCTTCTCGGAGCGGCTGACGACCGGCTGGGGTGGAGGTGTCG	15937
Db	26340	ACGGCGGCTGCAAGGCTTCTCGAGCGCGCGGACCGGACCGCTGGTCCGAAGGCTCG	26399
Qy	15938	GAATGCTGCTGGAGCGGCTGTCGAGCGCGGCGGCTCGGTCACCGAATCTCTCGCG	15997

Db	26400	GCATCTCTGCTCTGGAACGCTCTCTCGCGCGCGCGCGCAACGCGCCACAGGTCTCTGGCC	26459
Qy	15998	TGTTGGCTGCGAGTGGGTCAATCAGGACGGTTCGAGCAACGCGGTGACGCGCCCAACG	16057
Db	26460	TGATCGCGGACCGCGCTCAACAGGACGGCGGTTCAACGCGCTGACCGCGCCCAACG	26519
Qy	16058	GGCGGTCGCGAGGAGGTGTCATCCGCTGCGCTTGGCCAAACGCGGACCTGACCCCGCG	16117
Db	26520	GCCTCTCCAGCAGCGCTCATCGCCAGGCACTCGCCGACGCGCGCTCTCGCGCGCG	26579
Qy	16118	ACGTGATGCGGTGGAGGCGCACGGGACCGGACCACTTTGGGCGGACCCGATCGAGGCC	16177
Db	26580	ACATCGAGCGGATCGAGGCGCACGGGACCGGACCACTTCGGGACCGGATCGAGGCC	26639
Qy	16178	AGGCGCTCTCTGCGCACCTACGAGCAGGACCGCGCCGCAACGCGCTGTGGCTGGGCT	16237
Db	26640	GGCGCTGATCACCGCTAGCGCGGACCGGACCGGACCGGACCGGCTCTGCTGGGCA	26699
Qy	16238	CGATGAAGTCGAACATCGGCGCACCGGAGGCTCGCGAGAGTGGGGCGGGTTCATCAAGA	16297
Db	26700	CCGTCAAGTCCAAATCGGCGCACCCAGGCGCGCGCTGCGCGCGCTCATCAAGA	26759
Qy	16298	TGTTGATGCGCTCGGGAATGCTCTGTCGCGGAGGCTTGCATGTGATGAGCGCGTCCG	16357
Db	26760	TGCTGATGGCGATTCGCGCACCGGACCGCTGCGGAGGCTGCGAGTGGGACCGCGTCCA	26819
Qy	16358	CGATGTGGAATGCTGTCGCGCGGCGGCTGCTGTCGAGAGAGCGGTCCTTGGCGCG	16417
Db	26820	GCACGTCGATGAGGCGGCGGACCGCTCGCGCTCTCTGAGAGCGCGCGCTTGGCCAC	26879
Qy	16418	GCGGGAGGCGGCTGCGCGCGGCGGAGTGTCTATGTTTGGGCTCAGCGGACCAACG	16477
Db	26880	---GGACCGGCGAGCGCGCGCGCGCTCTCGCGCTTTCGCGCTCAGCGGACCAACG	26936
Qy	16478	CCACGTCATCTCTGAGAGAGCACCGCGCCACACACATCCGTCAGACACACCGCGCGACG	16537
Db	26937	CCACGTCGTCGTCGAGAGCGCGCGGACCGGAAACCGAAGCGCGCGCGCGCGCGCG	26996
Qy	16538	ACGCGCGGAGAGAGCAGCGCGCGGACGATGTTCCGGGGAGCGCGCGCGGACGCGCG	16597
Db	26997	CGGGCGCGGAGGCGACCGCGCGCGCTCTGTC-----CTTGGGTGCTCTCG	27041
Qy	16598	GTACCGCGGCGGAGCGAGCTGCTGCTGCTGCGGCGAGTCCAGGGGTGCGCGCTGCG	16657
Db	27042	GACGACCGGGAAGCG-----	27058
Qy	16658	TGTCGGCCAGTCCGACCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	16717
Db	27059	-----CTCAGGCGGAGCTGGACCGGCTCAGCGCGGACCG	27095
Qy	16718	CCGACACCGCGGCTCGACCTCGCGGAGTTCGGGTACACCTCGCGCGCGCGCGCGCG	16777
Db	27096	CGGCGACCGCGGCGCTCGGGGCGGAGCTGCGCGCTCGCTGGCGCACCGCGCGCG	27155
Qy	16778	TGTTGACACCGCGCGCGCTCATGCGCGCGGACCGGACACCTTCTGCAAGCACTCC	16837
Db	27156	TCCTTCGCGCACCGCGCGCTGCTGCTCGCGCG-----	27187
Qy	16838	AGGCACTCGCGCGAGGCGAACCCACCGCGCGCTATCCACAGCAGCGCGCGCGCGGA	16897
Db	27188	---CCGCGCGGGTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	27230
Qy	16898	CCGGGACCGGGGAGCGCGGAGGAAAGACCGCATTCATCTGCTCGGACAGGCGCACCAAC	16957
Db	27231	-----CCCCCGCGCGCGCGGTTCTGTTCTTCGGACAGGGCGCGCGCGCG	27275
Qy	16958	GCCCGGCGATGGCGCTTACACACCGCGCTTTCGCGCGCGCGCGCGCGCGCGCG	17017
Db	27276	ACGCGCTGATGGGCGAGACCTGTACGAGCGCTTTCGCGGTTCAGCGGACGCACTGGACA	27335
Qy	17018	ACATCTGACCCACTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	17077
Db	27336	CCGCTCTCGCGCGAGTTGACACCGTGTGGAGCTTCCGCGCGCGCGCGCGCGCGCG	27395

QY	12771	GGACGGGACCGGCTGGTCCGAGGGTGGGGATGCTGCTGGTGGAGCGGCTCTCCGACGC	12831
Db	23196	GGGTGAGCATGATGCTTCACTCGCGCGTGAAGACCCATGCTCGACGACTTTCGCGCGCG	23255
QY	12831	CCGCGCGCAACGGTCAACGCTGCTCTGGCCGTCGTCGCGCAGCGCGTCAACACGAGACGG	12890
Db	23256	TGCGCCGGGGCTGACTACCAACCGCCGAGATCCGCTGCTGTGTGTAACGTACAGCGCG	23315
QY	12891	CGAAGCAACGGCTGACCGGACCCAACGCTGCTTCA-----CAAGTCA	12934
Db	23316	GCCTGGGCCACCGCGCAACAGTCCGACGCCGACTACTGGGTTCGGGCACGTCGCGCGC	23375
QY	12935	AGGTCAATCCGCGAGGCTTTGGCCCAACGACACTCTCCCTGCGGATGTCGATGCGGTGG	12994
Db	23376	CGGTCCGCTTCGCGACGGCATCGATGGCTGCCCCACCGAGGCCAGCTCCACACTTTC	23435
QY	12995	AGGCCCAACGACGGGACCAACCTCTGGGCGACCCGATCAGGCTCAAGCCCTCTGTCGAAG	13054
Db	23436	TGGAGCTCGGCGCGGACGGCGTGCTCAGCGCCATGCCCCGGAGAGCCTCACCAGCCGT	23495
QY	13055	CCTACGGTACGACACGGCCCCAAACGGCGGCCCTCTGCTCGGAACCTCAAGTCCAAACA	13114
Db	23496	CCCCACGGCACTGCTGCGACCTCTGGGGGGAACGGGCCGAGAACTGCCCCGTGCTCA	23555
QY	13115	TCGGGCACTCCATGGCGCTCGGGGTGGCGGGGTCAACAAGATGGTATGGCGGTGC	13174
Db	23556	CGCGGTTCGCGCGGCCCAACGCGCAACGGCGCCGGTGCATGGAAGCGGTACTTCCGCC	23615
QY	13175	GGATGCTGCTGCGCGCGACCTTGCATGTGATGAGCGCTCGCGCGCATGTGACTGGT	13234
Db	23616	ACCACGCGCGCGCGGACCAACGCTCGCGACCTACGCTTCAAACGAGCGGTACTTGGC	23675
QY	13235	CCGCGGTGCGGTGACGTGCTGACGGAACGGTGCCTTGCGCCCGGGGAGGGGGCGGC	13294
Db	23676	CCGACACACCGCGCGCAACGAGCGCCACAC---GCCTGGATCCGCCCTCGACGCCGAGT	23732
QY	13295	TAGCGGGGAGGAGTGCATCATTTGGGTGAGCGGCACCAACGCCACGTCATCTCTCG	13354
Db	23733	TCTTGGCGCGCTGAGAGGGGACGAGTCCGCGCCCTCGCGCTTCCCTGACCTTGACCG	23792
QY	13355	AGGAAGCACCGCGCCCAACATCCCTCTACACACACCGCGCGACACGCTCCCGCGGAGAT	13414
Db	23793	ACGCCACCGTCAACGCGATGGTCCCGCGCTCACCCTTGCGCGCGCGCGCGAGC	23852
QY	13415	CAGCCCGGACGAGGATGCGGTAGTGGCGATGAGGCTGCTGCCGGCAGTCCAGGGGTGT	13474
Db	23853	AGACCGAACTGGAC-----TCCTTGGCGCTACCGCGCTCACTGGAAAGCGCGCGCGG	23904
QY	13475	GGCGTGGTGTGTCGGGCCAAGTCCGACGCGGCCCTCGCGCGCCAGGCCAGGCCCTGC	13534
Db	23905	CGCTACCGCACCGCCCGCTCACCGCGCGCTGGGTGCTGTGCTGT-CCCGCACACCACC	23963
QY	13535	ACGCCCACTTCAACGACCAACCCCGGCTCGACCTCGCGAGCTGGGTACACCTCTCGCC	13594
Db	23964	AGGACCGTCAGGACGAGCGGACCGCGGCTTGGGACCGCGAGTCCGACCGCTTGGGCA	24023
QY	13595	ACGCCCGCGCGGTGTCGACCAACCGCGCAACCTCATCGCGCGGACCGGACACTTCC	13654
Db	24024	CCACCACTGTCGGGTGACGGTCAACACCGACCGCGCGCGCTGGCGCCCGGATCA	24083
QY	13655	TGCAACGACTCCAGGCACTCGCGGAGGGAACCCACCGCGGTATCCACAGCAGCG	13714
Db	24084	CCGAACCGCGGCGAACGAGGCCCGTTGAGCGGTGCTGTCTGCTGTCGCTGCCGTGCCA	24143
QY	13715	CCCCAGGCGGGACCGGGACCGGGGAGCGCGAGGAAGACCGCATTCATCTGCTCCGGAC	13774
Db	24144	CCGGCGACCGCGGCCCAACCGGTGCGCGCGCGCTCACCCTCACCACCAACCGCGTCC	24203
QY	13775	AGGGCACCCAAACGCCCGCGCATGGCGCACAGGCGCTCT---ACCACACCAACCCGCTTCG	13831
Db	24204	AGGCCCTCGCGACGACCGCGCATTCGACGCGCGCGCTGTGGAAAGTCAACCGCGGGCGCTGG	24263

Qy	13832	CCGCGCAGCTCAAGGACATCTGACACCCACTCGACCCCACTCGACACACCCCTCTCTCC	13893
Db	24264	CCGTGCGCCGCGCGCAAGGTCAACCGCCGCCGAACAGGCGCCGCTCTGTGGGCGCTTGGGCC	24323
Qy	13892	CCCTCTCATCCACAGGACCCCAACACACACGAGACACACCACTCTGAAGAAGCGCGCGAC	13951
Db	24324	GGCCGTGCGCTTGGAACTTGC CGGCCCGGTTTGGCGGCACCTCTGACCTGCCCGCCACCC	24383
Qy	13952	TGCTCCAGCAGACCCGCTACGCCAGCCCGCCCTCTTGC-----CTTCCAGSTCG	14002
Db	24384	TGGACGSCAGGCGCGCCGCGGTTCGCGCGGTCTCGCGCTACCGACGCGCGAGGACG	24443
Qy	14003	CCCTCACCGCCTCTCACGAGGCGGTACACATACACCCCACTACTACGCGGACACT	14062
Db	24444	CGGTGGCCCTTGC CGGCCCTTCGGCGGTCTTCTCGCGCGCTGGCCACGCGCGCGCGCC	24503
Qy	14063	CCCTCGGCGAAATCACGCGCGCCCACTCGCGGCATCTCACCTCACCGACGCGCACCA	14122
Db	24504	CCGACACGCGCCCGCACCGCTTTCGACCGCGCGCGCGCACGCTCTGATCACTCCGCGGCA	24563
Qy	14123	CCCTCTCATCCCAACGCGCACCTCTCATCAAAACCATGCCCGCCCGGCACCATGACACCC	14182
Db	24564	CCGCGCGCATC---GGCGGCACGTGCGCCGCGGCTGGCGCGACGCGGCCACCCACC	24620
Qy	14183	TCACACACACCCCCCAACATACCCACCACTCACCGCGCAAGAAACAGACTCTGCGCA	14242
Db	24621	TGCTGTCTACACAGCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCTCGCGCGGAAC	24680
Qy	14243	TCGCGCGCATCAACACCCCACTCTCTGTCTATCAGCGGCACCCCAACAGCTCTCNAAC	14302
Db	24681	TGGAGAACTTGGGCGCGCGGGTCACTCTGCGCGCTTCGACGCGCGCGACGCGACGCGC	24740
Qy	14303	ACATCACCACTCTGCCAAACAAAGGCATCAAAACCAAAACCTCTCCCAACCAACACG	14362
Db	24741	TGGCGCGGTCTCTCGCGCACTGCGCGAGGACGCCCGCTGTGCGGGTGTTCACACCG	24800
Qy	14363	CTTTCACCTCCGCCACACCAACCCCATCTCAACAACTCCACGACACACCCAAACCC	14422
Db	24801	CCGGCTGCTCGAGGACACGCTGTGAGCGGCTCACACGAGAACTTTCGCGCGGTGC	24860
Qy	14423	TCACCTTACACCGACCCACACCCCGCTCATCAGCGCAACACCGCCACCGACCAACTCC	14482
Db	24861	TGCGCGCCAAAGACCGTTCGCGCGCCACCACTGCACAGCTGACCGCGACCTGGACCTCG	24920
Qy	14483	TCACCCCCCACTACTGGACCCCAACAGCCCGCAACACCGTGCAGCTAGGCCACCAACCC	14542
Db	24921	CGCTTTCGTGTCTTCTCTCACGCGCGGGTCTCTCGGCGCGCGCGGACAGGGCACT	24980
Qy	14543	AAACCTTCAACCAACGCGGTACCACTATATGAACTCGGACCGGACCAACACCTCA	14602
Db	24981	ACGCGCGCCAAACGCCACCTGGAGCGCTTCGCGAAACACGCGCTCCACGCGCTGA	25040
Qy	14603	CGACCTTACCCAGACAACTTCCCAACACCGCGCAACACCGCTTACCTTACCCACC	14662
Db	25041	CCGCGTGTCTCGCTTGGGCGCGCTTGGCGGGTTCGGGATGGTTCGCGACGCGCGCG	25100
Qy	14663	CCACCAACACCCCAACCACTCTCTCAACCACTCGCCAAACCAACCAACCACTTGC	14722
Db	25101	AACCTACCGGGTACGCGCGCGGGCTTTCGAACCGCTCGCCCCGAAACCGCGCGTGC	25160
Qy	14723	ACCCCAACCACTACACCCACCAACCAACCCCAACCCACCAACCACTCTGACCTCC	14782
Db	25161	GGCGCTTGTGCGGCATCGAAGACGCA---CACCACGCTGCGCTCGCGACATCG	25217
Qy	14783	CGACCTTACCCCTTCAACACCACTACTGTGCTTCAACCAACCGCGCAACGCGAGCAGC	14842
Db	25218	ACTGGAGAGCGCTTCCAGCGCGCTTTCGCGCGGTTCGCGCGGTTCGCGCGTTCGCGCGAC	25277
Qy	14843	CGTACCGAGCGAAGG-----CGTGAGCAAGCCACGACCCCACTAACCCGCTGCGTG	14896
Db	25278	TCCCGAGACCGCGCGGCGCACCCCGCGACCGCGCACCGGCGCGCACCGGCGCTGCGC	25337
Qy	14897	ATGTCTCTGTGGGCAAGTCTCCGAGAGCGAGACGAAGAGCTGTTCGCGCTGTGTGCGCA	14956







Db 16657 GCGCTGTCATGAGCCGACAGCGCTCTCTGTGAGACCACTGGAGTCTTGA 16716  
Qy 6564 ACAGCCGGCATCAACCCCAACACCTCCAGCGGACCCCAACCGAGTCTTCAACGGCAC 6623  
Db 16717 GCGGCCGGGATTCGCGCCGAAACCTCCGATCCACCTGACCGGACCTTCGTGGCTC 16776  
Qy 6624 CAACGAGACGACTACGACACTTCGCGTGACAAACGCGGGCCAGTCAACCGATGTTTCG 6683  
Db 16777 CAGCTACAGAGTACGCTGGG-----CGCGGGCAGCGCACCGAGGCCACAT 16827  
Qy 6684 ACTGACCGGAACCGCGGAGCGTCACTCTCGGTGATATCTCGTACAGTTCGTTGTTGA 6743  
Db 16828 GGTCAACCGGACGACCGCCAGTGTCTCTCGGCGGACGTCTGATGACGTTCTCGGTCTGA 16887  
Qy 6744 GGTCTCTCGGTGTCGTTGACACGGCTTGTCTCTCGTCTGTTGTTGTTGATCTGCG 6803  
Db 16888 AGGCCCGCGGTACCGTGCACACCGCTCTGCTCTGCTGCTGCGGCTGACACTGGC 16947  
Qy 6804 CTGTGAGCGTTGCTGCGGTGAGTGTCTGATGCGCTTTCGCGGGGTGTGACGTGAT 6863  
Db 16948 CTGCAAGTCTGCGCAACGCGGAGCAACTGCGCGTTCGCGGCGGCGCACGATCAT 17007  
Qy 6864 GTCTCTCGGTGCTCTGTTGAGTTCGCGGAGCGGGTCTGCGCGGAGCGGCA 6923  
Db 17008 GACGACGCCAACCCGTTTCATCGCTTCAGCGCGGCGGCTCTGCGCAAGGACGGCG 17067  
Qy 6924 TTGCAAGCGTTCTCGCGCGGCGGAGCGGACCGCTGGGGTGGGGTGTGGGATGCT 6983  
Db 17068 GTCAAGCGTTCTCCGACGACGCGGATGACGCTGCGCGGAGGCGTCTGCGGTCT 17127  
Qy 6984 GCTGTGAGCGGTCTCCGACGCCCATCGCAACGGTCAACGCTGCTCTGCGCGGTGCG 7043  
Db 17128 CCTGTCAAGCGGTCTCCGACGCGAGGCAACCGGCAACCGGCTCTGCGGTCTCTCG 17187  
Qy 7044 TGGCAGTTCGGTCAACGAGGAGCGTTCGAGCAACCGTTCGACCGCGCCCAACGGGCGTC 7103  
Db 17188 CGGCTCCGCAACGAGGAGCGGCGCTCCAAAGCGCTGACCGCGCCCAACGGGCGTC 17247  
Qy 7104 CCAGCAGGTGTATCCCGAGGCGCTCGCCAAACCGCGCTGTGCGGCGGTGATGTCGA 7163  
Db 17248 CCAGCAGAGGTATCCCGAGGCGCTCGCCAAACCGCGCTGCTGCTCGGCTCGGGA 17307  
Qy 7164 CGCGGTGAGGCGCACCGGACCACTTTGGCGGACCGATCGAGGCGCCAGGCGCT 7223  
Db 17308 CGCCCTGAGGCGACCGGACCGGACACCGTCTCGCGGACCCATCGAGGCCAGGCACT 17367  
Qy 7224 CTTCCGACCTACGACAGGACCGTTCGCGGCGAGGGCGGCTGTGCTGCGGTTCGGTCAA 7283  
Db 17368 GTTCGCCACCTACGCGCGGACCGCGACCCCGAGAGCGGCTGCTGCTCGGCTCGGTA 17427  
Qy 7284 GTCCATGTCTGTCACACAGGCTGCGCGGCGGCTCGCGGCGGTGATCAGATGTTGAT 7343  
Db 17428 GTCCAACTTCGCGGACACCGAGTCTCGCGGCGGCTCGCGGCGGCTCATCAGATGTT 17487  
Qy 7344 GCGCTGCGGCTGCTGCTGCTCGCGGAGCTGTGATGAGTGAAGCGTTCGCGCATGT 7403  
Db 17488 GCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17547  
Qy 7404 GAGTGTTCGCGGTGCGGTGCGTGTGATGAGGAGCGGTTCCTGCGCGGCGGGA 7463  
Db 17548 GAGTGTTCGCGGAGCGGTTCGCGGTGCTGATCCAGCGCGGCTGCGC---GGAGAC 17604  
Qy 7464 GGGGCGGCTACCGCGGCGGAGGTGCTCATTTCCGCTGACGCGGACCAACGCGGCGGT 7523  
Db 17605 CGGTTCGCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17664  
Qy 7524 CATCTCGAAGAGCAACCGCGGAGCGAGCTTCGCGGGGACCAACCGCGGCGGAGGTGA 7583  
Db 17665 CTTGCTGAGGAGGCGGCTGCGGACCAACCGCGGAGGAGCGGCGGCGGCTGCGGCG 17724  
Qy 7584 CGCGGCGGACGATGAGGTGCTGCTGCGGAGTCTCTGCGGTGCTGCGGCGGAGTACCGG 7643

Db 17725 GGTCCGATCGCC-----GCCGCGCTGCTCTCGGTGGTTCACCGCCCGCAGCGCGC 17778  
Qy 7644 GGCCAACTGTCAGCGGCGCTGCGCGCCAGGCGCCAGGCGCTTGCACGCCCACTCACCGA 7703  
Db 17779 GCGCTGCGGCGGCGGCGGCGGCGCTCTCTCGGCGCAGCC---GAAACCGTCCGACCGC 17835  
Qy 7704 CCACCCCGGCTCGACCTCGCGGATGTCGATACACCTCGCCCAACCGCGCGCGGTGTT 7763  
Db 17836 CTTGCGGCGCGCGGACCGCTCGACATCGGCTGCTGCTGCTCTCGCGCGCGCGCGTTT 17895  
Qy 7764 CGACACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 7823  
Db 17896 CGAGCACGTCGCTGCTGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 17955  
Qy 7824 ACTGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 7883  
Db 17956 GGTGCGGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 18000  
Qy 7884 GACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 7943  
Db 18001 -----GGACGTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 18054  
Qy 7944 CGGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 8003  
Db 18055 GGGGATGGGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 18114  
Qy 8004 CTGCACCACTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8063  
Db 18115 TGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18166  
Qy 8064 CAACGACGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8123  
Db 18167 -----GGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 18219  
Qy 8124 CTTGCGCTTCAGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8183  
Db 18220 GTTCGCGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 18276  
Qy 8184 CTACTAGCGCGGACACTCCCTCGCGGAAATCACCGCGCGGCGGCGGCGGCGGCGGCGG 8243  
Db 18277 TGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18336  
Qy 8244 CTTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 8297  
Db 18337 GTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18396  
Qy 8298 GCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8357  
Db 18397 GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 18456  
Qy 8358 GCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8417  
Db 18457 CGAGTTGAGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 18516  
Qy 8418 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 8477  
Db 18517 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 18576  
Qy 8478 CAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 8537  
Db 18577 CCGCGGATCGCGGTGAGTACGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 18636  
Qy 8538 ACTCCACCA-----GCACACCAACCGCTTACCTACCGCGGCGGCGGCGGCGGCGGCG 8598  
Db 18637 ACTGCTGAGGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18696  
Qy 8589 CATCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 8648  
Db 18697 GGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18756  
Qy 8649 CCGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8708  
Db 18757 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18816

QY	4380	GCCCCCTCCGCGGCTTGACACAGGTGGTGGCGGCACTCTCGCCTTGGGACCGGCAACA	4439
Db	14524	ACAGGACCTCAGCGCGTGGACTCTCTGTCTGCCGCCCTCACCTCGTGTGGCGGCGGCA	14583
QY	4440	ACAGCAACAAGCCGCACTAACACTTGACCTTACCAGGAAACCTTGAAACCCCTCACCT	4499
Db	14584	CCAGGAGAGCACTCTTGACACCTCTGCGTACCGGTGGAGTGACAGACTGAGCA	14643
QY	4500	CCCACCAACCAACCAACCCCAACAACTTGGCTCATCGCAATCCCGA---AACCGAGAC	4556
Db	14644	GCCAGCGCCCGGTCTCTGAGCGSACCTGGCTGTGGTCTCGAGCGCACCGACCGCGGC	14703
QY	4557	CCACACCCCAATACCAACATCTTCAACCACTTCACCAACAGGATCACCCCCAT	4616
Db	14704	CGACCGCAGCCCTCTCGAGCGCTTGGCGGAGCGCCCTCGGCTCGACAGGCGCGGGT	14763
QY	4617	CCCCCTCACCCCTCAAACACACACCAACCAACCCCAACCTTCCACACACCTCCACCA	4676
Db	14764	GCGTGGCTGCTTCTGAGCACTCTTGGCGGACCGGCGGTGCTCG-----	14810
QY	4677	CACCGGAAACAGAGCCAAACCAACACCGGAGCATACCGGGCTGCTCTCCCTCT	4736
Db	14811	--CGAAACGACTGGCGGGACCGCGAGGTGGACGCGGGAACAGGTCTGTCTGGTGT	14868
QY	4737	CGCCTCGAGGAACACCCCAACCCCAACACCCCAACACCAACCGGCAACCTCTCTCA	4796
Db	14869	GCGCTCGAGAGGGAGCGCGAGCATGCGCGCGCTCAACCGCGGAGTGGCGCTGAC	14928
QY	4797	CCTCACCTCACCACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	4856
Db	14929	CGTGGCTGTTCAGGCGCTTGGCGACACCGGCGCCAGGGCGGCTGTGACGCGCAC	14988
QY	4857	CACCAACGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	4916
Db	14989	CGGGCGCGCTCTCCACCAACCCGCGGACCCGCTCACCCACCGCTCACAGGCGCTGC	15048
QY	4917	CTGGGACTCGCGGACACCTCTCTGAAACACCCCAACCAACCGCGGATCATCGA	4976
Db	15049	CTGGGCTTGGCGCGGGCGTCCCTTGGAGCAACCAACCGCTTGTGGGGCGGCTGGTGA	15108
QY	4977	CCTCCCAACCAACCCCAACCCCAACCTTCAAGCACTTCAACCAACCTTCAAC-----	5030
Db	15109	CCTGCCAGTCTTCAGAGCGGGCGGACAGCGGCTGCGGGATCTCGCGTCA	15168
QY	5031	---CAAACCCCAACCAACCACTGCGCATTCGCAACCGGCAACCAACCGCGCG	5087
Db	15169	GGAACCGGCGGAGGACAGGTGGCTGCGGGGCAACCGGAGTCTCGGGCGCGCG	15228
QY	5088	CCTACCCCAACCTTCAACCCCAACCAACCAACCAACCAACCAACCAACCAACCAAC	5147
Db	15229	GCTGTCGCAACAGTGTGCAACCGTGTGCCACCGGCGGAGTTACCGCACCGGAC	15288
QY	5148	CACCTCATCACCGGGGAACCGGGCGCTTGGCAACCCACCTTCAACCACTTCAAC	5207
Db	15289	TGTCCTGATCACTGGTGACCGGTGGCTTGGGCGGAGTGTCCCGGTGCT---GCG	15345
QY	5208	CAACCAACCAACCTTCTCTCTCAACAGCGAAACCGGCGGCAACCCCAACCGC	5267
Db	15346	CGGGCGGGCGGACAGCTCTCTCTGACAGCGCGCGCGGCGGACCGCGGGGCG	15405
QY	5268	ACAACCTTCAACCAACCTTCAACCAACCAACCAACCTTCAACCAACCAACCTTCA	5327
Db	15406	GCGGAACTCGGGCGAATGGAGGGTACGGGCGGTGGTGTCTGCTGTGCTTGGCA	15465
QY	5328	CACGAGCAACCCAGACCACTTCAACCACTTCAACCACTTCAACCAACCAACCAAC	5387
Db	15466	GCTGCGGACCGGACCGGCTCGCGCTTCTTCAACCTTCAACCTTCAACCTTCAAC	15525
QY	5388	CACGACGTATCAACACGCGAGGATCTCTGACAGACCACTTCAACCAACCTTCAAC	5447
Db	15526	GACCGGTGTGTCACACGCGAGGCTCGGCACTACGCGCGCTTGAACCTTGAAC	15585

QY	5448	CACCCAACTCAA	CAACGTCCTCGCGGCCAAAGCCACAGCGGCCCACTCTCTCCACCAACT	5507
Db	15886	CGCCGAGTTGCGCGGCT	CACCGCCGCCAAGCTCGCGCGGCCGCCACACTCGACGCGCT	15645
QY	5508	CACCCAAACACACCC	CCTCACCGCTTCGCTCTACTCTCTCCGCGCGCGCCACCTTCGG	5567
Db	15646	GCTCGCGGACCGGAACT	GGACTTCTTCGCTCTTCGGCTCCATCGCGCGGTGTCTGGGG	15705
QY	5568	CGCACCCGGCCAAAGCCAA	CTTAGCGCGACGCAACGCTACTTCGACGCGCCTCGCCACCA	5627
Db	15706	CAGTGGCAACAGAGCGCT	ACGGCGCGCAAGCGCTACTCTGACGCGCTCGCCCTGCA	15765
QY	5628	CGGCGACACCCACCA	CCTCCCGGCACACAGCATGCGCTGGGGCACTCTGGCAAGGAAACGG	5687
Db	15766	CCGCGCGCCGCGGCT	TCGCGCGACTTCGCTCGCGCGCTGGGCGCGCTGGGCGGAGCGCG	15825
QY	5688	ACTCGCTGATT	CGGACAAAGCCCGGCGCATATCTCGACGCGCGCGGTTTCGACCCATGTC	5747
Db	15826	CATGGCGCGCGAGATG	CGGTTTCGAGACCTTCGCGCGCAGGGCCCTCGGCTGCTCGA	15885
QY	5748	ACC CGAGTTGGCCACCGG	CAGCGATCGCGGACATCGCGGACACCGCAACGGCCGTATGT	5807
Db	15886	CCGCGCCCGGCATGAC	CGAGCTGGCGCGCGCTGCTCGGCGAGGACGTACCGTCA	15945
QY	5808	CGTCATCGCGCA	CATCGACTGGAGCA-----GATCGAAACACCTCTCAGACGAGCA	5861
Db	15946	CGTCGCGACCTGGACT	GGCACTGGCAGCGGTACGACCGCTGTTCACCTCGCGCGCGCCAGCGC	16005
QY	5862	CCT-----	-----CGTGAGCGCGGCCGGGAAGGGAGCCAGCTGTCAGCG	5903
Db	16006	CCTGATCGCGGCGCT	CGCCGAGGTTCGCGCGCTTCGCGCGCAGCGAGCGCACCGAGCAGGA	16065
QY	5904	CCCACCTCCACGGGCGAG	TTGCACAAAGCGCTGCGCCATCAGACGTCGGCGCGCAACAG	5963
Db	16066	CGCACCGGGCGCTCGAG	GTGTCACCGCGTTCGCGCGCTGGCGCGCAACCGGAGCAACT	16125
QY	5964	GGCCGATTCGTCGAGCT	CGTACGAGACCATGTGGCGCAGTGTCTCGGCAAGCGGACCC	6023
Db	16126	GGCGCTGCTGACCGG	ACTTCGTCGACCGCTTCCTCGGCCACAGCTCCGC	16185
QY	6024	GAAGGCGATCGCGCGG	ACGACTGTTTCGCTGCACTCGGCTTCGATCACTCAGGCGGT	6083
Db	16186	CGAGCGCTGCGCGGCG	CGGCGCTTCGCGAGCTCGGCTTCGACTCGCTGACCGCGGT	16245
QY	6084	CGAGTTCGGAACCTGCT	GATCAAGCAACAGGACTTCGCTCTCTGCTCTCGCTGGTCTT	6143
Db	16246	CGAGCTCGGAAGCGCT	GGGCGCGGACCGGGCTGCTCTGCGGCGGAGATCTTCGGCGGT	16305
QY	6144	CGACACCCGACCCCTG	CGAACTCGCCGTACCTCGAGAACCACTGCGGGGCAACAGC	6203
Db	16306	CGACTACCGACACCG	CTGGAATCGCCAGTTACCTGCGGCGGAGATCTTCGGCGGT	16365
QY	6204	AGCGGAGTCGGCTCT	TACGCGGACCGGTTACCGCGGAGGCTTCGTCAACGAGCCGAT	6263
Db	16366	GCTGGAAGTCGCGCG	CGCGCTTCGCAACCGGCGGCGCA-----CGACGAGCCGAT	16416
QY	6264	CGCCATCTGTCATGG	CGCTGCTTCGCGGCGGAGTGACTCGGCGGACGACTCTG	6323
Db	16417	CGCCATCTCGGATGG	CTGCGCTTCGCGGCGGCTGAGTCTCCCGGAACAGCTGTG	16476
QY	6324	GGATCTGATCTCT	CCGAGCAGGACGATCGGCGGATTCGCCACCGACCGCGCTGGGA	6383
Db	16477	GGACCTGTGCTCG	CGGACCGGACCGCATCAGCGAGTTCCCGTCAACCGCGCTGGCA	16536
QY	6384	CTTGGAACGCTCTAG	ACCCCGGACCAACCGCGGACCTGTGCTACACCGGAAACGG	6443
Db	16537	GACCGGGCACCTCT	TCGACCGCGACCCCGGACCGGCGCGGCAACCACTACTCCACCGG	16596
QY	6444	CGGATTCCTACGAC	GAGGCCACTTCGACCGCGMATTCCTCGGCACTACGCCCGCGCA	6503
Db	16597	CGGCTTCCTCCAC	GAGGCGGAGTTCGACCCCACTTCCTTCGGCATCTCGCGCGCGCA	16656
QY	6504	AGCCCTCGCATGGA	CCCCCGCAACGACTCTCTCTCGAAACCGCTCGGGAACCATCGA	6563

33388	CGTTTCATCGGCTCCACCTTACAGAGAAAGTACAGGACTCGGCGTTCAGAGACGGCTC-----	33337	
OY	1856	GCGCCGCGGAGCGTGGAGAGGCCCAACTCTTCAACGGTACCAAGGCAAGCGTCTCTGTGGAGCC	1915
Db	33336	-----:GGCGGTATCACTGGGTGACCGGACACAGGCCCAAGCCGATGCTCTCCGGGC	33290
OY	1916	GTATTCGCTTACAGTTTTCGGGCTGGAAAGGCGCGGCAATCAACCTTGGACACAGGGGTGTCGG	1975
Db	33289	GCCGTGGCTTACCTTTTGGGCGCTCGAAGAGCCCGGCGCTTACCGTTCAGCACCGCATGCTCTCT	33230
OY	1976	CATGCGCTTCGAGCGCTGATCTTGGCGGAGCGAGTGCAGTGGCGGTTCGGGTGATGTCAGCTCG	2035
Db	33229	CTCTCCCTTGGTGCCTTTCGACTTGGCCTTGGCCAGTGTCTGTGCGCAACGCGGAGAGTCTCTTGG	33170
OY	2036	CGCTGGCCGAGCGGCGGCTCTCGGTCATGTTCACCCCTCGGCAATTTTCATCGAGTTCTCCCGGC	2095
Db	33169	CCCTTGGCCGAGGCGGCGGCGACCGTATGTACCAACCCCAACCGTTTCGTGTGGCTTACGCGGC	33110
OY	2096	AGCGCGGAGCTGTCCGTTGAGACGCGCAGAGGTTCAGAGCGCTTACTTGGCTGACGCCAGCGGACCG	2155
Db	33109	AGCGCGGCTGTGGCAGGCGAGCGCGCGCTGCGCAAGCGCTTCTTCGGAAGCGCGCGACCGGATGGA	33050
OY	2156	GCTGGGGGAGAGGCGGTGGGGATGCTGTTGGATGGAGCGGGTTTTCGAGTGGGGTCCGCTGG	2215
Db	33049	CCCTTGGCCGAGAGGCGGTGAGGCGTCTCTGTCTTGAAGCGCTCTTGGACGCCCAAGCGGCACAG	32990
OY	2216	GGCATTCGGGATCTTGGCCGCTGGTATCGCGGCAAGTCCGCTTCAACAGACGCGTGGCTCGATG	2275
Db	32989	GGCACAGAGATCTTGGCGGTCGTCCGCGGCTCTCGGCATCAACAGACAGAGAGCGCTCCACAG	32930
OY	2276	GGCTGACGCGCGCCGAAAGGTTCGAGCTCAGAGACGCGGTTGATTCGGGCAAGCGTTTGGCGAAGC	2335
Db	32929	GCTGTGCGGCGCCCAAGCGGCCCTTCCAGACGCGCGTCAATCCGCGCAGGCGCTTGGCCAACT	32870
OY	2336	CGGGGTGTCCGTGGCGGATGTGGATATGTGGATGGAGGGGCGACCGGGAACGGGACAGACGCTGG	2395
Db	32869	CGGGGCTGACCCCGCGCGGACATTCAGCGCGCTTCAGAGCGCCACGGGACCGGACCGCGCTTG	32810
OY	2396	GTGATTCGGATTCGAGGCGACAGAGCGTTTGTTCGCCACGTACGGGCGA---CGGCGCGGTGACA	2452
Db	32809	GGCACCCCATTCGAGGCGCCAGGCGCTGTCCGCCACTTACGAGACCGGGCGCGGACCGGAGACA	32750
OY	2453	GGCGGCTGTGGCTTGGGCTCTTGAAGTCCAAACTCGGGCACACCATAGCTTCCGCGGGGTG	2512
Db	32749	GTCCGCTGTGGCTGGGCTCGGATGAAATCCAAACTTCGGGCCAACCCAGTCCGCGCGCGGG	32690
OY	2513	TGGGTGGGATCATCAAGATGTGTATGGCGTTTGGGAGAGGGGGGTGTTCGCGCGGACGTTTC	2572
Db	32689	TGGCGCGGCTCATTCMAATGGTCTCTTGGCCCTGTGGCGCAACGGAACGCTGCGCGGACCTTTC	32630
OY	2573	ATTGTGATTAAGCGGTTCGCGCGGAGGTGAGCTGTCCGCGGGGCGGAGTCCGAGCTGTACAGG	2632
Db	32629	ACGCCGACACCCCTTTCAGGCAATTCGACTTGGACCCCGGCGACCGTCTCCCTGTGTACCG	32570
OY	2633	AGGCGGTGCGCTGGCCGCGGGGAGACGCGGACAGAGCGGTTTTCGCGCGGCGGAGAGTGTCTGTCT	2692
Db	32569	AAACCAACGACTGGCC-----CGAGGGCGAGGGCGCGCGCGCTGCGGGGTCTCTCTCT	32516
OY	2693	TCCGGATTCGGCGGCGACGAAATGCGCATGTGATTTTGGAGAGCGCGCGCGCGGGGGGCT	2752
Db	32515	TCCGCACTCAGGGGCGACCAAGCCCAACCCCTCTCTGAAAGAGCGCCCCCGCGCGGACAGAG	32456
OY	2753	GTGTGTGCGCGGAGGTGGGAGTGTGGAGAGGTCTCCGGGTCTTGGCATTTTGGATGGCTGAAT	2812
Db	32455	CGACCCCGCGGGGCGCGGTGCC-----	32433
OY	2813	CGATGTGCGGCTTCAAGTGAATGTGTCTTCCGCGCGGATGCTGAGTTCGATGCGGATCCGATTC	2872
Db	32432	-----CGGCGCG	32426
OY	2873	CGGTGCGCGGTTTCTGTGTCGCGGTGTCCGCTAGGTTCAGTGGCTTGGGTTTCGCGCGCAGGCGG	2932
Db	32425	GGGAGACCATTCCTCTGGATGTGTGTCCGCGCGGACCCCGGCGCGCGCTGCGCGCCACAGCGG	32366

[illegible]



QY 4010 CCGAAGACGTACCGCGATCGGACGCTTCGCGCGGCGACAACGACACCGCGCTTCC 4069  
 Db 31300 GGGCGCGCGCGCGGAGTCTCGGACGCTCGGCGGCGACAACGCGCGCACTCGACCTTCC 31241  
 QY 4070 TCACGCGCTTCGCGCGACACCATACCGCGATCGGCGACACCCACACTTGGCACACC 4129  
 Db 31240 TGGCGCTTCGCGCGGAGCTT-----CGTCCGGGCGCGGACCGCGACTGGTCCGCG 31187  
 QY 4130 ACTACACCCACACGACGACCCCAACCCCGGCGACGACGCTCGACCTGCCACCTAC 4189  
 Db 31186 TCTTGGCGGCGACCGCGCGCGCGCGGCGGCT-----TGCCCACTACG 31142  
 QY 4190 CTTTCAACACGACGACGACTAGTGGCTCGAGAGCTCACAGCGGAGTCCGAGTCCG 4249  
 Db 31141 CTTTCAAGCGGACGACCTGTG----- 31119  
 QY 4250 GTGCGCGGTCCGCGTTCGCGGTTCGCGGCGGCGAGGACTGCGGCGGAGCGGACG 4309  
 Db 31118 -----GGGATCCCGAGCGGTTCGCGGACCGGCGCGGCGGAGCGGATC 31079  
 QY 4310 AGGTGAGTCCGCGTTCGCGGACGCGGTGCGCGGCGGCGGCGGCGGCGGCGGCGG 4369  
 Db 31078 CCGCGGACGCGGAGTTCGAGACGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 31019  
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 Db 31018 GCGTCCGCTGAGACCGGACCTC---CTGCGCGGCTCTCCGCGCGCTTCGCGACTGCG 30962  
 QY 4430 ACCGCGACCAACGACGACGCGCGGATCAACTGAGACTTACCGAGAAACTTGGAAAC 4489  
 Db 30961 GGAAGCGCGCGCGAGCTGTCACCGTGAATCTCTGGCGCTACCGCGCGACTTGAAGC 30902  
 QY 4490 CCGTCACTTCGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4549  
 Db 30901 CGCTACCGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAA- 30843  
 QY 4550 CCGAGACCGACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 4609  
 Db 30842 -----GGAGCGGACCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30794  
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 Db 30793 GGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30752  
 QY 4670 TCCACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4729  
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 QY 4730 CCGTCTGCGCGCTTCAAGAAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4789  
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 QY 4790 TCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 4849  
 Db 30631 CCGTACCGGTGCGGCTTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30572  
 QY 4850 AGCGACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4909  
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 QY 5207 CCGACCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5266  
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 QY 5327 ACACGAGAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5383  
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 QY 5384 CCGTCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5443  
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Db 29260 ACTACCCCAACCCGCTCGCACTCTGCGGCTTCCTGCGGAGTCCCTCGCCGGGCTCCGCA 29201  
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 Db 29200 CCGGACCGCGCCGCAACGACGACACCGCCG-----GCCACGAGCCCATCG 29150  
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 Qy 7346 CGCTGCGGATGATGTCTGCTGCGGAGCTTTCGAGTGTGTATGAGCGGCTTCGCGGATG 7405  
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 Db 27172 GCGGCGGAGGAGGAGGAGGAGTGTATCATTTGCGGCTGAGCGGAGGAGGAGGAGGAGGAGG 27113

QY 8363 ACGAAACGACCTCGCATCGCCGCCATCAACACCCCACTCCCTGCTCATCAAGGCGCA 8422  
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 QY 8423 CCCCCACACCTTCCACACATCAACACCTTCTGCGCAACAAAGGATCAAAACCAAA 8482  
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 QY 8543 ACCAGACACCCAAACCTTCACTACCAACCAACCCCAACCCCTCATCACGCGCAACA 8602  
 DB 26932 CCGCGCGCGCGAGAGGATCACTTCAACGCGCGGAGGTGCGCGCTGCTTCAACCTTCA 26873  
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 DB 26872 CCGGAGAGCTGATCTCTGCGCGAGACCTGTGCTCGCGCGCGTACAGGACCCGCGAGTCC 26813  
 QY 8651 GCAACACCGTCACTACGCAACCAACCAACCCCAACCCCTCAACCAACGCGCTCAACCACT 8710  
 DB 26812 GGGGACCGCTCGGCTTCCGCGACGCGTACGAGCACTTCAACGAGACGCGTGAAGACTT 26753  
 QY 8711 ACATGAACTGGACCCGAGAAACACCTTCAACCAACCCCAACCAACCTTCCCAAC 8770  
 DB 26752 TCTTGAGCTCGGCGCGGACGCGTACCTAGCGCGCGGTAACGAGACACCGCGAGC 26693  
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 DB 26692 AGACCCCGCGACCGCGCTCGGACGCGCGCGAGCGCGCGAGCGCGCGCGCGCACTGA 26633  
 QY 8831 CCACCTCGCCAAACCAACCAACCTTCAACCAACCCCAACCAACCAACCAACCAAC 8890  
 DB 26632 CCACGAGACCTGCGCGCGCTTCAACCTTCAACGAGGAGCGGTCGACTGAGACGCGCTTCC 26573  
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 QY 9104 CTGACATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 9163  
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 QY 9164 TTCAATGCGGACATACCTTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 9223  
 DB 26272 CCACGCGCGGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 26213  
 QY 9224 TGTGCTTCTGTGATGAGGCGGTGATGATGATGATGATGATGATGATGATGATGATG 9283  
 DB 26212 CTTGACGAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 26153  
 QY 9284 AGGGCGCGCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 9343  
 DB 26152 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 26093  
 QY 9344 CGTGGGCGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 9403  
 DB 26092 TCGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 26033  
 QY 9404 GTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9463

DB 26032 CCAACGACGAGGCGCTCTGCTGACGCGGACCGCGCTCAAGCCCTGGGCGACACAGTGA 25973  
 QY 9464 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9523  
 DB 25972 TGAAGCGCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25913  
 QY 9524 GGTGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9583  
 DB 25912 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25853  
 QY 9584 AG-----GCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9639  
 DB 25852 CGACGCGTGGGCGCGCGCTGCTGATCTCCCGACGAGCTGACGCGCGCGCACCTGCGCC 25793  
 QY 9640 GTCAAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9675  
 DB 25792 GCTTGGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25733  
 QY 9676 ---GAGTTTGGAGAGGCGCGGATGCGGAGGAGGATGCGGAGGCGGCTGTGAGGAT 9732  
 DB 25732 CGACCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25673  
 QY 9733 GGTGTGCTTCAACCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 9792  
 DB 25672 TCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25613  
 QY 9793 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 9852  
 DB 25612 CCGCGTGGCTGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25553  
 QY 9853 GCGTGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9897  
 DB 25552 ACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25493  
 QY 9898 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9957  
 DB 25492 TCGCGCGGCGGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25433  
 QY 9958 GAGTGGGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10004  
 DB 25432 ACGAGACACCGCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25373  
 QY 10005 GAGCGTGGATGAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 10064  
 DB 25372 ACAAGCTACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25313  
 QY 10065 TCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10124  
 DB 25312 ACTGACAGAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25253  
 QY 10125 TGGG---GTGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 10181  
 DB 25252 CCGGACACCTTGGGCGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25193  
 QY 10182 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10241  
 DB 25192 CTTTGGCGGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25133  
 QY 10242 GGTGAGTGTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10301  
 DB 25132 GGGCGGAGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 25073  
 QY 10302 TGTCTCTGACCTTGAACACCGACACCGGACACCGGACACCGGACACCGGACACCG 10361  
 DB 25072 GCTTACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25013  
 QY 10362 TTGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10420  
 DB 25012 ACGCGAGGCGGCTGACCTTGGCGGACATGACACTGAGCGCTTACGAGAGGTCTTCA 24953  
 QY 10421 CGGTGCGGAGCGGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10480

Dh 24952 GACACCCGCCGACCTCTTCGTCGCGACCTGCCCCGAACTCCAGCAGGTCAACGCCGCCG 24893  
Qy 10481 TTCAGCACCAGCGGTCCGGTGAACAACAGCCCGGCGGTCCGACGCTGCTGCCACGCGT 10540  
Db 24892 CCGGAGCAACCGGAACCCGCTCTGCGGGAACCGGCCCTGGCCACAGGCTCCGCGGACTCT 24833  
Qy 10541 CCGGTGGGTGCTCTGCGGCGGTGATTGATGATCCGGTCCGGAAGCTTTGCTGGT 10600  
Db 24832 CCCCCGCGCGCGCGCTTCGTCCTGACCTGTACGCAACCCAGGTG--GCCGCGGT 24775  
Qy 10601 TGTGGGTGGGTGGGTGTTGGTGAAGGGTGGGACGGGTGTG-----TGGTGGGGGG 10654  
Db 24774 CCTCGGAGCAAGCGGACCTCGGCCCATGCGGCCCAAGCGGTTCAGTGACCTTGGCTT 24715  
Qy 10655 TGGCGCGCATCTGCTGGTGTGTGGAGGTCCGGATCTGCTGTGTGGTGAACCGCGCTG 10714  
Db 24714 GCACTCGTGACCACTGCTGAACTGCGAACCTCAAGGCAACACCGGCTGAACCT 24655  
Qy 10715 GTCCGAGTCTCCGGGTGCG-----GAGGGTCTGCGGGCGAGCTGGCCGCTTGGGGGC 10769  
Db 24654 GCCCGCAACCCCTGCTACGACTACCGAACCCGACCCGCGCTCGCGACTTCTCTCGC 24595  
Qy 10770 GGAAGTGGGATGTTGTGGTGTGAATGGGGGAGCGCGGAGGTGTCCGCTGTGA 10829  
Db 24594 GGAATCTCGGGCGCTCGCCGAGTCCGGTCCCGGCTTCTGTGGCCGCGCGCGGA 24535  
Qy 10830 GGGTGTCTCTGCGGGGTGCTCGCTGACGAGGTGTCTGTGATGGCGGTGTGTGTGAAGA 10889  
Db 24534 GAGCATCTCCATCTCATCTGTGCGGATGAATGCGGCTTCCCGCGGCTATACGTTCCC 24475  
Qy 10890 TGGCAGATCGCTCTTCAAGCCGAGCGGCTGGGACAGGTGTTCGCGCCAGAGTGA 10949  
Db 24474 CGAGGACTCTGAGCTGCTGAGAGCGGCGAGGACGCAATCAGCGGATTTCCCGCGGA 24415  
Qy 10950 TGGCGCTTTTGTCTGTGAATGACTTACCGGGGTATGAGAGCTGTGGGCTTGTCTGT 11009  
Db 24414 CCGCGGCTGGGACTGTGACGCGCTGCGCGCGCGCTCCGCACTTGAAGGCGGAT 24355  
Qy 11010 CTCTCGCGCGCGGGATCTTGGGGTTCGCGCGGAGGAGCACTACGCGCGCAATGC 11069  
Db 24354 CTGTGACGGCGTGGGCTTCTGACGCGCCCTTCTTGGGCTGTGCGCCCGGAGGCTT 24235  
Qy 11070 CGCTCTGACGCGCTGAGCTACCGGCGGCGGCG-----GC 11105  
Db 24294 GGGCATGACCCCGACGAGCGCTGCTGTGAGACCTCTGGAGGCGTTGACGCGC 24235  
Qy 11106 GGGTGTGCGGGGTGTGCTGTGGGCTGTGGGCTGTGGGAAGAGCGACGAGATACCG 11165  
Db 24234 CGGAATGACGCGACCACTGTGCGGAGCGGCTGACCGGCTGATTCGTGCGCACCAAG 24175  
Qy 11186 GCACTTGGCGGACCGACCAACCGGCGCATCATCGGTTCCGGTCTGATC-----CCATGT 11221  
Db 24174 CCAAGACTACCGCACTCTGTGCGCAGAGGACCGGACCAACGACATCCGGGCGCATGT 24115  
Qy 11222 GACACCCGGAAGCACTGCGCTTTCATGCGGCCCTGGCTC-----TGAACCGGCC 11273  
Db 24114 CGGCAACCGGAACACCGCAGGCTGATGTCCGGCGCGCTCTCTACGCTTCCGCTGGA 24055  
Qy 11274 GGTCTGTGCGCGCGGACCTGTGCTCGGCCCGCGCTCGCGCTGAGCAATGC 11333  
Db 24054 GGGCGCGCGCTGACCGTGTGACACCGCTGTCTCTCGCGCTGTGCGCTGTGCAATGC 23995  
Qy 11334 CTGCGCGCAACCGCGCGCGACCAACCGGACCAACCACTACCGGTGTGGGAGCAAGG 11393  
Db 23994 CCGCGGCGCGCTGTGCGGAGCGGAGTGAACCTCGCTGCGCGCGCGGCTGTCCGTAT 23935  
Qy 11394 CGCCAGTGAAGCGCC-----GGCTGCGCGCGAGACACAGAACAGAACAA 11438  
Db 23934 GTCCAGAGCGGACTCTTACCGAGTTACAGGTTCAGGAGAGGAGCTGGCCCGGAGAG 23875  
Qy 11439 GCAACACACCTCTCTGCGCTGTGCTCCCACTGCGCACGCTCTGCGGACACACAC 11498  
Db 23874 GTGCAAGCTGTTCGCGGATGGCGCGAGCGTACGAGCTGTTCGAGGCGCTCGGCTCT 23815

Qy 11499 CCGCGACACATCCCGCCCGACCGCGCGTTCGCGACCTCGGCTTTCGACTCTTCACCGC 11558  
Db 23814 CCTCTGGAAGGGCTCTCCAGCGCCGCGCGAGAGGCGCAGCATGTGTGGGCTATGTGCG 23755  
Qy 11559 GGTGAATACGAAACCGGCTCTCCGCAACACGGAATCCGCTTCCCGACACCTTGC 11618  
Db 23754 CGGACCGCGGTCAACAGAGCGGCTCTCAAGCGGCTGACCGGCGCCACCGCGGGC 23695  
Qy 11619 CTTGAGACACCGCAACCCCAACCACTTCAACCACTTCAACCACTTCAAGCA 11678  
Db 23694 CAGAGCGCGCATCTGCGCAGGCTTGGCGAGCGCACTCGCTCCCGCGAGTGA 23635  
Qy 11679 ACCGACACACCTTTCGCGCGCGGTGTGGCGAGCTGACAACTGAACTCGGCTCTC 11738  
Db 23634 TGTGTGAGGCGCCACGCGCAACCGGACACAC-----CCTCGGCAACCCCATGAGCGCAAGC 23578  
Qy 11739 CGCCCTGCAAAAACCGACAGCGCGAGGAAAGTCACTTCGGCTGAAATCAT 11798  
Db 23577 CTTGATCGCGCTTACGGAACGAGACCGGCGAGGACCGGCGGCTGTGCTCGGCGCGT 23518  
Qy 11799 GTTGAAGTGAACCGACCCCGCATTCGACAGCCGGAAGCGGTGATGACAGAAATT 11858  
Db 23517 GAATCGAACCTGGGTCAACACCGAGCGCGCGGTGTGCGGACACATCAAGTGTCT 23458  
Qy 11859 CACATCGGCAACAGAGCTGAGATTTTCAAAATTCATTGACAGCA-----CCTCGGCTGT 11914  
Db 23457 GCTGGCGATGGGCGACGCGGTGTGCGCCAGACCTCTGACACCACTGCGCTCGCGCA 23398  
Qy 11915 CTTGAACCGAGCGCTTCGCACTCGCGCGTATCCGCTGGGCGCTGTAGAGAGTGAAGC 11974  
Db 23397 CGTGAATGAGCGCGCGGACAGTCTGCTCTTCAACGAAACAGAGAGTGGCCGAGAC 23338  
Qy 11975 AATTGGGAATGAAAGCGAAG--CTCTGGAATTACTCAAGCGGTCACTGTGGACCTGGA 12032  
Db 23337 CGGACAGCGCGCGCGGCGGTGTCTCGGCTTGGGCTGACGCGACCAACGCTCAAGT 23278  
Qy 12033 CCGCACTCGCGCTGCTGTGAGGTGTGAGAGCGTGTAGAGAGGACCGATCGGCAATTGT 12092  
Db 23277 CATCATGAGAGAGCGCGCGACCGGAGAGTCCGTGCGCGCGGAGCCACACAGGTGCC 23218  
Qy 12093 GGGGATGCGCTGTGTTACCCAGGCGGGCGACGTCACCCACGGACTGTGSCATTTCTGT 12152  
Db 23217 GGGCTCGTG---CCGTGGCGGTGTGCGGCAATCGAGGCGCGCTTGAAGGAGGAAAT 23161  
Qy 12153 CAATCCCAAGCGAGCTATTCGGGAGTTCCGACCGACCGTGTGATGAACTGTGAGACA 12212  
Db 23160 CGAGCGGCTCTCGCGCTGACCGGCGGCTCACCGGTGACGCTGGGCCCATCTCTCACAC 23101  
Qy 12213 GCTCTAGACCGGAGCCCGACCGCTCAGGAACAGTTTACCGGCGAGCGGAGGTTTCT 12272  
Db 23100 GGGGAGGCGGCTTTCACCCACCGCGGCTCTTGGCGCGCAGCGCGGCGGCTGACGGA 23041  
Qy 12273 CTATGACGCGGCGACTTTCGACGCGCGGCTTCTTGAAGTTTCAACGCGGTGAGCGTGGC 12332  
Db 23040 ACTGCGCGGCGGTTCGCGCCACGAGCGGACGGAAGTGGCGGTGCTGTGCG--GGCC 22982  
Qy 12333 AATGACCCGGAAGAGCGCTGTCTGGAACAATTGGGAAAGTTTGAACAGGCGG 12392  
Db 22981 AGGCGGTCAACGCGGTGGGATGGGCGGAGTTTGTCTCGGTTCCCGGTTCGCGG 22922  
Qy 12393 AATGACCCGAGGTCATGAGCGGAGACCGGAGCGGAGTTTGTGGGAGTCAATTCGGA 12452  
Db 22921 AGGCGCTGAGAGGAGGTGTGCGCATCTTCAATGCGGATTCGGAAGTATGTTCCGTG 22862  
Qy 12453 GAACTACCAACCGGATACACATCAGCCCTTCAAAGCATGAGGCTTACCTGCTCAC 12512  
Db 22861 ATGCGAGAGGCTTGAAGAGCGGAGTTTCAAGCAGCCCGGCTGTTCGCAATGAGGTGG 22802  
Qy 12513 TGGAGCGCGGCAAGCATTTGCGTGAAGCGGTATCTCTTCAACATTGGGCTTGAAGGCC 12572  
Db 22801 CGTTGTTCCGCGTGGCGGAGTCCCTGTGAGTGTGCGGC--GGAATTCGTGGGCGGCACTC 22744

OY	12573	TGCGATCATATCGACACCGCGTGTCTCTCTCGCTCGTGTGCCCTGCACTTGCCCTTGCCA	12632
Db	22743	GATCGGTGAGATCCGCGCGCGCATGTGCGCGGAGGTTCCTCGCTGCGGAATGCGGTGC	22684
OY	12633	AGCGCTCCGGTCCGGTGATATGCACATATGGCGCTCGCAGCGCGCGCTCCGTATGCGCCAC	12692
Db	22683	GCTGTTGGCGGCGCGGTGCGCGGCTGATATGACAGCGCTTCGCCGCGGCGCGCGCATGTGGC	22624
OY	12693	TCCCTTGGTCTTCAACCGAGTTCTCTCGCACGCGGCGCTGGCCGCAGACGCGCGTGCA	12752
Db	22623	CGTCCAGGCACACAGCGGAGGCGCGCGCACGGCTGTGTGACGGGGTGTGCATCGCGGC	22564
OY	12753	GGCGTTTTCGGCGCGCGCGCGACGAGACCGGCTGTCCAGAGGTGTGGGATGTCTGTGT	12812
Db	22563	GGTCAACGCGCGCGGAGCGGTGTGTATCGCGGAGACAGCGGAATCCTCGGATTCGC	22504
OY	12813	GGACGGGTCTCCGACCGCGCGCCACACGGTCAACCGTGTCTTGGCGGTGTGCGC----	12867
Db	22503	CAGGAGTTTCAACCGGCTGGGTGCTATGACACGGCGCTGCGGTTAGCCAGCTTCCA	22444
OY	12868	--GGCAGCGCGTCAACCGAGACGCGCGCAAGCAACGCGCTGACCGCACCCGATCGTT	12925
Db	22443	CTGCGCGGTATGAGAGCCATATGCTGAGAGACTTCCGCGGGGTTCGCGAGGAGCTGTCTGA	22384
OY	12926	CACAAATC-----AAGTCAATCGCGAGCTTTGGCCACGCACA	12965
Db	22383	CGAAGCCCGCGGATCGCGGTGTGTGAACCTTCACCGCGCACTCGCACCGAGGACT	22324
OY	12966	CCCTCCCGTCCGATGTGCATGTGCGTGGAGGCGCACCGACGAGGGACACACCTGGGCGA	13025
Db	22323	CGTCCGCTCGGCGAGATCTGGGTTCGGGCAATGGCGAGAACCTGTGCTTGCCGACGG	22264
OY	13026	CCCGATCGAGGCTTCAGACCCCTGTCGAAGCTTAACGTTACAGAACCGGCCCAACGCGCGCC	13085
Db	22263	CGTAGAGCGCCCTGGCGCGCCGAAGAGCGCTCGTCTTCTGAGACTGGGCCGAGCGGGT	22204
OY	13086	CCTCTGGTCGGAACCTCAAGTCAACATCGGCACTCCATGCGCGCTGCGGGTGTGG	13145
Db	22203	GCTACCGCGATGCGCCAGACACCTTGAGCGGCAACCGCGCATCGGCGTACCGGCTTGCG	22144
OY	13146	CGGGGTCAATCAAGATGTGTATGGCGTGGCGGAATGTGTCTGTCGCGGACGTT-----G	13200
Db	22143	CAGGAACTGTCGAGAGAGACCGGCGTCTGACCGCGCTGCCCACTGCACGTGATAG	22084
OY	13201	CATGTGATGAGCGCGTGCSCGCAATGTGATCTGTGCGCGGATGCG-----GTGCACTGCT	13256
Db	22083	CGTGGGGTGGACTGTGTCCGGATCTTTCGCGCGGACCGGTCGCCGCGTGTGACTGCG	22024
OY	13257	GACGAGAACGGTGCCTTGGCGCGCGCGGAGAGGGCGGCTAACGGCGGACAGATGTCACT	13316
Db	22023	CACCTACCCCTTCAGACACAGATGTACTGGCGGACCGCGCACCCGCGCGAGGGCGAC	21964
OY	13317	ATTGGGGTCAAGCGGCAACACGCCCACTCATCTCTGAGAGAACCGGCCACAAACT	13376
Db	21963	GACCGGTGCGCAGGACCCCGTGAACGCGGATTTGAGAGCGCGTGAAGCGCGGACT	21904
OY	13377	CCCGTCAAGAC-----ACCGCGGACGACGTCGCCGGAGAAATCAACGCGCGA	13424
Db	21903	CTCGTCCGCTCTCCGACACGCTCGAATCTGACACAGCGCGCACTGTGCGCCCTGTGCGCG	21844
OY	13425	CGAGGATGCGCGTATGTGCGATGAGGCTGTGCGCGCACTCCAGGGGTGTGCGCGTGC	13484
Db	21843	CCTGTGCGCTGCGGCGCGCAAGCGCGTGGAGCGCTTACCGTGAAGGCTGGGGCTACCA	21784
OY	13485	GGTGTGCGCCAAATGTCAGACCGGCGCTTGGCGCGCCAGGCGCTTGACGCCCACT	13544
Db	21783	CGTACCTTCAAGCGCGTGAACCGGACCGGCGCCCGGACCTTTCGCGAAGCGTGGCTGCG	21724
OY	13545	CACGACACCCCGGCGCTGCACCTCGCGGACGTGCGGTAACCCCTGCCACCGCGCGCG	13604
Db	21723	GCTGTCTCCAGGGAAGCGCGCAACGACGATGAACACTGCGGTACTGCAACCTCTCG	21664
OY	13605	CGTGTTCGACCAACCGCACCCCTCATGTGCGCGGACCGGACACCTTCTGCAAGACT	13664

Db	21663	CGATGCGGTGTATCCCGGAAATCGATCCGACCGACCGGATGCTTGGCCGACGCT	21604
Oy	13665	CCAGGCACTGCGCGCAGGCGMACCCAACCCCGCGTATCCACAGACGCGCCAGCGG	13724
Db	21603	CGGGAACTGCGCGMAACGGGMAACGAGTTACACCGCGTGTCTCTCTCGCAATCCG	21544
Oy	13725	GACCGGGAACGGGGAGGCGCGAGMAAAGACCGATTACTGTCTCCGACAGGGACCA	13784
Db	21543	TACGCTTTGCGCTTCCCTTTCGAGCCGCGCTTGCCGAGAGCGGTGCGGACTGGC	21484
Oy	13785	ACGCCCCGGGATGGGCCACGGGCT---CTACCAACACCAACCCGCTTGTGGCGCGCACT	13811
Db	21483	CGAGCGGGATCGACCCCGCGTGTGTGTCGTACACCGCGACGCGGTTCGGTGGACG	21424
Oy	13842	CAACGACATGTGCAACCCACCTCGAACCCCACTGACCAACCCCTCTCCCTCTCANC	13901
Db	21423	CTCGGAGAGGGAAGTACAGCCCGCCAGGCGGCGGTGTGGGGGCTCGCAGGATGCGCGC	21364
Oy	13902	CCAGGACCTCCAACCCAGGACACCAACCACTCTGAAGAAGGGCGCAGCTGCTCAGCA	13961
Db	21363	CTTGAACACCCGGAACCGCTGGGGCGGCGTGTGCACTACCGAGAGACAGACCGGCG	21304
Oy	13962	GACCCGCTAGCGCCAGCGCCGSC---CTCTTGGCTTCCAGGTGGCCCTCAACGCTCT	14018
Db	21303	TACGCGGAAACGGTTTGCGCGCTACTGTCCGCGCGCGCGAGAGACAGTGGCACT	21244
Oy	14019	CACGAGCGGTACACATCACTACCCCACTACTACGCGGAGACCTCCTGGGGAATCNC	14078
Db	21243	GCGGCTCTCGGCGGCTTCCGAGAGAGCGGTGTGGCGCGCAGAGACACCCCGCGAC	21184
Oy	14079	CGCGGCCACTGCGCGGATCTCTCACTCAGCGACGACACCTCTATCAACCAAG	14138
Db	21183	CCCTGTGCAACCGGCGGACGGTCTGTGTGTGTGCGCCCGGCTCGGACCGGAGACA	21124
Oy	14139	CGCCACCTCATGGAAACCATGGCCCCCGGACACATGACCACTCTCAACAGACCCCA	14198
Db	21123	CTGGCGCTGTGTGCGCGGAGAGGATGCGACGACTGTGTGTGGCGGACCGACGCG	21064
Oy	14199	CCATCATCCCAACCACTTCAACCCCGCACGMAAAGCATCTGCGCATGCGCGCATCAACAC	14258
Db	21063	ACCGGAGACGGGCGAGTGTATCGGCGAACTCGACGCCCTTGGGCGTGGTACGATGCT	21004
Oy	14259	CCCCACTCTCTGTCTACAGCGGACCCCGCACACGCTGTCAACATCAACCACTCTTG	14318
Db	21003	GACTGTGCGACCGGCGGACGATGAGCGCTGTGAGCGGCGCTGCGCGCTCCGAGGCG	20944
Oy	14319	CCAAACAAAGGATCAAAACAAAACCTTCCCAACCAACAGCTTTCATCTCCCCCA	14378
Db	20943	GCTAGCGCGGTGATCTACCGGACGGGCGGTCCGACGCTGACGCTTAGAAACGCGCAC	20884
Oy	14379	CACCAACCCCATCTTCAACCAATCTCACAGACACCAACCAACGCTTACTTACACCAACC	14438
Db	20883	CACCGGGAACCGGCGCATCTCTGGCGGCTGTACCGGAGAGTGGAAAGCTTGGCGCG	20824
Oy	14439	CCACACCCCTCTATCAACCGCAACACCCACCGGACCAACTCTCACCCCACTACTG	14498
Db	20823	CGTGGCGGAGCGGCGGACCGGCGCTGTGCGCCCTGGGCGGTTGCT---CTCTTCTCTTC	20767
Oy	14499	GACCAACAAAGCCCGCAACCGTGTGACTTACGCAACCAACCAACCAACCTTCAACCAACA	14558
Db	20766	GATGCGCGGACCTGGGAGTCCGGAAGCGGAGCAACGAGGCGCGGCGGAGGCCCACT	20707
Oy	14559	CGGGGTACACACTCACTGAACTGGAACTCCGAAACCACTTCAACCACTTCAACCAACA	14618
Db	20706	CGAGCGCTTGGCAGTATGTGTGTGTGTCGAGGATCTGCTGCACGCGGCTTCTGTGGG	20647
Oy	14619	CAACCTTCCCAACACCCCAACCAACCTTCAACCTTCAACCAACCAACCAACCAACCA	14678
Db	20646	CGGTGTGGGCGGACGCTCTCGGAGCGTGGC---TGACACCTGTGGGCGAAAGGGCT	20590
Oy	14679	AACCCACTCTTCAACCACTGCGCAAAACACACCACTTGGACCCCACTTACAC	14738



Db 20589 GCCCCGATGAGACCCCGCGGGCCCTGACCGCGCTCGCCGCTCCCTGGAGACCGGACAC 20510  
Qy 14739 GCACCAACAACAACCAACCCACACACCCACTCGACTCCCACTACCTCCCTCA 14798  
Db 20529 CCCCTCGGAGCGGTGCGGAGCTACAGTGGGACAGATTCCGCGCTTACCCCGAG 20470  
Qy 14799 ACACCAACAATACTGCTTCAACCAACCCGAGACCGGAGCGA-----CCGTCACCGAG 14852  
Db 20469 GCGGACAGCGCCCTGTTGCGGAACTCCCGAGGCCCGGAGCGCTGGCGAGTCCGA 20410  
Qy 14853 CGAAGCGGTGAGCAAGCAACCAACCCCACTCAACCCCGCTGCTGATGTCTCTGTGGCA 14912  
Db 20409 CCGGACCGCGCGGGAGACCGGAGATGCGCGTCCGCGCTGCGGCGGAACTGCGCGCG 20350  
Qy 14913 GTCTCCGAGAGAGAGAGAGAGAGCTGTGGCGCTGGTGGAGCAACCTGCGGCGCTGT 14972  
Db 20349 CCCGACCGCGAGCGGACCAAGAGCACTGTGGCCCTGGTCCGAGACCGGTGGCGGCT 20290  
Qy 14973 GCTGGGCAATGCACTCCGAGATGATGTTCCGAACAAGGCTTCAAGAGCTGGATT 15032  
Db 20289 GCTCGGATTGCGGAGCGCGACGCGTACCTCGGCGAGGCGTTCAAGGACTCGGCTT 20230  
Qy 15033 TGATTTCTCGCGCGCAATTCAGCTTGTATGATGATGCTGCTGTGAGAGTTGAGCTGCGCT 15092  
Db 20229 GCACTGCTGACCGGCTGACCTGCGCAACCACTGCGCGTCCGAGCGGCTTGGCCCT 20170  
Qy 15093 TCCGCGCAAGCTGATCTTGAATTACCCCACTCGAGTGGCGCTTGGCACTTCTCGGAGC 15152  
Db 20169 GCGCGCACTCTGCTGTTGACTTACCTCCAGCGGCGAGCTCGCGGTTACTTCCGAGC 20110  
Qy 15153 GCGGATCGTCGGA-----GCGGACACAGGCAAGCACTCGCTCGCT 15197  
Db 20109 CGAATCTCTCGGCGAGGCGGGAGAGACGCGGAGGAATCCCGCGGTGGTCCGAGCA 20050  
Qy 15198 AACTCGGCTCCCCGCGAGAGCGAGCCGATCGCATCTGCGCACTGCTGCTGCTGCTGCTGCT 15237  
Db 20049 GAGACCGCAACACCGCGAGAGACCCGATGCTCATGCTGCGCACTGCTGCTGCTGCTGCT 19990  
Qy 15258 TGATGTACGAGCGGTGATGATCTCTGCGAGGTGGTGAAGTGGTGGCACTGAGCGGATCGG 15317  
Db 19989 TGGGATCGGCTGCGCGAGAGACTTGGCAGCTGATGAGCGGAGAGCGGACGCTATCGG 19930  
Qy 15318 CGGATTCGCGAGGAACCGTGGTGGGACTCGACACGCTGTACMAACCGGAGCCCGAGCA 15377  
Db 19929 AGGCTTCCCAACGACCGCGGCTGGGACTGGACCGGCTGCGCAACCGGAGCCGAGAGCG 19870  
Qy 15378 CCAAGCAACAGCTACACCCGAGAGCGGCGGATCTCTTTACGAGCGAGCAATTTGATTC 15437  
Db 19869 CCGCGCGGAGACCGTCAACCGGCGAGGCGGATTTCTCTTACGACGTGGCGGACTTCGAGCC 19810  
Qy 15438 CGACTTCTTGGATTCAGTCCGCGTGAAGCACTGGCGATGAGCCCGGAGAGCGGCTGCT 15497  
Db 19809 CGGGTCTTTCGCGATCGCGCCGCGTGAAGCGATGATGAGCCCGGAGAGCGGATCTCT 19750  
Qy 15498 GCTGGAACAGCGTGGAGAGATGAAACAGCTGTACACCCGACAGCTCCGTG 15557  
Db 19749 GCTGGAAGCACTGGAAGGCGCTGGAAGGACCGGATTCGACCCCGCGCTGCGG 19690  
Qy 15558 CACACCAACCGGCGCTTTCGCGGCTGACCTACCAAGCACTAGCGCGGCGCTTTCCAC 15617  
Db 19689 CCGGCAACACCGCGGTTTCACTGCGGCGGCTCGGCGGCACTACCGGCGGAA----- 19638  
Qy 15618 AGCTCGGAGGAGTTGAGAGGATCTGAGGAGCAAGGAAGCGGAGAGTACGCTGAGG 15677  
Db 19637 -----GCGGCGACGCTGGGAGATCGGAGACCGCGAGTGGAGGCTGCTTCCGG 19585  
Qy 15678 TCGTGTGCTTACGCTTTCGCGCTGGAAGTCCGCGCTTCAAGTCACTGCTGCTC 15737  
Db 19584 CCGGCTGAGCTTCACTTTCGCGCTGGAAGGACCTTCCGTCAGCTGCAACGCGGCTGCTC 19525  
Qy 15738 TTTGCTCTGCTGCTGCTGCACTTGGCTGTAGGCGCTGCGGCTGCGGAGTTCAT 15797  
Db 19524 GTGCTCTGCTGCTGCTTCACTTGGCGCGCCAGGCGCTTGGCAACCGGAGATGCTCAT 19465

Qy 15798 GCGCTCGCGGAGTGGCTCAAGTATGTCAACCCCGGCGGAGTTGAGATTTCGCG 15857  
Db 19464 GCGCTGACCGGCGGTGTGAGCGGTATGTCCAGCCCGGTGAATCTTCTGATGTTCCGGA 19405  
Qy 15858 GCAAGCGGAGCTTGGCCGTGAGCGGCGGTGCAAGCGTTCTCGGACGCGCTGACGCGAC 15917  
Db 19404 GATGGAGGCTTGGACCGGACCGGCGCGTCCGCGCTTCCGTCGCGCGCGGCGGAC 19345  
Qy 15918 CCGCTGGGAGTGAAGGTGTCCGAATGCTGCTGTGAGAGCGGTGTCCGACCGGCGGCT 15977  
Db 19344 CCGCTGTGTCGAGGAGCGTGGCGTCTGCTGTCTGTAACGCTTCTCCAGCGCGCGCA 19285  
Qy 15978 CCGTCAACGAATTCCTCGCGGTGTGCTGAGGAGTGGCTCAATAGAGCGGTGCGAGCA 16037  
Db 19284 CCGGACGAGAGTGTCTCGGCTGACTGCGCGGCTCGGCTCAACAGAGCGCGCACGCA 19225  
Qy 16038 CCGGCTGAAGCGGCCCAACCGGCGGCTCCAGAGAGCTGTCACTCGGCTTGGCGAA 16097  
Db 19224 CCGGATCAACCGGCGCAACCGGCGCTCGAGCGCGCGCTCATCCAGCGGCGCTGGCGAA 19165  
Qy 16098 CCGGACCTGAACCCCGCGGAGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 16157  
Db 19164 CCGGAGGCTGAGCGCGCGGAGCTGAGAGCGCTGAGAGGACACAGGACCGGACACCT 19105  
Qy 16158 GCGGACCGGATCGAGGCGCGGCGCTTCTCGGCACTTACGAGACGCGCGCGCA 16217  
Db 19104 GCGGACCGGATCGAGGCGCGGCGCTTCTCGGCACTTACGAGACGCGCGCGCA 19045  
Qy 16218 GGAACCGCTGTGCTGAGGCTGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 16277  
Db 19044 ACTGCGCTTGTGCTGAGGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 18985  
Qy 16278 TGTGGGCGGAGTCAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 16337  
Db 18984 CATGCGGAGTGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 18925  
Qy 16338 GCATGTGATGAGGCGCTGCGCGATGTGAGCTGCTCGCGGAGGCGGAGTGAAGTGAAGT 16397  
Db 18924 GCAATGTGAGAGGCGCTTCTGCGCATGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 18865  
Qy 16398 GAGAGCGGTGCTGAGCGCGGCGGAGGAGGCGGCTGCGGAGGAGGAGGAGTGAAGTGAAGT 16457  
Db 18864 GAGAGCGGCGAGCTGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 18808  
Qy 16458 CCGGCTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16517  
Db 18807 CCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 18766  
Qy 16518 GTCAAGACACCGCGCGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16577  
Db 18765 -----CGTACCGACCGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 18727  
Qy 16578 AGCGGCGGCGAGCGAGCGCGGATCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16637  
Db 18726 GCGGCGGCGG-----CGTACCGACCGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 18717  
Qy 16638 AGGAGTGTGAGCGGCTGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16697  
Db 18716 -----CGCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 18661  
Qy 16698 GCGCTGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16757  
Db 18660 GAGCTGAGCGGCTTACGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 18601  
Qy 16758 CTTGCGCAAGCGCGCGGCTGTTGAGCAACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16817  
Db 18600 CACGCGCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 18541  
Qy 16818 CACTTCTGAGAGCACTTCAAGGAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16877  
Db 18540 GGAATCTGCGGAGGAGTGGCGGCGGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 18482

QY 16878 CAGCAGCGCCCGGAGCGGAGACCGGAGAGCGCGAGGAAAGACCGCATTCATCTG 16937  
 Db 18481 -----GGGGCGGGGTGCGGAGCGCGCGCGGAGCTGCGCGTCTGTT 18439  
 QY 16938 CTCGCGACAGGGGACCCAAACCGCCCGGCGATGGCCCAAGCGCTCTACACACCCACCCGT 16997  
 Db 18438 CTCGCGCGCGGAGATGCAAGCGCGGTGGGCAATGGGAACTGCAAGCGCGCTTCCCGT 18339  
 QY 16998 CTTGCGCGCGGACTCAACATCTGACCGCAACCTCGACCCCGCACTCGACACCCCT 17057  
 Db 18378 GTTCGCGAGGCGCTGAGAGAGGTGACGCGACGCTTGAGAGTGAATCTCCGCT 18319  
 QY 17058 CTTCCCGCTCTCAACAGAGACCGGACCGGAGACCGACCACTCCCTGAGAGAGCGC 17117  
 Db 18318 GCGGAGGCTCATGTTGCGGAG-----TC 18295  
 QY 17118 CGCACTGCTCCAGCAGACCGCGTACGCCAGCCCGCGCTTTCGCTTCAGAGTGCCT 17177  
 Db 18294 GAGCGGCTGAGACGAGCGGCTACACCGCGCGCTGTTGCGGATCGAGTGCCT 18235  
 QY 17178 CCACGCGCTCCCTCAACGAGCGGTACACATCAACCGCCCACTACTAGCGCGAGACTCCCT 17237  
 Db 18234 GTTCCGCTCGGT---GCGTCTGAGGCAATCGCGCGGACTTGTGTCGCGGCGACTCAT 18178  
 QY 17238 CGCGCAATCAACCGCGCGCCCACTGCGGCGCATCTCACTCACTCACTCACTCACTCACT 17297  
 Db 18177 CGCGCAATCAACCGCGCGCGGAGCATGCGCGGCTCTTCTCCGAGAGTGCCTGCGCT 18118  
 QY 17298 CATCAACCAACGCGCAACCTCATGCAAAACATGCCCC---CGGCACTGACACCTCT 17354  
 Db 18117 GGTGCGCGGAGCGGCGCGCTGATGAGCGCTGCGCGCGGCGCGCGCATGCTGCGCT 18058  
 QY 17355 CCACGACCGCCCGGACCATCAACCGACCGCGCGCGCGCGGAGAGAGCTGCGCAT 17414  
 Db 18057 CGAGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 18007  
 QY 17415 CGCGCGCATCAACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17474  
 Db 18006 CGCGCGCGCATCAACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17947  
 QY 17475 CATCAACCGCTCTGCGCAACAGGATCAAAACCAAAACCTTCCCGCAACCAAAACCG 17534  
 Db 17946 CTTGCGGAGAGATTCACCGCGCGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAG 17887  
 QY 17535 CTTGCACTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17594  
 Db 17886 ATTTCATCTGCAATGAGAGCGGCTTCTGAGAGCTTCGAGAGAGTGCAGAAAGCGT 17827  
 QY 17595 CACTACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17642  
 Db 17826 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17767  
 QY 17643 CGACCACTCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17702  
 Db 17766 GCGGAGAGGTGCTCCCGGAGTCTGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 17707  
 QY 17703 CACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17762  
 Db 17706 CGACGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17647  
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 Db 17586 CGTACCGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17527  
 QY 17877 AACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17936  
 Db 17526 GGTGCACTGACGAGAGTGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17467  
 QY 17937 CACCGACCT---CGACTTCCCGACCTACCGCTTCAACAGCAGCACTAGGCTGGAAG 17993

Db 17466 GCCCGCGCGACCGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17414  
 QY 17994 CACACAGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCG 18053  
 Db 17413 -----CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17386  
 QY 18054 CGGACCGCGCAGAGGTGAGTGCAGGTTCTGAGAGCGCGGTGCGCGCGCGCGCGCGCGCG 18113  
 Db 17385 CCGCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17326  
 QY 18114 GGTGCGACCAACGCTGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18173  
 Db 17325 CTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17269  
 QY 18174 CTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18233  
 Db 17268 CGCGGACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17209  
 QY 18234 AACCTGAGAAACCGCTCAACCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18293  
 Db 17208 CACTTGTGAGCGCTGAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17149  
 QY 18294 CATCCCGGAAACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGAC 18353  
 Db 17148 GATCCCGGAGGCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 17089  
 QY 18354 CCACGCGATCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18413  
 Db 17088 GAGACCGTACGCTTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17029  
 QY 18414 CCACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18473  
 Db 17028 CCAACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16969  
 QY 18474 CTTCTGCGCGCTGAGAGAAACCGGACCGGACCGGACCGGACCGGACCGGACCGGAC 18531  
 Db 16968 GAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16909  
 QY 18532 -----CTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 18584  
 Db 16908 GCGCGCGCGCTTCAACCACTTGTATGAGGCGCGCGCGCGCGCGCGCGCGCGCG 16849  
 QY 18585 CTTCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18644  
 Db 16848 CTTGAGGTGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16789  
 QY 18645 CACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18704  
 Db 16788 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16729  
 QY 18705 CGCGCGAGTATGAGACTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18764  
 Db 16728 GGGTGTCTGATATCACTTGCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16669  
 QY 18765 AACCTACCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18824  
 Db 16668 TGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16609  
 QY 18825 CGCGCGCGCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18884  
 Db 16608 CGCGAGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16555  
 QY 18885 CGGAAACCGCTTATCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18944  
 Db 16554 CGGAAACCGCTTATCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16495  
 QY 18945 CACGACCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19004  
 Db 16494 ---GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16438  
 QY 19005 CACGCGCAACACTCTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19064

Db 16437 CGGCGGAGACGACTGCGGGCGGAACTACCGCGCTCGGCGGAGCTGACCTTCACCGC 16378  
Qy 19065 CTGCGACACGACGACACCGAGACCACTCCAACTCTCTCAACACCATCCCCCAACA 19124  
Db 16377 ATGGACCGCCCGGACCGGAGCGGCTGGCGAAGTCTGGGGGACATCCCGAGACGTC 16318  
Qy 19125 CCCCCTCAACACCGTATCAACACCGGAGCATCTTGAAGACGACCTTCACCAACT 19184  
Db 16317 CCCCCTGACCGGCGTGTCAACACCGCGCGGTCTATCAACGAGGTGTCTTGAACAGCT 16258  
Qy 19185 CACCCCAACCACTCAACAGTCTCTCGGCGCAAGCCCAAGCGCCCACTTCTCA 19244  
Db 16257 CACCCGAGCGGTTCTGAGAGGCTTCCGCGCAAGCGCGCTCGGCGCTTCA 16198  
Qy 19245 CCAACTCAACCAACACACCGCCCTCAAGCGCTTCTCTCTACTCTCTCGCGCGCGCAC 19304  
Db 16197 GCACTTCAACCGAGACCTGAGACTTGGCGGTGTTCCGCTTCTCTCTCTCTCTCGGAGC 16138  
Qy 19305 CTTGCGGCAACCGGCGCAAGCCCACTAGCGCGAGCAACCGCTTACTTGAAGCCCTGCG 19364  
Db 16137 GGTGGGCAACGCGGCGCAGGCGCACTAGCGCGCGCAACCGCTTCTTGAAGCGCTGCG 16078  
Qy 19365 CCAACACCGGCAACACCACTCTCCGCGCAACGATCGCTTGGGCACTTGGCAAG 19424  
Db 16077 CGAACGCGCGCGGCGCGGCGCTGCGCGCATCTCTCGCTGGGTTGATGGGAGG 16018  
Qy 19425 AAACGAGCTGGCGGACTGTGCA---AGTCAGGGAATCTCTCGCGCGCGGAGTTGGC 19481  
Db 16017 CGGCGGAATGGCGCGGACGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 15958  
Qy 19482 CATGCGCGCGGAGTTGGCGGTCAACAGCTTTGAACGCGCGGATCGGAGCGGCGCGGAG 19541  
Db 15957 GCTGGACCGGAGCTCTGCGGTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 15898  
Qy 19542 TCTCTCTGCTCGCGGATATGAGTGTGAAGAAATTGGGACCGGTTCTTCTCAAGAGTCTG 19601  
Db 15897 CGAGGTCTGTGCGCGCATGGAACGCGACCTGTTCTCTGCTCTTCAACGCGGCTGAGC 15838  
Qy 19602 GGTCT---TTGCTGAGGACCTTCCCGCAGGCAAGGAACTGAGGAGGCGCGGAGTACG 19658  
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Qy 19659 TGAGCAGACGAGAGACCAAACTTCGCGCACTCTCATGAGTCTGCTCACTTCGAGCA 19718  
Db 15777 CGAGGACACACGCGGCGAGCGGCTGCGCGGAGGTGACGCGGCTGCGCGCGGCGGCAAG 15718  
Qy 19719 GGAGAGAGGCTGTCAAGCTCTGCTCGCATCTTCGCGGAGTGTCTTGGCGGAGCA 19778  
Db 15717 CTCCAGGCGCGTACGCGGACCTGTGTGCGCACCGGCGCGGCGGCGGCTGTAGCA 15658  
Qy 19779 CTCCAGGCGCATCCCGCGCGGCTGTGTCAGGATCTAAGGTTTGAAGTCTGCGTGGCG 19838  
Db 15657 AGCCGACCGGAGGCGCGGCGGCGGCGGCTGCTGTAACCTGCGCTTCACTCTCAAGCG 15598  
Qy 19839 GGTGAGTCTGCGACACACTTCGAGCAACAGAGGCTGTCTGCGGACGACTCTGCT 19898  
Db 15537 CGTGAACCTGGGCAACAGCTGGGCGCGGCTACCGGACTGAACCTGACCGGCACTCTG 15538  
Qy 19899 CTTGATTAACCCCAACCCCAACCAAGCTGCGCAATTTCTGCT--- 19940  
Db 15537 CTTGACACACCCCAACCCCGCGCGCTGAGCAACCACTCTGAGCTGTGCTGCTCCGA 15478  
Qy 19941 --- 19940  
Db 15477 CGAGGACCCGCGGAGGAGGAGCAGCGACGACCGGACCTCTCGGCGATGAGGC 15418  
Qy 19941 ---CTCGAGATCGCGGAGTTTCAGCCGCAACT 19972  
Db 15417 CCGTCTCGCTCCGCTCTCCGTGGCCAGCTGGCGAGATCGGCGTGTCTGAAACCTCTGCT 15358  
Qy 19973 CAACCTCCGCTTTCGCGGACCCCG--- 19995  
Db 15357 GAAAGCTCGCGCGCGAGACGCGGTGCTCGCGCGCGAGGCGCGCGCGGCGGACCGGAGC 15298

Qy 19996 --- 19995  
Db 15297 GGAGCGCTACGAGAGTGCATCGACGGGATGACATGCGGACCTGTGTGAGGGGCAATT 15238  
Qy 19996 --- 19995  
Db 15237 CGAGCGAATTCCCCCAAGACCGCTGAAGAGCGGACATGACCATTCAGTGAAC 15178  
Qy 19996 --- 19995  
Db 15177 GTGTCGACGCTTCGCGGCTCGCTGAAGAGACCGAAGACTTGGCGCGGACAGACCC 15118  
Qy 19996 ---GCAGACTGATAGCCGATCGCATGTTGGCATGCGCTGTGCTTCCC 20046  
Db 15117 AAGCTGTGCGCGCGGCGGCGGACGAGACCGATTCGATCTGGGAGTGGCTTGGCGTACC 15058  
Qy 20047 GCGGAGTGAATCTGCGGAGACGACTTCTGGGATGTATCTTCTCGAGCAGAGCGGATC 20106  
Db 15057 GCGGATGTCAGTGCGCGGAGGACCTGTGGAGCTGTGACCGCGGCGAAGGACGCGCATC 14998  
Qy 20107 GCGGATTTCCGACGAGCCGCGGCTGGGACCTGAGACGCGTCTAGACCCCGGACCCGAC 20166  
Db 14997 GCGCGGTTCCGACGAGACCGCGGCTGGGACCTGAGACGCGTCTGCGGAGCGCGGCTGAC 14938  
Qy 20167 CACCCGCACTGTCTACACCGGAAACGCGGGAATTCTCTTACAGCAGCGGCACTTGCAC 20226  
Db 14937 CCGCGCGGCAACGCGCTGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 14878  
Qy 20227 GCGGAAATTTCTGCGCATAGCGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 20286  
Db 14877 GCGGACTTCTTGGGATCTCACTGCGGAATCGTACGATGAGACCGGACAGGCGCTC 14818  
Qy 20287 CTTCTGAAACCGGCTGGGAAACGATGAAACCGCGGCACTCAACCCGACACCTTCAC 20346  
Db 14817 CTGCTGAGACCTCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 14758  
Qy 20347 GGCACCCGCAACGAGGAGTCTTCAACCGGACCAACGAGGACGAGGAGGAGGAGGAGGAG 20406  
Db 14757 GCGAGCGGACACGCGGCTGTTCATGCGGACCAACGCGGAGGAGGAGGAGGAGGAGG 14698  
Qy 20407 CAGGCGCGGAGCGGATCCGAGGAGTTGCTGTGACCGGAGGAGGAGGAGGAGGAGGAG 20466  
Db 14697 CGCTCTCTGCGCGGACGCGGACGCGGAGCATCGGACCGGAAATGCGCGGAGGAGGAG 14638  
Qy 20467 GCGGAAATCTCTACATCTCTGCGGTTGGAAGGCTGCGGCTGACCCCTGAGACAGAGCT 20526  
Db 14637 GGGAGGCTGTGTACAGCTGTGGGCTGTGAGGAGGCGCGGAGGAGGAGGAGGAGGAG 14578  
Qy 20527 TCTCTCTGCTGTGCGGCTGTGACCTGCGGAGTCTCTCAGGTCGGGTAATGACG 20586  
Db 14577 TGTCTCTGCTGTGCGGCTGTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 14518  
Qy 20587 ATGAGCTTGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20646  
Db 14517 CTGGGCTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 14458  
Qy 20647 GCGGAGCGGAGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 20706  
Db 14457 AGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 14398  
Qy 20707 ACCGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 20766  
Db 14397 ACCGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 14338  
Qy 20767 AACGATCAACGATGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 20826  
Db 14337 AACGAGATCCGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 14278  
Qy 20827 AACGATCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20886  
Db 14277 AACGCTTCAACGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 14218

OY	20887	AACGGGAGACCTGACCCCGCCGAGAGTGAGTGGGAGAGGCCACCGGACACCTG	20944
Db	14217	GCCTGCGGCTGTGGCTTGGAGCGTGGACGTGGTCCAGAGGCCACCGGACCTCCG	14158
OY	20947	TTGGCGGACCCGATCTGAGGCCACGAGCCACTCTCGCGACCTACGGACAGACCGTCCGCG	21006
Db	14157	CTCGGTGATCCGATGTAGAGGCCACGCGGTGTGGCCACGTACGGTCAAGACCCGACCCC	14099
OY	21007	AACGGGCGGTTGTGGCTGGGCTCCGTCAAGTCCAACTGCGACACACAGGCGCGCGCG	21066
Db	14097	GAGCGGCGCGCTGCTGGTGGGGTCCGATCAAGTCCAACTCGGACCTAACCCAGGCGCGCC	14038
OY	21067	GGCGGTGGCGGAGTGAATCAATATGTGATAGGCGCTCCGCGACCGGACATCTCCACCGACT	21128
Db	14037	GGCGGGGAGGAGCTGATCTAATATATCTTGCGCATGGGAGACGGTGTCTCGCCCAAGAG	13978
OY	21127	CTCCACGCGGATGAGCGGCTCGCCGATGTGGACTGTGCTCGCGGGGTGGGCTGAGCTGCTG	21186
Db	13977	CTGTATCGCGCATGTGGCTCTCTCCACGTGGACTGTGACAGTCTGGGGAGGTGGAGCTGTG	13918
OY	21187	AACGAGACGGTGCCTTGGCCCGGCGGGAGGGGCGGCGCGGAGAGTGTATCA	21246
Db	13917	AACGAGCGCTCAGAGTGGCC---CAAGGCGGACCGCCGCTGTGGCGGCGCGTCTCTG	13861
OY	21247	TTCCGGCTCTACGGGACCAACGCCCACTGATCTCTGAAAGACACCCCGCCAGCTTT	21306
Db	13860	TTTCGGCATCAGCGGACCAACGCCCATGTGATCGTGGAGCAGCGGAAACCGACGAAAGG	13801
OY	21307	CCGGGGGGGACACAC---CGCCACGAGAGATGCCCGGATGGGG	21346
Db	13800	CCGGTGGCGGAAACCGGGGGTTGGCGCCCGCGGTGTCCATGCTGGTGTCCGCAAGACC	13741
OY	21347	AGGAGGCTGCTGCGCGGACGTCTGGGG-----TGTGGCGGTGGCTGTGGCC	21396
Db	13740	GAGAGGGGCTGGCGGACAGCTGCGCGGATCTCTTCGCGAGGGGACACGGGTACCG	13681
OY	21397	AACTTCGACCGCGGCGCTCGCGGCCACAGGCCCTGAGCGCCACTCACCAACAC	21456
Db	13680	GTGACGTGGAGATTCTGCTCGCTCTCGGGCCGTTTCGGCGTTTCAGACACCGCGGGTGTG	13621
OY	21457	CCCGGACCTCGACTCGCGCGGACGTGGAATACCTCGGCCACCGCGCGCGGTTCGAC	21516
Db	13620	CTGGCCCACTGGCCCGGACGCGAGCTCTCCGAGCGGCGCCGGGGCGCGCGAGACGAC	13561
OY	21517	CACCGCGCAC-----	21527
Db	13560	CGCCCGCTGGCGGTGTCTCTCGGGCAGGGGTCTCAACGGGTGGGTATGGGCGGGAG	13501
OY	21528	-----CTCATGCGCGCGGACCGGACACTTCTCTGACGACTTCAGGCACTCGCC	21579
Db	13500	TTGTATGTCCGGTTCCTCCGGTGTTCGCGGAGCGCTTGACAGAGGTGTGCGGCACTTCGAT	13441
OY	21580	GCAGGCGAACCCACCCCGCGGTTCATCAACAGAGGCGCCACGGCGGAGACCGGAGCCGGG	21639
Db	13440	GCCGGGTTGGGAGACGTGATGTTTCGGTATGCGAGGGGTTTGACAGACCGGGTTCAAG	13381
OY	21640	GAGGCGGACAGAAAGACCGGATTCATCTGCTCGGACAGGGGCAACCCAGCCCGGCACTG	21699
Db	13380	CAGCCCGCGCTGTTTGGCATTTGAGGTGGCGTGTTCGCGTGGCCGAGTCTCTGGGTGTG	13321
OY	21700	GCCCAAGGCTCTACACACACCCACCCGCTTTTGGCGCGGACTCAACAGATCTTGACCC	21759
Db	13320	CGGCGGATTTTCGTGGCGGGGCACTGATCGGTGATGCGCGCGCGCATGTCCGCGG	13261
OY	21760	CACCTGCAGC-----CCCACTCGACACACCC	21786
Db	13260	GTTGTTCTGCTGACGATGCGGTGTGGTGGGCGGCTTCGGCGCGGCTGATGAGGCGC	13201
OY	21787	CTCTCTCCCTCTCTCAACCAAAACGACACGACACGACACGACGAGACCGGCGGACTG	21846
Db	13200	CTCCCGGCGGGCGGTGCATGTGTCCGTATACAGCGCTCGGAGAGCGAGGTGGCCGACGG	13141
OY	21847	CTCCAGACGACCCCGTACGCGCCACCGCGCTTTCGCTTCACAGGTGACCTTCACCGC	21906

Db 12060 GAGGGCTTCTACGAAAGGACCGGTTACGGCCCGGCTTCCAGGGCCCTGCGTTGCGGTGCG 12001  
 Qy 22823 -----TGCGCGAAACCTCTGACATGACGCGCTCTGCTCTGAGACG 22863  
 Db 12000 AGCTGCGGGGAGCGGTGCTTACGCGGAAGTGGCTCTGCGGACCACTGGCCGAGAGACGCC 11941  
 Qy 22864 GTGTGCTCCGCACTCTCGGCTTGAGACCGGCAACCAAGACCAAGCCCGCATCAAC 22923  
 Db 11940 GGGGCTTCGAGCTCCATCCGCGCTGCTGAGCGGGGTGTTGCACTGCGACCGCATCCGC 11881  
 Qy 22924 TGGACTTACAGAAACTGGAACCCCTTCACTCTCC-----CACACCCACCA 22974  
 Db 11880 GGGGTGCGAGCGCGGAGACGACCAAGTTCCTGCGCTTTCGCTGCGAGGGCTCTCGCTGAT 11821  
 Qy 22975 CCGCACAAACCTGCTCATGCGCATCCCGGAAACCGACCAACCGACCGCCACATCAC 23034  
 Db 11820 GCGGCGGGCGCTTCTGCTCTGCGGCTCGGGTCTGGAAGACCGGAGACGATCTCGATGCC 11761  
 Qy 23035 AACATCTTACCAACCTTCCACGACGACATCACCCCATCCCTCTCATCTGTCAACGAC 23094  
 Db 11760 ATCGGGCGCTGCGACCGGAGCGGACCCGTACTGTCCGCGAGGCGATGCTGATGCGG 11701  
 Qy 23095 ACCGACCAACACCCCGCAACCTTCCACGACACCTTCCACGACCGGACCAAGACCCCA 23154  
 Db 11700 GCTTACCGCGACCCCGGACCCGCGACGCGGCGGACCGGACCGGCGGATGAG 11641  
 Qy 23155 AAC----- 23158  
 Db 11640 CTGTGTGCTTGAAGTGGGTGTCGGGCTCTGAGTGGCGCGCGGGGTGCGGTGCGTG 11581  
 Qy 23159 -----ACACCAAC 23166  
 Db 11580 TCCCTGGGCGGGATGAACTGGGTGTGGGCGCGGTGCGCTCTGTTGGCGGACCTCTCC 11521  
 Qy 23167 GGAACCATACCGGCGCTGCTCTCTCTCTCTGCGCTTCCAGAAACACCCACCCCAAC 23226  
 Db 11520 GGGGACGAGGATTTGATGTGCTTCCCGTGTCCGGTGTGGGTGATGTGCTCTGCTGCG 11461  
 Qy 23227 CCGCACACCCACCGGAGACCTCTCTCAACCTCACCCCTCCCAACCCACCCCAAC 23286  
 Db 11460 GGGACGAGTTGACGCGCCGAGCGCTCGGTCTTCAAGAGTGGTCCGGCCGCGAGGGC 11401  
 Qy 23287 CACCCACCAACCCCTCTGTGTACGCAACCAACGCGCACGACCCACCCCAACGAC 23346  
 Db 11400 TCAAGTGGTCTCGGTTTGTGTGTCTGCAACCGGTACCGGCTCTCGGCGGACGAAGCGAG 11341  
 Qy 23347 CCGCTTCAACACCCCAACCCCAACCTGTGGGATCTGCGCGACCAACCTCTCTGAA 23406  
 Db 11340 TCCGTACGCGATGTGGCGCGGCTCGGTGTGGGTGTGGTCTGCGCTCGGCGGATCGAG 11281  
 Qy 23407 CACCCACCCCAACCGCGGGAATCATTCACCTTCCCAACCCCAACCCCAACCCCTC 23466  
 Db 11280 AGTCCGGGCGGATCGC---GCTGTGTGACCTGTGAGGCGGATCTCGGCGATCTCGCGAG 11224  
 Qy 23467 CACCACTTCAACCAACCTTCAACCCCAACCCCAACCAACCTTCCATCTCGAC 23526  
 Db 11223 GTGCTTGGGGGTCTGCGCGGTCTGTGTGTGCTGCGGGAGCGCTCAAGTCTGATGTGGCGAA 11164  
 Qy 23527 ACCGCAACCCACCGCGGCTTCAACCCCAACCTTCAACCCCAACCAACCAACCC 23586  
 Db 11163 GGTGTGTGTGGGTGGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 11104  
 Qy 23587 ACCCCACCCCAACCGGAAACCACTTCAACCGGCGGAAACCGGCGGCTTCCGCAACCA 23646  
 Db 11103 GAGTGGATGTGGAGCGGACGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 11044  
 Qy 23647 CTACCCCAACCAACCTTCAACCCCAACCAACCAACCAACCTTCTCTCAACCGGAG 23706  
 Db 11043 TTGGGCTCGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10984  
 Qy 23707 GGGCCCAACCCCAACCGCAACCACTTCAACCCCAACCTTCAACCAACCAACCAACCA 23766  
 Db 10983 GGAACCGAGCGCGGCGTCTTCCGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10924

Qy 23767 CTACCATCACCACTTGGACACGAGCAACCAACCAACCAACCAACCTTCAACCAAC 23826  
 Db 10923 GTACACGTCGCGGCTGTGAGAGTGGCGGACCGGGCGGGGTGTGACGCTCTGTGCTGCC 10864  
 Qy 23827 ATCCCCCAACCAACCCCTTCAACCGGATCTTCAACCGGAGCGGTCAATCTTGTGCC 23886  
 Db 10863 GTACCGGCGGAAACCCGTTTACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10804  
 Qy 23887 CCGGTGTGGAACCGAATGCGGAATCTTCTTCTGTTTACGGGAGCGGAGCAACGGGC 23946  
 Db 10803 CTGTGACCTTGTGACACCGGAGCGGCTGTGACCGGATCTGCGCGCGAGGTGATCG 10744  
 Qy 23947 GCGGCAATCTGTGATGATGCTCTGAGACCAATGAAACGTTTGAACACTTATCTTCT 24006  
 Db 10743 GCTGTGATGTGTGACGAGGCGGACCAAGGACCTTCA---CTGTGCGGCTGTGTGTGTGT 10687  
 Qy 24007 TCGTGGGCGCGCGCTTGGGGGACGCGGAATGATGCGCATCTCGGCGGCAACGCA 24066  
 Db 10686 TCGTTCATCTCCGGGGGTCTCGGTCTCCGGAACGCGCAACTACGCGGACGACGCTG 10627  
 Qy 24067 TACCTGACGCGGCTCGGACGCACTGTGACACATGAGACTTCCCGGGGCAATTCATGCC 24126  
 Db 10626 TTCTGTGATGTGTGCTGTGACCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 10567  
 Qy 24127 TGGGCGCCCTGGGCGGAAAGGCAATGTGCGC-----CGGTGATGCGG 24169  
 Db 10566 TGGGGCGCTGTGACCGAGAGCGGCGGCACTGACCGGACCCCTCTCCGACACGATGTGAG 10507  
 Qy 24170 CTATGTGTACCTGTGAAAGCGGCGGATCTTCCGAGTGAAGCAACGATGCGC----- 24221  
 Db 10506 CGGATGCGCTCTACGCGACCGGACCGGCTGAGCGGCGCGGCGCTGCGCTGTTCAC 10447  
 Qy 24222 -----GCTCGGCAATTCATCTGTGCGCGGGCGGAGCGG 24255  
 Db 10446 GCGGCTGTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 10387  
 Qy 24256 CCGAATTCACCTGTATCATGCGGACATCATGAGGAGCGGCTTGTCTTCCGCTTCAAC 24315  
 Db 10386 CGGGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 10327  
 Qy 24316 G-----CTGACGCGCAACGCGGCTCATGAGGAC 24345  
 Db 10326 GCGGTGAACGAGCGGAGAGACGCGGCTGTCTTCTGCGGACCGGCTGCGGCGGCGGCG 10267  
 Qy 24346 ATTGCGAGGTTGCGCAAGCGGCTTCAAGAGCTGTG--AGCACTGTGTGTGTGTGTGTGT 24404  
 Db 10266 CCGAGGAGCGCGCGGCTGTATGACGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10207  
 Qy 24405 GACCAAGCTGAGCGGATGTGAGCGTCTTCTCGTGTGAG-----CGATTGGCC 24450  
 Db 10206 GGAACGCTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10147  
 Qy 24451 CGACTGAGCTCTCAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24510  
 Db 10146 TCCGTGACCTCGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10087  
 Qy 24511 ACCGTTCTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 24570  
 Db 10086 GCGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10027  
 Qy 24571 GGGTTGAGCTGTGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 24612  
 Db 10026 CTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9967  
 Qy 24613 GCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 24672  
 Db 9966 GCACTGCGCGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9907  
 Qy 24673 GAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 24732  
 Db 9906 CAGATCTTGTGAGATGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9847



QY	24733	CTGTGAAATGCT-----	24744
Db	9846	CGGCTGAAAGCCGCGACGACGATCTTCGCTTCATGCAACGAGCTCGGCGT	9787
QY	24745	-----	24744
Db	9786	CACAGCATCGTGAAGTCGAGCCCTTAATTCACGGAAGTTTCCAGCATGCGAAGC	9727
QY	24745	-----CTCCGCAAGTGGCCATCGGCG-----	24767
Db	9726	ACAAGCCGACGACAAAAGCTGTTGACTTACTCAAGTGGGTACGAAAGACTTGACCC	9667
QY	24768	-----TACGCTGAGGACGAAACCGATGCGCATATCG	24799
Db	9666	AGACCCGCAACGCGCTTCGGGAAGTGAAGTCGCGCAAGGACGAAACGATAGCATCTGTG	9607
QY	24800	GTATGAGCATGTGCTTCCCCCGGAGTACGTTTCGCGACGACCTGTGGGAATTGCTCG	24859
Db	9606	GGATGCTTCGCGACTACCGGGTGGGTGCGGTGCGCGGAAAGATTCTGGCAGTTGTTGA	9547
QY	24860	CTTCGGGTAAAGGACGCTATCGGCGTCTTCGCGACGACCGGCGTGGGACCTGACACGCG	24919
Db	9546	AGGACGCGCGGACCGGACTTTCGACCTTCCACGACCGCGCTGGACCTTCGACCTGC	9487
QY	24920	TCTACGACCCCGACCCCGACCAACCCCGGACCTGTCTACACCCGAAACCGCGGATTCCTCT	24979
Db	9486	T-----CGCGGCGACGCGCAGTGGCAGAGTGGCCACCGCGAAGCGGCTTCATCG	9436
QY	24980	AGCGGCGAGGCACTTTCGACGCGGAAATTTCTTGGGATCAGCCCGCGGAGCCCTCGCA	25039
Db	9435	AGCGCGC-----CTCGTTTCGACGCGGCGCTTTCGGGATCTCGCCCGCGGCGGTGACGA	9379
QY	25040	TGGACCCCCGAGCAACGACTCTCTCGAAACCGCCCTGGGAAACCATTCGAAACGCGCGCA	25099
Db	9378	TGGACCCCCGAGGACGACATCTCTGCTGAGATCTCTCTGGAGGCGCTTGGACGCGCGGAA	9319
QY	25100	TCAACCCCCCAACCTTCACGCGCACCCCAACCGAGTCTTCGCGGAAATCAACGCTCAAG	25159
Db	9318	TGACCCCGGTGCTCGCGGGGACCGAGACCGGTGTCTTCGTGGGCAAGACGGGTATCG	9259
QY	25160	ACCAAGCGCGCATATCGGCAAGCCGTGATGTGAGACATTCGAGGGCTTACGCTTGA	25219
Db	9258	ACTTACATCAACACCGGTATGAATCTCCG-----CGAGGACATTCGAAAGCCACGCGACGA	9205
QY	25220	CGGACGATTCGGAAGTGTGGGCTCGCGCGGGGTGGCTTACACGCTCGGCGCTCGAAGGCG	25279
Db	9204	CGGCGCTTATCGCCAGCATCTCTGCTCGGCGGGTCTCTGTAACCTTCGCGCTTGAAGGCGC	9145
QY	25280	CGGCGGTGCGGTGATACGAGCGTTCGTCTGCTGTGGTGGCGTTCGATTCGAGCGGCGC	25339
Db	9144	CGGCGGTACCGTCAACCGCATGTCTCTCTCCCTGTCTACCTGCACTGGGCGGCC	9085
QY	25340	AGGCGTTGCGTGGGTGATGTTCGATGGCGCTTTCGCGGGGTGTGACGCTGATGTGCT	25399
Db	9084	AGGCGCTGTGTGGGGAGTGTCTGCTGCGCTGCGGAGGGGTGACGCGGATATCGA	9025
QY	25400	CTCCGCGTATCGTTTGGAGTTCTACGCTCAGCGGGGTTCGCGCGGCGCGGCGGATGA	25459
Db	9024	CGCCGATAGCTTCTGCTCGATTCAGACGAGGCGGCGCTGGCGCGGACGCGCGATGA	8965
QY	25460	AGGCGTATTCGCGGCTGTGAACGATACCGGCTGGGCGAGGCGTGGGAGTGTCTGCG	25519
Db	8964	AGGCGTTCCTCGACAACGCGCGACCGGACCGCATGTTCGAGGGCGGTCTGTGCTCG	8905
QY	25520	TGGAGCGCTTCTCGACGCGCGGTGCAACGATCACCGTGTCTTGGCGGTGTGCTGCA	25579
Db	8904	TGGACGCGCTGTCTCGACGCGCGCGCAACGCGCATCTCGCTCTCGCGTTCGACGCGGCT	8845
QY	25580	GTGCGGTCAACGAGGACGCGTGGAGCAACGCTGACGCGCGCGCAACGCGGCGCTCCGACG	25639
Db	8844	CGGCGGTCAACGAGGACGCGCGCTCCACACGCGCTTACGCGCGCGCGCTCTCCACGCG	8785
QY	25640	AGCGGTATCTCGTCAAGCGCTGGCCAAATGCGGGAATGACCCGCGCATGTTCAGCGAG	25699
Db	8784	AGCGGTATCTCGGAGCGCTGGCGCGCGCGCGGTCTGTGCGCTTCGACCTGACGCTGCG	8725
QY	25700	TGGAGGCGACGAGACCGGAGCACTCTGGGGGACCCGATGAGAGCCGACGACCTCCGCG	25759
Db	8724	TGAGGGCCATGAGCACCGGACCGCGCTGGTGTATCCATGAGGCGGACGCGCTGTGG	8665
QY	25760	CGGCTTACGACCAACACCGCCCCCAACACCGCCCTTGTGGCTGGGATCTCTCAATTCGA	25819
Db	8664	CCAGCTTACGCGCGGAGCCGAGACCCGAGCGCGCTGTCTGTGGGTCTGATCAAGTCA	8605
QY	25820	ACATCGGACGACACAGGCGCGCGGCGGTGGGCGAGTCACTAAGTGTATGCGCC	25879
Db	8604	ACCTCGGTCAACGACGAGCGCGCGCGCGCGCGCGCTGTATCAAGATGATCTCTGGGGA	8545
QY	25880	TGCGCAAGGGGCTGTGCAACAGCCCTCCACGATGGAAGACCCACCCCGGAGGCGACT	25939
Db	8544	TGCGCACGGGCGTCTGCTCGAGACGCTGACATGTAAGGCGCGCTGTCAATGATGACT	8485
QY	25940	GGTCCACAGCGGAGTACCACTCTCTGACACAAACGCGTGCCTTGGCCCGCGACCGGCGCG	25999
Db	8484	GGTGTCTCGGTCGCTGCACTGCTGACGAGCTCAGAGATGCGC-----CAAGGCGCG	8431
QY	26000	GCGGCGCACGCGCGCGGTGTATCATTCGCGGTGAGCGGACCAACGCGCCACATCA	26059
Db	8430	ACCGGCGGTGCGGCGCGCGGTGTCTCTCGCATACGCGGACCAACGCGCCACATCA	8371
QY	26060	TCTTGAAGAGCAACCACTCCGACGACGACGATACCGAGAGAAACCGGCTGCGCAACG	26119
Db	8370	TCTTGAAGACCAACCGCGCGCGGAGAGCCGAGAGAGAGAGAGGCGGATACCTTCGC	8311
QY	26120	CACAGCGCTGCGCCATCCCTCTCTCTCGCGGCGGTTCGCGGAGGTCTGAGGCGCG	26179
Db	8310	CGTGGCGCTG-----CCTTGGCTGTCTCGCGAAGTCCGAGAGG	8269
QY	26180	GCTTGGGCGCGACGAGCGGCTTGGCGGACGTAAGTGAAGCCCGCGGACATGTAC	26239
Db	8268	CATGACCGCGCA-----GCTCGACCGGATCTCGCGCTGACCGACGCGTGC	8221
QY	26240	CTGCGACATGTGTGCGGTTCGCGCGCGCGCGCGGTACTGGAACAACCGCGCGCTCA	26299
Db	8220	CTTGGACCTGCGCTCTCACTGCGGACACCGCGCGGCGCATCTGAGACGCTCGGCTGC	8161
QY	26300	TCTTGGCGCGGACCGCGAGGAACTGGCGGAGGACGACGACGCGCTGGACCGGCGGAC	26359
Db	8160	TGCTGTCCGAGGCGGCGGAACGCTGAGTGGAC-----	8125
QY	26360	CCACCCCGACATCAACAGGCGACACCGGCGCGGTGACCGCGCGCGCTGCTTTCG	26419
Db	8124	-----CGGCGACGCGGACGACACGCGCGGAGGCTGGCG-----TGC	8086
QY	26420	TCTTCCCGGACAGGCGGCGGACGAGTGGCGCGGAGTGGGCTGACCTGTCTACCTCTAC	26479
Db	8085	TGTTCTCGGCGGAGGCTTCAACGCTGTGGGAGTGGCGGAGTGTGACGCTGCTTC	8026
QY	26480	CCGTGTGCGGACACATCAACGATGCGGAGAGCCCTGACCCCTGGGCTGCGTGT	26539
Db	8025	CGGTGTGCGGAGCGGTGGAACGCGGCTGTGGGCACTTGTGATGCGCGGTGCG-----	7972
QY	26540	CCTGACCGACATCTGACCGGACCCCGACGACCCCGGATGGCAACAGCGGACGTTG	26599
Db	7971	-----GGATGTGATGTTCGCGAGGCGGAGGCGCT-----GAGGAGACCGGATTCGA	7924
QY	26600	TTCAGCCGCTGTCTTACGATCATGTGTCTCTCGCGCGCGCTGTGGCGCTCTTACGGA	26659
Db	7923	CCAGCCCGCGCTTGTGCACTGAGGTGGGTGTTTCGCGCTGTGAGTCTGTGGGTG	7864
QY	26660	TGCAACCGGACGCGGCTCTGCGGACCTCCAGGAGAAATGCGCGCGCGCCACATCTGCG	26719
Db	7863	TGCGGCGGATTTGTGTGGCGGAGCACTGATGAGTGTGCGCGCGCGGATGTGCGCG	7804
QY	26720	GCGCACTGAGCTGAAAAGCGCGCCCAAAACCGTTGACCTGCGAGCGCGGACTGCGCG	26779

Db 7803 GGGTGTCTCGTGGCGGATGCGTGTGCTGTGGCGCGCCCGCTGATGACAG 7744  
 Qy 26780 CCGTACGAGCGCGGCGCGCATGCGCTCACTGCGCTGCGCGCGGAGAGTGCAGAC 26839  
 Db 7743 CCTTCCCGCGCGCGCGCGATG-----TGGCGTTAAGCGCGAGAGAGCG 7696  
 Qy 26840 TCAATTCGGAACGTTGGGAGAGGAGTTGTGGTGGACGCGCTCAACGCGCCCACTCA 26899  
 Db 7695 AGGTGGCTGCAAGCGCTGGTCAAGCGGGGTGTGATGCGCGCGGTCAACGCGCCGAGGCGG 7636  
 Qy 26900 CCAAGCTCTCGGCGACACCAAGGCGGTGATGAGTGTGTGGCGACTGACACCAACCG 26959  
 Db 7635 TGTGTATGCGAGGGAGAGCGCGAAGTCTTGGCGATGCGCGAGAGTTCAACCGCGCTGG 7576  
 Qy 26960 GCGTACGGGCGCAAGCGATCCCGTGCATAGCGCTTCCACTGCGCCCGCGCTCAACCC 27019  
 Db 7575 GCGCTAAGACAGCGCGCGCTGCGGTGACGACGCTTCCACTGCGCGCTGATGAGCGGA 7516  
 Qy 27020 TCCAGGACGAATCTCTGCACTGTGGAGACATGACCCCGCGCGCTGACCGTGGCGT 27079  
 Db 7515 TGTGGAGGACTTCCGAGGGGTGCGCGAGGACTGTGTAAGAACCCCGCGGATCGCGC 7456  
 Qy 27080 TCTTCTCCAGCGTGGAGAGCACTGCGTGGAGACATGACCCCGCGCGCTGACCGTGGCGT 27136  
 Db 7455 TGTGTTCGAACCTCAACGCGCAACTGCGCAACGAGAGACTGTGCTGCGCTGCGCGGTA 7396  
 Qy 27137 GGTACCGCAACTCTCACCAGCGCGTCCGCTTACGCGAGCGCATTCGAGACCTGACCGAG 27196  
 Db 7395 GGGTCCGCGATGTGCGCGAGACGTCGCTTCCGAGCGGTGTGATGCTGCGCGCGCG 7336  
 Qy 27197 ACGGACCGCGCGCTTCAATGGAATCAGCCCCCAACCCCGCTGCTCCCGCGCATGAG 27256  
 Db 7335 AAGGGCGCTCGCTTCTGAGAGTTGGGCTTGAAGGTGTGTAAGGATGAGCCAGC 7276  
 Qy 27257 ACAACCGAAGAACACCGAATATACCGGACCGCGAGCTCGCGCGCGGACA 27316  
 Db 7275 ACACCTCGGACCGGACCGGACCAACCGTACCGCGCTGTGAAGGACCGGTTCGAGGAGA 7216  
 Qy 27317 ACGACACCAACCGCTTCTCAACCGCGCTGCGCGCAACCGACCAACCGGCAATCGGACA 27376  
 Db 7215 CCGC-----GCTGCTCACCGCGCTGCGCGCACTGATGTGCGGCGTGGGGTGG 7165  
 Qy 27377 CCACCACTGCGACCACTACACCAACCAACCCCGCAACCCCGCAACCCCAACCC 27436  
 Db 7164 ACTGATCGGGATCTTTCGCGGCGACCGGTGCG-----CGCG 7126  
 Qy 27437 TCGACTCGCGCACTACCTTTCACACACGACACTGAGTCAACCAACCCACCA 27496  
 Db 7125 TCGACTCGCGCACTACCTTTCACACGACGCTACTGAGCTGCTGCGCGCTGCTCA 7066  
 Qy 27487 CAACCGACTCAACCAACCGGCTTCAACCCCGCAACCCCGCTTCTCAACCGGCAAC 27556  
 Db 7065 GCGGGAATGTGTGCTGCTGCGGTGCGGTCTGCGCGAGACCGCTGCTGCGCGGAGCG 7006  
 Qy 27557 TCACTCTGCGCGCAACAAACACAACTACTACCGCGCGCTCTCCCTACGACCAAC 27616  
 Db 7005 TCACTCTGCGCGAGTCCGCTGAGGTGTCTACCGGAGGCTGTCTTCAAGGATAC 6946  
 Qy 27617 CTTGCTCAACGACCAACCGTCCGCGAGTCTCTTCTGCGGCGCAACCGGCTCTCG 27676  
 Db 6945 CGTGTCTACGACCAACCATGGGCGGAGGCTCTTCTCCGCGCAACCGGCTTCTCG 6886  
 Qy 27677 AACTGCGCTTCCAAACCGCGGAAACCGGTGGAATGTCTTGGTGGAGAACTGACCTTGC 27736  
 Db 6885 AGCTGCGATGCGCGCGCGCAATGAGTGTGCGAGCGGAGTTCACGAGTTCTGCTGA 6826  
 Qy 27737 ACGCACTGTTGATTCGCGCAACCGAGAGTGAAGTTCAGGTTCAACGTTCCGGAG 27796  
 Db 6825 TGACTTCGCTGTGCTCGGAGAGAGGAGGCAACCAAGTTCAGAGTGTGCTGAGACCG 6766  
 Qy 27797 CCGATGAGAGTGCATCGCGCTTGCAGTCACTGTAATTCGCGCAACCGGCTGTCG 27856  
 Db 6765 CCGAGAGGCAAGGCAACCGCAAGATCTCATGCGCGCCGAGCGG-----ACC 6712

Qy 27857 CGGACCGGAGTGAACCGCTACCGCAACGCGCTTCTACACACCAACCGCAACCGATC 27916  
 Db 6711 CCGACAGCGCGTGAATGACGACCGCGCGCGAGCTGTACAGAGGTGAAGATCTGCG 6652  
 Qy 27917 ACCGTGCGGACGCAACGAGCGCGTTCGCGGAGAGTGGCGCGCGCGCGCGCG 27976  
 Db 6651 ACTTTCGGGTCCACCGT-----CTGCGCGCGGACGAGGCGCGCG 6616  
 Qy 27977 AGCCCATGAACTGAGGAGCGCTACGCTGATGCGGCGGAGACTCGGACATTCGCTACG 28036  
 Db 6615 AGGCGTGCACCTGAGGCGCTTTCACACAGACGCG-----TTACG 6574  
 Qy 28037 GCGCGCTTTCAGAGGCGTGAACCGCGCTGAGAGTTTCGCGAGATGCTCTGCGCGAG 28096  
 Db 6573 GCGCGCGCTTTCAGAGGCGTGTGTTGAGTGTGAGTGAAGAGAGTGTCTTACGTAAG 6514  
 Qy 28097 TGGCTTCCGGAAGAGCTTCCGCGATGCTCCGCGCGCGCGCTTCCGCTTCAACCGG 28156  
 Db 6513 TGGCGCTCCGGAACAG-----TGGCGAGAGACCGCGGCGCTTCCGCTTCAACCGG 6460  
 Qy 28157 CTTGTCTGAGCGCGCGCTTGCACCGACGCGCTTCAACCCCGCAACCGGAGCGCTGCA 28216  
 Db 6459 TGTGTCTGAGCGCGGTGTCTCA----- 6438  
 Qy 28217 CGGAGAACTGCGCGCGAGAGAGATGCTGACCGCGAGCGCAACGAGCGGACTGCGCT 28276  
 Db 6437 -----GTGCGCGCGAGATGCGCGGAT--CGGCGCTGCGGAGAGACGTTTCTGCGCT 6388  
 Qy 28277 TCACTGAGAGCGGTGTCTCTGCAACGCGGCGAGTTCGCTGTGCGCTGACGCGTGT 28336  
 Db 6387 TCGCTGCGCGAGTGTGCTGCTGATGCGGCGCGCGCTGCTGCTGCGGCGCGGAG 6328  
 Qy 28337 CGCGGAGTCCGAGACGAGTAACTGCGGCGCTTCAACCGCGCGGAGAGAGTGTGCGG 28396  
 Db 6327 TCAAAACCGGAGAGAC-----ACGCTGTCTTGTGTGCGCGTGAACGCGAGCGCGC 6274  
 Qy 28397 CGGTGTGAGATGAGTGTGCTGCGCGCTGCGGCGCGTGTCAACGAG-----GAGTGTGCGG 28453  
 Db 6273 CCGTCTGTCTGAGAGAGACTTGTGCGGACCAACTACCACTACAGAGCAACCGT 6214  
 Qy 28454 CGGCGCGGAGTGTACCGCGGAGACGAGTGTCTTCCGACTGAGCTGAGTTCGCTGAC 28513  
 Db 6213 TGAAGCGCGGAGCGTGTGCGGAGCGGAGCGCACTGTGTGCTGTAAGTGTGTGCGG 6154  
 Qy 28514 CAGTGTCCGCGCAAGCGCTTTCGCGCACCGGAGACCGGCGCTGAGCGGTCACTGCGGCGG 28573  
 Db 6153 CTGAG----- 6149  
 Qy 28574 GCTTTCCCACTGCGCGCGCTGACGAGACAGACGTAACCGGTATGACAGCGCG 28633  
 Db 6148 ----- 6149  
 Qy 28634 CGGACTGCTTCTGAGCTTGAACCGGAGTCTCGCGCGCGGCTGTGTCGTGAGTGG 28693  
 Db 6148 -----GTGCGCGCTGCGGAGTGTGCGGTGCGG 6118  
 Qy 28694 GTTGTGCCACACGAGAACCGCGGAGATTTCCGCGGAAGCCCGGAGAGCGCGGAGCG 28753  
 Db 6117 TGGGTGCGAGTGAAGCTGAGTGTGAGCGGATGAGTGTGACCTGTGCGGAGACCTTTCGCGG 6058  
 Qy 28754 AGGCGTGGAGAGCGCGCGGAGCGTGTGCAACGTTGGGCGTGTGACACAGCGCTGCGG 28813  
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 Qy 28814 ACGCGCTGCGCGCAGATGTTTGGCCAGGCTTCAAGGCTGAGCTGAGCGGAGCGCGCTCG 28873  
 Db 5997 ACGAGTTGAAGCGCGCGAGCGTGTGCTTCAAGAGTGTTCGCGCGGAGAGGAGAGCA 5938  
 Qy 28874 CAGAGCGCGGCTGTCTTCAACGTCGCGCGGCTGTGCGCGCGCTTCCGCGAGCAATG 28933  
 Db 5937 GCGCTTTCGCTTGTGTGTCTCAACCGGTAAACGCGGTCTCGCGCGAGAGCGAGTCCG 5878

QY 28934 CGACGACCTGCCCCGGGCGCCGCTGTGTGGGGCTGTGTGCTTCCGGCGACGTCGACACC 28933  
 Db 5877 TACGGCATGTGGCCGGGCTGGCGTGTGGGCTGTGTGCTTCCGGCGACGTCGACAGATC 5818  
 QY 28994 CGGACCGCATCAAGCTGTGTGACTTGTGACGGGGGCAAGAGCGGAGCCGGTCAAGTGG 29053  
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 QY 29054 CGACGCGCTGAATCTGCGGGGAGCGGACGCTTCCGCTCCGCGCGGAGGGCTGTTCACGC 29113  
 Db 5769 CGGAGGTGTTGGGGGTCTGGCGGCTGTGTGTGCTTCCGGGAGC----- 5725  
 QY 29114 CACGCTGTGTGCGCGGCCACGTGTGCCGACCGCTACCCCGCTACCCCGCGCTGGCGC 29173  
 Db 5724 -----CTCAGTTGTGTGTGGCGAAGGCCCTGTGTGCGGGCGGCT 5683  
 QY 29174 TACCGTCAAGGGGTCAACGACCGCTACCGGCAAGCGGTCTCTTCTTCCGGCGGAAACG 29233  
 Db 5682 TGGTCAAGTCAACGAGGGCGCGGGGCTGTGTGCGGGAGTGGGATGCGACGCGACCG 5623  
 QY 29234 TCGTATCAACCGCGGAAACCGGTGTCTTGGCGCGGCTCGTGGCCCGGACATCTGTGAGAG 29233  
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 QY 29234 CGCACGCGGTACGCGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29353  
 Db 5562 AGCGCGGTGTACGCGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5503  
 QY 29354 CGGATTTGGGGCGGAGCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29413  
 Db 5502 GGGACCTGTGCGACGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5443  
 QY 29414 CGGCGGACCGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29473  
 Db 5442 TAGCGGACCGGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5383  
 QY 29474 CGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29533  
 Db 5382 CGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5323  
 QY 29534 AGCGCTCGGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29553  
 Db 5322 AGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5263  
 QY 29594 CGCGCGGGGACAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29653  
 Db 5282 CCAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5203  
 QY 29654 CGCCCGGGGAGGCACTAAGCGCGCGCGCAACCGCGCTCTGTGTGTGTGTGTGTGTGTGTGT 29713  
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 QY 29714 GCGCGCGGAGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29773  
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 QY 29774 GGATGACGGGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29833  
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 QY 29834 CGCTGCGCATGTGCGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29893  
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 QY 29954 TGGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 30013  
 Db 4911 TCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4873  
 QY 30014 CGGCGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 30073

Db 4872 GCACGCGCGGTAAACGACGCGGAGAGAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 4813  
 QY 30074 AGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 30133  
 Db 4812 CGCGCGCGGAGAGGAGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4753  
 QY 30134 TGTCTGCGCATAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 30193  
 Db 4752 TCTCTGACACGCGCTCATCCGAGAACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4693  
 QY 30194 TCGACTGCTTACGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 30253  
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 DIRECT SUBMISSION  
 Submitted (01-SEP-2001) Harnu Ikeda, Kitasato University, Dept. of Microbial Chemistry, School of Pharmaceutical Sciences; 5-9-1 Shirokane, Minato-ku, Tokyo 108-8641, Japan (E-mail: ikeda@mc.pharm.kitasato-u.ac.jp, Tel: +81-3-5791-6242, Fax: +81-3-3444-6197)  
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Oy	2865	GCCGAGTCCGAGTCCGAGTCTCTGTGCGGGTGTCCGCTAAGTCTGAAGCTGGGTGGCGGCG	2924
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Oy	2925	GCAAGCGGAGGCGTGTGGCTCAGTACGTGGGACATGCCCGCGACGTTTCCCTTGGCGGATGT	2984
Db	20235	CCAGGCGGACCGGCTGAG-----CGACCGGCTGCCGAGGCGGCGCGCGCGCGAGGT	20285
Oy	2985	GAGTGGCGAGTCTGGCGCTGTGGGCGGCGGTGTGTTGAGAACATCTGCGAGTGTCTCTGGCGCG	3044
Db	20286	CGGCGGCTCTCTGTGAACGACAGAGGCGGACCTGGCGGAGACGGGCGGTACTCATCGGTGA	20345
Oy	3045	GGAACGTGAAGACTGGTGCMAAGGTTTGGGGCGCTGGCGCGGAGTGAACCGGATGCGCG	3104
Db	20346	CGGCTCCCGGCACTTCCGCGCGGGGCTTGGCGCGGTGAGCGCGGGGCGCGGGGACCGCGCG	20405

QY	3105	GGTGAACACGGGTCATGCGCCGGGTGTGAACCGGGCCGGTGTCTTTCGTGTTTCCCG	3164
Db	20406	GGT-----GGTGCGGGACCCCGACACCCCGCGCCGGGTGTCTTTCGTGTTTCCCGG	20459
QY	3185	AACGGTGTGGAGATGTGGGCGCGGATATGGGTGTGGTCTTCGCTTCTTCGCGTGTCCG	3224
Db	20460	CCAGGCGGCCACATGTGGGCGCGCATGTGGCGCGCTGTGGAGTCTGTCCGCGTGTTCG	20519
QY	3225	CCGGCGGATGCAAGCGCTGTGAGAGAGGCTCTGGCGCGGTGGAGTGAATTGGCTGTGGTGA	3284
Db	20520	CCAATGGATGGACCGCGCTGCCCGAGGTGTGGGCGCGCTGACCGAATTGGTCCGTACCGA	20579
QY	3285	CATCTGCGCGGAGACCGGGGGGATGCGGTGTGGAGCGGGCCGATGTGTGTCAGCTGT	3344
Db	20580	GGTATCCATTGAGACGAGGACCGAACCCCGAATTGACCGGGTGAAGTGTGTGAGCCCG	20639
QY	3345	GCTGTTCAGGCTATGTGTCTTTGGCTGCTGTGTGCGTTCTTACGGTATGGAACCGA	3404
Db	20640	GTCTTGGGCGGTGAGCTGTGACCTGGGCGCGCTGTGGCGTGTGGGTGTGAGCGCGCG	20699
QY	3405	CGCGATCTTTGGCCATTCCAGGGGCGAGATCGCGGCGCGCATGTGTGGGCGCTGAG	3464
Db	20700	CGCGGTGTGAGACACTTTCAGGCGAGATGCGCGCGCTGTGTGGGCGGAGCTGTTC	20759
QY	3465	CCTGAAGAAGCGCGCGAAGAATGTGTGCTGCGCAGCGCGCGCTGGCCGCTG--TGGC	3521
Db	20760	CCTGAGAGAGCGGCGCGCCTGTGAGACGTGTGGCAGACAGGCTGATGCGCGAAGAACTGTTC	20819
QY	3522	GGGCGGGGGCGGCATGGCTCTCAGTGCCTGCTGCCAAGAGATGAGACAGTCAATTGG	3581
Db	20820	CGGGCAGCGCGGCACTGTGTGTGCTGTGGCCCTGTCCCCCGCGACACCGCGGAAGCAT---	20876
QY	3582	TGAGCGGGGGCGGGGCGGTTGTGGGTGGGCGGCGGTCAACGCGCCCGCTCCACCGCGGT	3641
Db	20877	CGCCCGCTGAGACGGCGGGATCTGTGTGCGGGGGAACAAACGCGCGCTCCACCGTCTGT	20936
QY	3642	CTCGGGGAGATGCCAGAGCGGTGAGACGAGGTGCTGGGCTGACTGTGCGCGCACCGGGGTGG	3701
Db	20937	GTCCGGGGAAACCGAAGACGCTGGGCCGAATCTGTCCGAGATGAGAGCCGAGGGCGTACG	20986
QY	3702	GGCCCGCGGATCCGGTGCATATGCTTCGCACTGCGCCCCCATGTGCAGCCCCCTGCGGGA	3761
Db	20997	GGCCCGCGGATCCCGCTGGAATACGCTCCACTCGCCCAAGTGAACGGATCGAGCG	21056
QY	3762	GGATTTCTGAGAGCTGTGCGGGGACATCAAGCCCGAGCCGTCCGGGTGCGGTTCTTCTTC	3821
Db	21057	GCACCTAACCGAGCTGAGCGGCGCGGTGTGCAACGCGCGCGGGGGAATCTCCCTTCACTTC	21116
QY	3822	CACGGTGAAGGACACTGTGCTGAGACACAAACCTTGAGACGCGCGCTACTGTGTACCGAA	3881
Db	21117	CACACAGAACCGGCGGCGCGCTTCACACACAGGGCTTGGACGCCGACTATGGTACCGAA	21176
QY	3882	CTTGCACACGCGGTCGGTTTACGCAATGCGCTTCAGGCCCTTGGCGGATGACGACACCG	3941
Db	21177	TCTGCGCGCGGCGGTGTGTTTGGGCGCGGTCAACGAGGAATCTCTGCCACAGGCGACGA	21236
QY	3942	CGTCTCTGTGGAAGTCAAGCCCCCAACCCCTCTGTCTCCCGCATGGAAGACCAACCGA	4001
Db	21237	CGTGTCTCTGGAAGTGAAGCCCGGACCCGGAATCTGTCTCCCGCGGTGACAGAGCGCGTCA	21296
QY	4002	AGACACCGCGAAGAGCTCACCGGATCGGCAAGCTTCGCGCGCGCGGACAAACGACACCGG	4061
Db	21297	CGGACCGGACAGACCGCGCGCGCGCTGTGGGCACTGTGCGCGGAGACAGCGGCGCCCGA	21356
QY	4062	CGGTTCTCTACCGCGCTTCGCCACAAACCATACCAACCGGACATGCGACACCAACCTTG	4121
Db	21357	GCGGTTACCGGTCTCTCTGCGCGAGGGGTGTGTGTGGCGGCGCGCCGTGTGATGTGACGGC	21416
QY	4122	GCACACCACTACACCAACCAACCAACCAACCCCAACCGACACGCACTTGACCTGCG	4181
Db	21417	CGTCTCTGAGACACGCGCGCGCGCG-----CGGTTGTGACCTGCG	21455



Db 23484 GAACTCTGGGACTGATCGCGGCGGAGACGGAATCGGGACTTCCCGCCGACCG 23543  
 Qy 6375 CGGCTGGGACTTGACACGCTCTACGACCCCGACCCCGGACCACTTCTGTACAC 6434  
 Db 23544 CGGCTGGGACCTCG-----CGGCGAACCGCGGCTTCTC 23576  
 Qy 6435 CCGAAACGGCGGATTTCTCTACGACGAGGCCATTTCAGCGCGGAATTTCTTGACATCAG 6494  
 Db 23577 CGAGACCGGCGGCTTCTCCCGGACGTGGCCGAGTTTCGACGCGCGGCTTCTTGCGGATCTC 23636  
 Qy 6495 CCCCCGGAAGCCCTCGCATGGAAGCCCGACGAGACCTCCCTCGAAGCCGATGGGA 6554  
 Db 23637 GCGGCTGAGGCGCTGCGGATGATTCGAGACGCGTTGTCTGAGACGTCGTGGGA 23696  
 Qy 6555 AACCATCGAACACGCGGATCAACCCCAACACCTTCCAGCGGACCCCAACCGAGTCTT 6614  
 Db 23697 GCGGCTGAGGCGGCGGCGGTGAGACGCGCTGAGACTGCGCGGACCGGACCGGCTCTT 23756  
 Qy 6615 CACCGGCAACGAGACGAGACTGACACTTGCCTGACAAACGCGGCGCACTCAACCGA 6674  
 Db 23757 CGTCCGCGCGGCTCCACGACTACG---GCACCTGCTACCTCACTGAAAGAGGCCA 23813  
 Qy 6675 TGGTTTCCCATGACCGGAAACCGCGGAGCGTCACTCCGCTCGTATCTGTACAGTT 6734  
 Db 23814 GGACTACGCGCTCACCGGAGCGGTGAGCGCTGTCTCCGCGGAGATCGCTTACGCTCT 23873  
 Qy 6735 TGGTTTGAAGGCTCTGCGGTGCTGCTGAGACACGCGCTTGTCTCTGCTGTGGCTTT 6794  
 Db 23874 GGGGCTGAGAGGCGCGGCGCTTACCTGTGACACGCGCTGTCTGTCTCTGTGTGGCT 23933  
 Qy 6795 GCATCTGACCTGTCAAGCGCTTGCCTGCGGAGTGTCTGATGAGCGCTTCCGCGGAGTGT 6854  
 Db 23934 CCACCTGCGCGGCGGACGCACTGCGGAGCGGCGAATGCGACGTGGCCCTGCGCGGCGGCT 23993  
 Qy 6855 GACGCTGATGTCTGTCTCGGAGCTTCTGCTGAGATTTTCCGCGGACGCGGAGTCTGGCGC 6914  
 Db 23994 GCGGCTGATGTGCAACCCCGACGCTTGCACGCTTCCGCGGACGCGGAGGCGCTTGGCCCC 24053  
 Qy 6915 GGACGCGCATTTGCAAGCGCTTCTCGGCGGCGGAGCGGAGCGGCTGCGGAGTGT 6974  
 Db 24054 GGAACGCGCGGTGCAAGGCGTTTCCGACGCGGCGGAGCGGACGCGCTGCGGAGGCGT 24113  
 Qy 6975 GGGGATGCTGTGTGAGAGCGGCTCTCCGACGCGCATGCGAACGCTGTCTGTGC 7034  
 Db 24114 CGGCGTACTCGTGTGACGCGGCTGTCCGAGCGCGGCGTCCGCGCATGAGCTGTGC 24173  
 Qy 7035 CGTGTGTGTGCGGATGTGCGGTCAACGAGACGCGTGTGACGCGCTTCAACGCGCCCA 7094  
 Db 24174 GGTGTGTGCGGAGTTCGCGGTTGAACTCGGACGCTGTCTGAACTGACGCGCTGCA 24233  
 Qy 7095 CGGCGCTTCCGACGCGGTGATCCGCGAGGCGCTCCGCAACGCGCGCTTGTCCGCGG 7154  
 Db 24234 CGGCTCGTTCGACGAGCGGAGTATCCGCGAGGCGCTTCCGCTTCCGCGGAGTGTCCGCGC 24293  
 Qy 7155 TGATGTGACGCGGTGAGGCGCCACGCGACCGCTTTGGCGAACCCGATCGAGC 7214  
 Db 24294 GGAAGTGAACATGTGAGGCGCACGCGACGCGGACGTCGTCCGCGAACCGATGAGGC 24353  
 Qy 7215 CCAAGCCCTCTCTCGGACCTTACGAGACGAGACCTGTGCGGCGAGGCGGCTGTGTGC 7274  
 Db 24354 ACAGCGCTTGTGTGCGGAGCTACGAGTCAAGACCTGCGGCGGACCGTCCGCTGTGCG 24413  
 Qy 7275 CTCGCTCAAGTCCAAATGTCTGATCAACAAGGCTGCGCGGCGGCTGCGCGGAGTATCA 7334  
 Db 24414 TTCGTTGAATGACATGAGTATACGAGCGGCGCGGAGTGTGCGGAGTATCA 24473  
 Qy 7335 GATGTGTGTGCGCTGCGGACATGTCTGTGCGCGGAGCTTGTGATGATGAGCGCTC 7394  
 Db 24474 GTCGTAATGCGCTTCCGGAACGAGACTGCTCCGCGAGCTTGTGATGATGAGCGCTC 24533  
 Qy 7395 GCGCGATGTGACATGTCTCCGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 7454  
 Db 24534 GCGGAGGTGAGCTGTCTCCGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 24593

Qy 7455 CGCGGAGGAGGCGGCTACGCGGCGGAGAGTGTATATTGCGCTCAAGCGGACCA 7514  
 Db 24594 GAGAGCGGACGCGCG---CGTCCGCGGCGGCGGTGTCCGCTTCCGAGTACAGGACGAA 24650  
 Qy 7515 CGCCCACTGATCTCTGAGAGACACCCCGGAGAGAGCTTCCGCGGAGACACCGCGG 7574  
 Db 24651 CGCGCACTGATTTTGGAGCGGCGCTTTCGATGAGAACCGGAGACCGCGCTTCGGA 24710  
 Qy 7575 CGAGGATACCGGCGAGCGAGATGAGGCTGTCCGCGAGTCTTGAGGTGTGCGG 7634  
 Db 24711 TGACG-----GTTTGTGTCTG 24721  
 Qy 7635 GCTGTGTGCGCAAGTGCAGCGGCGCTGCGGCCAGGCGCCAGCGCTTGCAGCGCA 7694  
 Db 24732 GGTGTGTGCGCGGCGGTGAGAGGCGTTCGCGGCGGAGCGCGGACCTTGTCCGACCA 24791  
 Qy 7695 CCTCACCGACCAACCCCGCTTGCAGCTTGCAGATGTGAGATACACTTCTGCCACGCGG 7754  
 Db 24792 TGTGCGAG---CAACGATCTACCTGCGGATGTCTGCTTATCTCTGCGGAGCGG 24848  
 Qy 7755 GCGGTTGTGACACACCGGCGCACCTCATGCGCGGAGCGGCGACAGTCTTCTGCAAGC 7814  
 Db 24849 TGCAGGCTGAGACACGCGGCTTGTGACGAGCGGAGCGGAGACTTCTGTGCA 24908  
 Qy 7815 ACTCAGGCACTCGCGGAGCGAGCGCCACCGCGCTCATCCACAGCAGCGCGCGG 7874  
 Db 24909 GTTGGCGCGTGTGCGAGGAGTGC-----AGTGGCGCGG 24944  
 Qy 7875 CGGACCGGAGACCGGAGGCGCGGAGAAAGACCGCATTTACTGTCCGACAGGCGAC 7934  
 Db 24945 GATGTGTGCGGATGTGCGGAGGAGGCGGAGCGGCGTCTCTGTTACCGGTCAGGAGTGC 25004  
 Qy 7935 CCAACGCGCGGAGATGCGCGCACGCGCTTACACACCAACCCGCTTCCGCGCGCACT 7994  
 Db 25005 GCAAGTGTGATGTGAGGCGCTGAGCTGTAGAGCGTTTCCGCGTGTGCGGCTGCGT 25064  
 Qy 7995 CAAGACATCTGCAACCCCACTGACCCCGACCTGACGACACCGCGCTCTCCCTCTGAC 8054  
 Db 25065 CGAGGCGGTGTGTGCGAGTGTGAGATCTGTGTGAGAGGCGCGT----- 25109  
 Qy 8055 CCAAAACGACAAACGACGAGAGCGGCGGACCTGTCTGACGAGACCGCGTACGCCA 8114  
 Db 25110 ---GAGAGAGTGTCTTACCGAGCGCGCGCGTGTGAGCGC---ACGATTTACGCA 25163  
 Qy 8115 GCGCGCGCTTCTCCCTTCCAGTGTGCGCTTCCACCGCTCTCTACCGACGCTACCAAT 8174  
 Db 25164 GCGCGGTTGTGTGCGGTGAGTGTGCGCTGTGAGCTGTGAGCTGTGAGGAGTGTG 25220  
 Qy 8175 CACCGCCCACTAATACGCGGACACTCCCTGCGGCAATTCACCGCGCGCACTTGCAGG 8234  
 Db 25221 GCGCGGATGTGCTGTGCGGACATGTGATGCGGAGCTGTGCGGCGGCTGTGTGTGCGG 25280  
 Qy 8235 CATCTCACTCAACGAGCGCACCACTCATCAACCAACGCGCACCTCATGCAAC 8294  
 Db 25281 GGTGTGTGCTGTGCGGAGCGGTGCGGATGTGTGAGCGCGCGGCGGCTGTGTGAGAGC 25340  
 Qy 8295 CATGCGCGCGGACATGACACCTTCAACCAACCGCGCACCATCAACCAACCACT 8354  
 Db 25341 GCTGCGGAGGCGGTGAGTGTGCGGTGAGAGCGGCGAGGACGAGCTGCGCGACCT 25400  
 Qy 8355 CACCGCCCAAGAAAACGACTCGCATGCGGCGCATCAACCGCGCACCTTCTGTGAT 8414  
 Db 25401 TCCG-----AGGTGTGTGTGAGTGTGCGGTGAGAGCGGCGGCTGTGTGTGCT 25451  
 Qy 8415 CAGCGGACCGCGCACCGTCAACACATCAACCACTTCTGCAACCAAGCATCA 8474  
 Db 25452 GTCGATGATGAGAGCGCGGAGACCGCGCTGCGCGAGCTTCCGCAACAGGAGAGCG 25511  
 Qy 8475 AACCAAAACCTTCCCGACCAACAGCGCTTCACTTCCCGCACCAACCAACCACTCTCA 8534  
 Db 25512 GACCAAGCATTTGCGGTGAGTCAAGCTTCACTTCCGCGGAGAGGCGGAGTGTGC 25571

QY 8535 CCAACTCCACGACACCAACCCCTCACTCAACCAACCCCAACCCCTC----- 8589  
 Db 25572 GAGATTCCGGAGACGCTCGCCGGTGAAGTTCCGTTCCGCCGATATCCCGTGGTTC 25631  
 QY 8590 ----ATCACCCGCAACACCCCAACCCCACTCTCAACCCCACTATTTGAACCAACA 8645  
 Db 25632 GAATGTGAGGGGTGGAGATGGCGGGCGGAGTTTCACTCTCCGCTTACTTGGGTGGGA 25691  
 QY 8646 AGCCGCAACACCGTGTGACTAGCAACCAACCAACCTTCAACCAACAGGGGTCAAC 8705  
 Db 25692 TGTGGGAGAGGCGCTTCCTGTTGCGGATGTGTGGGAGAGGTGTGGCGGGGTGTGA 25751  
 QY 8706 CACCTACATGAACTTGGACCCGCAACAACCTCAACCAACCTTCAACCAACCACTCC 8765  
 Db 25752 CAGGTTCTCTGAGCTGGGTCCCGGGGGTGGCTGACCCGGAATGGCCGAGAGACCTTCA 25811  
 QY 8766 CAAACCCCAACCAACCTTCAACCTTCAACCAACCAACCTTCAACCAACCAACCTTCA 8825  
 Db 25812 CCAACACCGGTGCGACCGCTGTGTGCTCCGTAATGACCCCGAAGCGC---CCGAGGA 25868  
 QY 8826 CCTTCAACCACTCGCCAAACACCAACCAACCACTGGACCCCAACCACTCAACCAACCA 8885  
 Db 25869 CGCCACGCTGTGACAGCGGTGGCCACCGCTCGGTGAGGGGTGGCGCTGACTGAC 25928  
 QY 8886 CAAACCAACCCCAACCAACCAACCACTTCAACCTTCAACCAACCAACCAACCA 8945  
 Db 25929 GACCCCGTTTGGCTGCGCCGCGACCAACGAGCTGCGGACCTTCAACGCGAGGG 25988  
 QY 8946 CTACTGGCTTCCGAACGACAG---CCGGTGGCGGCAACGTGTAGAGCCGGAATCGA 9002  
 Db 25989 CTTCGGCGCGCGCCCGCGGACGCGGGCGCGGCGGACCTGGCGCGCGCGGACTGGC 26048  
 QY 9003 CCCCAACCAACCAACCCCTTCACTGGCGGCACTTGAACCTGGAACCTGAGCGTGAACGCT 9062  
 Db 26049 CGAGGCGCGGACACCACTGCTCAACGGAATGGCTCCCGTGGCGCGGAGGGGAGAGGGGTGT 26108  
 QY 9063 TCTTGCAGGGCGCTTGTCTTTGAGGTGCGATCCGTGGCTGCTGAACATGCGGTGGCGG 9122  
 Db 26109 GTGCAACCGGCGGCTGTCCCTCGGCAACATCCGTGGCTGGCGGACCAACGCGTCTCGG 26168  
 QY 9123 CACGCTGCTGTGTGGGGGCACTTCTCGAATCTGCGCTTCAATGGCGGCACTAGCT 9182  
 Db 26169 CACGCTGCTGTGTGGGGGCACTTCTCGAATCTGCGCTTCAATGGCGGCACTAGCT 26228  
 QY 9183 GGGCTGCGCACCGAGTGAATGAGCTGACGCTGATGCGCGCTGTGTGTCTCTGTGATNG 9242  
 Db 26229 CGGCTGCGCGGAGATACGGAATCTGACCTTGGCAGCGCACTGGCACTGCGGAGAGAC 26288  
 QY 9243 GGGTGTGAATGACAGTTGGGTTTGGCGCTGCGGATGGGAGAGGGCGGCTTTGTGTAG 9302  
 Db 26289 GGGGTGTGAATGACAGTTGGGTTTGGCGCTGCGGATGGGAGAGGGCGGCTTTGTGTAG 26348  
 QY 9303 TGTGTATGCGCGGGGTGGAGATGTGTGTGTGGGGGTGTGTGTGGGTGTGTGAC 9362  
 Db 26349 CGTGTATGCGCGGAGCGGACACCGAGAGACGAGCTGAGACCCGCGACGCGAGGG 26408  
 QY 9363 GTGTATGCTCGGGGAGTGTGTGTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 9422  
 Db 26409 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26468  
 QY 9423 GCGCGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9482  
 Db 26469 CGCA-----TGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26522  
 QY 9483 TTTGCTGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9542  
 Db 26523 GCTTCCCGACCGCGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26582  
 QY 9543 TGAATGGGGGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9602  
 Db 26583 GCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26636  
 QY 9603 TGGTTTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9656

Db 26637 CGGTTTCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26696  
 QY 9657 GTTGTCTCGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9716  
 Db 26697 CAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26756  
 QY 9717 GCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9776  
 Db 26757 GACGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26816  
 QY 9777 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9834  
 Db 26817 CACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26876  
 QY 9835 GAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9891  
 Db 26877 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26936  
 QY 9892 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9951  
 Db 26937 CGCCACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26996  
 QY 9952 TGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10011  
 Db 26997 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10071  
 QY 10012 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10071  
 Db 27055 CTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27114  
 QY 10072 GCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10131  
 Db 27115 CGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27174  
 QY 10132 TTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10191  
 Db 27175 CTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27234  
 QY 10192 GTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10207  
 Db 27235 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27294  
 QY 10208 -----TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10254  
 Db 27295 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27354  
 QY 10255 -----GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10299  
 Db 27355 CTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27414  
 QY 10300 TTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10324  
 Db 27415 ATCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27474  
 QY 10325 ----- 10324  
 Db 27475 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27534  
 QY 10325 ----- 10324  
 Db 27535 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27594  
 QY 10325 ----- 10324  
 Db 27595 AGCACGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27654  
 QY 10325 ----- 10324  
 Db 27655 CCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27714  
 QY 10325 -----ACACGGGCT 10332

D	27715	GTCTGATCGCCCTTCACATGTAATCCCGCGCGGACCTCGGACCGAGTCGCGG	27714
Q	10313	ACCGACTTCGACACCGGTGTGTGTGCTGTTGGAGCGTGGATGTGAGCGATGGCGAG	10312
D	27775	GTCTCTCGAGAGAGGGAACCGGTGTACCGGGCTGGCCCCCGGGGACCGGGATGGG	27834
Q	10393	GTGTGGCGTGTGTGTGAGCCGCAATTGGCGGTGCTGGGAGCGGTTCGTGC-----	10445
D	27835	ATGTGTCCCGGGGGCGTTTCGGGGCCACCGCGGTGCGGACCGGCGCGTGTGGCGGATA	27894
Q	10446	-----	10445
D	27895	CCGGACGGCTGTCTTCGAGACCGCGCGGACCCCGGTGCTTCCTGACCGCTAC	27954
Q	10446	-----CGCAGCGCTGTGAAAGACTTGAATCATCCGTGTGATGTTTCAGCCGAC	10492
D	27955	TACGGCTGTGTGACCTGGCCGGGTCTGGCGGGCGGAATCGGTGCTGTGACGCGCG	28014
Q	10493	GGTCCGGTGAACAGAGCCCGGCGGTTCGACGTGCTGCCAGCGCTCCGGTGGCTGC	10552
D	28015	GCCGGGGGGGTGGGAATGGCGCGCGGTGACATGGACCGGACCTGGGGCCGAGGTTC	28074
Q	10553	-----	10552
D	28075	GGCACCAGAGCGAACCGAATGTGAGCACCTGTCTGACACCGGTTCGACCGCGGAC	28134
Q	10553	-----	10552
D	28135	ATCGGCTCTCAGCGGACGCTGACTTGGCGGAACTGTGTGCGAGACAGACCGCGCG	28194
Q	10553	-----	10552
D	28195	GGCGTCACTGCTACTGAATCGCTCGCGGAGATTCAACGACCTCGTGGCGCG	28254
Q	10553	-----CTGCTCGGCGGTGGGTGATGTATTCGGGTGGGA-----	10586
D	28255	ATGCTCGCGCGCGCGCTTCTGTGAGATGGAGAACCGACCCCGGACCCCGAACGC	28314
Q	10587	-----	10586
D	28315	GTCCGCCCGACACCCCGCGTGGTACCCTCTTCGACTGGGGGAGCGCGCG	28374
Q	10587	-----	10586
D	28375	GACCGCATCCGCGAGATCTGCGCCATCTGTGAGCTGTTCGAGTCCGGCGGCTAC	28434
Q	10587	-----	10586
D	28435	CCGCTGCCGTCAACCACTGGGACATCGGAGCGGACGCGCTTCGTGTGAGC	28494
Q	10587	-----GGTGTTCGTTG	10602
D	28495	CAGGCCACTCACCGGAGCGGTCTTACCGTCCCGCGGGTCCGTCCGTTCCAG	28554
Q	10603	TCGGGTGGTGTGTGTGTGTGACCGGTGGAGCGGTGTGCTGGGTCCGCGGTGCG	10662
D	28555	GCGGTGAGACGTCTGTATCACCGGGGACCGGACCTGGGACCTCGTGGCGG	28614
Q	10663	CATTCGCTGTGTGTGTGGGGTGGGAACTGTGTGTGTGACCGGTGTCCGAT	10722
D	28615	CACCTGTCAACCGACCGGACTGTCTGTCACTTGCCTGGCCGGAAGCGGGGACGAG	28674
Q	10723	GCTCCGGGTGGAGGTCTGCGCGGAGGAACTGGCGCGTGTGGGGCGGAGGTG	10782
D	28675	ACGCCGAGTGGGCAATGCGCGGACCTGCGGAGATGGGCGCGAGTACGGGT	28734
Q	10783	GTTGCTGTGTGTGTGGGGAGCGGCGGAGGTGCTCGGCTGTGAGGAGTGTCTTC	10842
D	28735	GAGGCTGTGCGACGCGCGGAGACAGAGACCGGTACAGACGCTCTTGAAACGCTAC	28794
Q	10843	GGGTGTCCGCTGACCGGTGTGTGTGATGCGGCTGTGTGTGTGACATGACGATCG	10902
D	28795	CACCAACGCTGGCGGAGTGTCTACGCGCGGCGCTCACACGACCGGGTGTGTCC	28854

QY	10903	TCCTCTCAACGCCCGCAAGCGCTGTGGCCACGGTGTTCGCGGCGCAAGGTGATGACCGGCTCTTTTG	10962
Db	28855	GGCGCTCAACCGGCGCGGGCTGTCTCGCGGTACTGACCCCAAGGTGCGGGCGCTTGGAAC	28914
QY	10963	CTGGATAGAGCTGACAGCGGGGATAGAGAGCTGTGGGCGTTTGTGTCTTCTCTCGCCGG	11022
Db	28915	CTGCAACGGGCTCAACCGGCGACCTTGGCGCCCCGGGATTTGTCTCTTCTCTCCGCTCG	28974
QY	11023	GGGATTCCTGGGGGTCCGCGCGGGCAAGGCACTACGCGCGGCAATCCGCTCTGACCGG	11082
Db	28975	GCCCACTCTGGCGCGCGCGCGGCAAGGCACTACGCGCGGCAACGCGCTTCTCTGACCGG	29034
QY	11083	CTGGCGTACCGGCGCGCGCGGGGTCTTCCCGGCGGGTGTCCGTGGCGTGTGGGGCTGTGG	11142
Db	29035	CTCGCGGAGCACCGGCGACGCGCGGGGGCTGTCCCGGAGCAGCTCGCTGTGGGGACTGTGG	29094
QY	11143	GAAGAGGCGAGCGGGGATGACCGGGCACCTGGCCGGGACCGACCAACCGCGGCACTATCGGT	11202
Db	29095	GACCAAGGCGAGCGGGGATGACCGGGCGCTTCGCGGAACCGGACCGGAGCGGATGAGCCGG	29154
QY	11203	TCCGGTCTGCATCCCATGTGAGACCCCGGACGCACTGGGCGCTTCTGTGATGATGGGCGCTGGT	11262
Db	29155	GCGGCGGTCCGCCCCCTTGACTCTGACACAGGCGCTTGCGGTGTGACACCGCGCTGTCT	29214
QY	11263	CTGGACGGGCGGGTCTGTGGCTGGCGGCGGCACTTGCCTCCGC-----	11303
Db	29215	ACGGGTATCCCGGGCGGTGAGCGCCCGCGCGCTGACCTTGGCGGACCTGGGGCGAGGGCG	29274
QY	11304	-----CCGGCCCCCTGGCCCCCTGTGTCGAGAACTTCTTCCCGGCAACCCGCGCGCACCT	11358
Db	29275	GCGGACAGGCGGGTCCCGGCGGTACTGCGGGAACTGTCCGCGCTGGCGCGCGTGGCGGCG	29334
QY	11359	ACCGGCA-----CCACCATCACCGGGGTGGCGGACAAAGGGGCCAGCTGCACGCGCGG	11412
Db	29335	ACCGGCAACGAGGCGCTCGACCAAGGGGAGCGCCGGGTGAGCGCGGAGCGCTGACGAGCGGG	29394
QY	11413	CTGGCGGGCGGACGACACGAAACAAGACACCACTCTCGCGCTGTGGCTCCGCTCCAC	11472
Db	29395	CTGGCGCGGCTGTCCCCCGCGGAGCGGACCGGCTGTACTGTGATTTGGTGGCGAGGAC	29454
QY	11473	ATGCGCACCGTCTTGGGCGACACCAACCCCGGACCATCTCCCCCGGACCGCGCGTTCCG	11532
Db	29455	ACCGGAGGCGGTCTCGGTACAGGCTGGCGGACGATGACCCCGACAGGCGTTCAAG	29514
QY	11533	GACCTCGGCTTTCGACTCCCTTCACCGCGCTGTGAACTAGCAACGGGTCTTCCGACACAC	11592
Db	29515	ACGCTCGGCTTTCGACTGTGCTACCGGGGTGAACTCCGGAACCGGTGGCGAGCGGCAAC	29574
QY	11593	GGACTCGGCTCCCCCAACACCTCGGCTTGTGACACACCCCAACCCCAACCTTCAACCCAC	11652
Db	29575	TCCCTGACGTCCTCCCGGACCTTGTGTTTCACACACCCACCCCGGCGGCTTCAACCGG	29634
QY	11653	CACCTCGACACACAACTCCAGGCAACCGGACAAAGCTGTGCGCCCGTGTGGCGGAG	11712
Db	29635	CATCTGCTGGAACTCGCGCGGCGCGCGGAGACGACCGGGTGCTCAGGTTCCGCGGCA	29694
QY	11713	CTGCACAAACTCGAATTCGCGCTTCTCGCGCTTGTACAAAACGACAGCGCGACCGAAGA	11772
Db	29695	CTCGAAGCGCTCGAAGGGGCGTGCAGGCGCTTGGGCGCGCTGACCGGCCCCACGACGA	29754
QY	11773	GTCACCCGCGGCGCTGAGAGTCACTCATGTTGAGGTGGAAGGCAACCCAGCATCCGACAGCC	11832
Db	29755	GTCGTGCGACGACTG-----CGCGGATCTTGCAGAGGCGGAGCGGCTCGCGCG	29808
QY	11833	GAAGCGCTGATGACGAGAAATTTCATCTCGGCAACAGAGCTGAGATTTTCAAAATT	11892
Db	29809	GACGCGGCGCGGCGAGGACTCTCGTGTTCAGAGCGGCTCGCGCGGGAAGTGTGCGGTT	29868
QY	11893	ATTGACACGACCTCGGCGCTGTCTTGAACGGAACGCGCTGCACTCCGCCGTATCCGCTG	11952
Db	29869	ATTGACAGCGAATTCCG-----CGATCTTCGCT	29936



OY	11353	GGCCCTCGTGAAGAGTGAATGCAATTGGCGAATGAAGCGAAGCTCTCTGAATATCTCAAG	12012
Db	29897	AGTACATATACGAGGTGATGCGAGTGTGTGAATGACAAAGCTCTGTCACTATCTCAAG	29956
OY	12013	CGCCTCATCTGGCGACCTTGACCCGACCTTCGCGCTGCTATGACAGGTGGTCGACCGTGAAG	12072
Db	29957	CGGCTTCAACCGCGACCTTGAAAGCGAACCCCGGACCGGTGTGAAGGAATCTGAAGCGGCGCC	30016
OY	12073	CAGAGCCCGATCGCGAATTGTGGGGATGGCGTGTCTTACCAGAGCGGGCGAGTCAACC	12132
Db	30017	GCCCAACCCATCGCGCTGTCTCGATGGGCTGGCCGCTTCCGGGCGGACATCGCTCCCG	30076
OY	12133	ACGGCAGCTGGAGCATCTCGTCAAGTCCCAACCGAAGCTATCGGGAGTTCCCGAACCGAC	12192
Db	30077	GAGGACCTGTGGAGGTGCTGTGCGACCCGACCGGACCAACATCTCGGGTTCCCAACCGAC	30136
OY	12193	CGTGGATGGAACCTTGAGACAGCTCTATGACCCCGGACCCCGACCGCTCAGGAACAGTTAC	12252
Db	30137	CGCGGCTTGGCGCACCCGGCACCTGCGGGGACCTTCCG-----30175	
OY	12253	ACGGCAGACGGAGGGTTCTCTATGACGCGGCGGACCTTCGAGCGCGGTTCTTCGAGTTG	12312
Db	30176	---CTCGGGGCGGCTTCTTCGCGGACGCGGCGGGTTGACGCGCGGGGTGTTCGGCATTG	30232
OY	12313	TCACCGGCTGAGGGCGCTTGGCAATGGAACCGGACGAGCGCTGTCTGTCGAACACTTTGG	12372
Db	30233	TGCGCGGGGTGAGGGCGCTGGAGATGGAACCCGACAGCGGCTGTCTCTGGAAGACTTCTTG	30292
OY	12373	GAAGCTTTCGAACGAGGCGGGAATGACCCCGAGGTTCATGCGCGGAAGCCGGACCCGGGTT	12432
Db	30293	GAGGTCTCTGAAGCGGGCGGGCGCTGACCCCAACACGCTGCGCGGCGCCACGCGCGGGATG	30352
OY	12433	TTCTGTGGGGATCAATCCGAGAGACTTACACCAACCGGATACACATCAAGCCTTCAACCGCA	12492
Db	30353	TTCTGTGGGCAATGCGGACCAAGAAAGTACGGCCGCGGAGAC---GGTAACTCTTCGACGACG	30409
OY	12493	GTGAGGGCTTACCTGCTCATCTGGCAGGCGGCGCAAGCATTTGCTGACGCGGTATCTTAC	12552
Db	30410	GTCAAGGGCGCTGTGCTCTGACCGGACCAACGAGCAGGTGCTCTCCGCGCGGATCGCTTAC	30469
OY	12553	AACCTTCGGGGCTCGAAGGCGCCMGCGCATCATATGACAACCGCGGTTCTCTCGCTCGTC	12612
Db	30470	TGCTTCGGCTTCCAGGGGGCCCGGATACCATGACACCGCTGTCTCTCTCCTTGTC	30529
OY	12613	GCCCTGTGATCTGGCGCTTGCCAAGCGCTTCGGGTGCGGTGAATGACCATGTGCGCTCGACGCT	12672
Db	30530	GCCCTGACCTCGCGGTATCGAGGGCCCTGCGCTCGGGGGAAGTCTGTTCCGCGCTCGTCCGCG	30589
OY	12673	GGCGCTTCCTCATGCGCACTCCCTTCTGTCTTACCGAGTTCTCTGCGCAGCGGGGCTTG	12732
Db	30590	GGTCCCGCGGTATGGCGGAACCCCAAGCTTTTGCGCGAGTGGGAGACAGGCGGGGATG	30649
OY	12733	GGCGCAGACGGCGCGGTGTCAGAGGCGTTTTCGGCGGCGCGGACGGGACCGGCTGTCCGAG	12792
Db	30650	GCGGCGCAGCGCGCTGTCAGAGGCGTTTGCGCGCGCGGCGGACCGGACCGCTGTGGGCGAG	30709
OY	12793	GGTGTGGGGAATGCTGCTGTGTGAGCGGCTTTCGACGCGCGCGCAACGCTACCGTGTGTC	12852
Db	30710	GGCGTCCGGCGTGTCTCTGCTTCAGCGCGCTTCCACGCGCCGGGAACAGGAGCTGCGCCGTC	30769
OY	12853	CTGGCGCTGTCCGCGGCGAGCGCGCTTCAACCAAGACCGGCGCAAGCAAGGCGCTTACCGCA	12912
Db	30770	CTGGCCACCGTCCGCGGCAACCGCGGTCAACAGGACCGGCGCTTCCACGACCCAGCTCAAC	30829
OY	12913	CCCAACGCTCGTTCACAAATCMAAGTATCTCCGCAAGCTTTGGCCAAACGACACTCTTC	12972
Db	30830	CCCAACGCTCCCGGCCACGCGCGCGGTATTCGAAAGCGCTCTGCGACGCCAGCTCAAC	30889
OY	12973	CTTCGCGATGTCATGCGGTGAGAGGCCACACGCGACCGGAGCAACCTGTGGGCGACCCGATC	13032
Db	30890	GTCCGCGAGGTTCGACGCGGTGTGAAGCGGACCGGACCGGAACTCCGCGTCCGACACCCATTC	30949
OY	13033	GAGGCTCAAGCCCTCTGTGAAGCTTACGATCAGAACCGGCCCAACGAGCGCGCCCTTGG	13092

Db	30950	GAGCGGGGGGCTTGGCTGGCCACTTACGGCCAGAGACCGGAGCCGGAGACAGACCGCTGTGG	31009
QY	13093	CTCGAAACCTTCAGATCCAAATCGAGCACTCCATGAGCCGCTGGGGTGTGGAGCGAGCTC	13152
Db	31010	CTGGGCTCGGTCAAAGTGGAACTCGGTCAACAGCAGGACCGCGGCGGGATGGCCGGAGTTC	31065
QY	13153	ATCAAGATGGTGAATGGCGCTCGGGAATGGTGTCTCTCCCGCGAGACTTTCATGTGGATGAG	13212
Db	31070	ATCAAGATGGTGTGGGATGCGGAGCGGACGTCTCTCCCGGACCTTCGACGTGGACGAA	31129
QY	13213	CCGTCGCGCGCATGTGGACTGTGTCCGCGGGGCGGGTCACTGTGTGACGAGACGGTGGCC	13272
Db	31130	CCCAACCCCAAGGTGCACTGTGTGGCGGGGCGCGGTACGGCTGTGACGAGAGAAAGACCC	31169
QY	13273	TGAGCCGAGGGGAGGGAGCGGACTTACGAGCGGAGAGATGTCAATTCCTGGCTCAAGCGAG	13332
Db	31190	TGGCGAGAGCA---GGCGGGCGGCGCGGTGGCGGTCTCTTCCTTCGAGTACGGGT	31246
QY	13333	ACCAACGCCACGTCACTCTCGAGAGAACCCCGCCCAAACTCCCTTCAGACACACC	13392
Db	31247	ACCAACGCCACGTCGTCTTCGAACAGAACCCCGCGGAGCGGCGGACCGGACGCC	31306
QY	13393	GCCGACGACGTCCCGGGAGAAATGAGCGCGGAGAGAGATGCCGATGTGGCATGAGCT	13452
Db	31307	GAGCCGAGCCCGACACTTCGCTCGCCGCGCCCGCTC-----	31342
QY	13453	GCTGCGGAGTCCAGGGGTGTGGCCGCTGTGGTGTGGCCAAATGCGAGCGCGCTTG	13512
Db	31343	-----CGTGGAGCTTTCGCGCGGAGGAGGGGCGTG	31378
QY	13513	CGCCGCCAGGCCAGGCTCTGACGCCACCTTACCGACACC CGGCTCGACTCGCC	13572
Db	31379	CGCCGCCAGGACGCGCGGTGACCGGATCGCCGAGCGGACCCCGCGCGCTG	31438
QY	13573	GAGCTCGGGTAAACCCCTCGCGACGCGCGCGCTTGTGACCAACCGGCGCACCCCTATC	13632
Db	31439	GACATCGCCGATCTCTGCGCGCGGTGGCGCGCGCTGCGACCGCGCGCTGTGCTC	31499
QY	13633	GCGCCGACGCGACACTTCTCTGAAGACCTTCAGAGCACTGCGCGGCGGACGACCCGAC	13692
Db	31499	GCGCCGACGCGACGAACTCTCAAGTCCCTGCGCGCTCGCGCGCGGCGGACCGCGAC	31558
QY	13693	CCGCGCTCATTCACAGACGCGCCCAAGCGGAGCCGGAGCGGAGGCGCGAGGAAAG	13752
Db	31559	CCCGGCTGTGACGCGCGCGAC-----GTGCGAGCGGCGCC	31597
QY	13753	ACCGCATTCATCTGTCTCCGAGCAGGGACCCAAAGCCCGCGGATGGCCCAAGCGCTTAC	13812
Db	31598	GTCCCTCTCTGTTCACCGGCGCGAGGCTCGCAACCGGCGGAGCTCGGAGAACTGTAC	31657
QY	13813	CACACCCACCCGCTCTCGCGCGGCACTCAAGCATGTGACACCACTTCAGACCCGAC	13872
Db	31658	GAGACCTTCCCGGTGTTCGCGCGGCTTCGACGAGGTGCGGACCGGCTTCACCCGAA	31717
QY	13873	CTGACCAACCCCTCTCTCCCTCTTCAACCGAGAACCCCAACCCAGGACACCAACC	13932
Db	31718	CTGCGCCACCGCTCGACGACATCTCGAGGG-----GCG	31753
QY	13933	CTGCAAGAGCGCGGCACTGTCTCAAGCAAGACCCGTTAGCCGACCGCGCTTTCGCG	13992
Db	31754	GTCTGTGACGGAATGCGCGTGAAGCAGACCGGGTACGCGTTCGCGCGGTGTTCGCG	31813
QY	13993	TTCGAGGTGCGCTTCACGCGCTCTCAACGAGGTACCAATCAATCACCCTCACTTAC	14052
Db	31814	CTGAGAGTGGGTCTTTCGCGGTGT---GAAACGCGGTGTGTCTCCCGACTTCGTC	31870
QY	14053	GCCGAGACTCTCCCTCGCGGAATCACCGCGCGCCACTCGCGGCACTCTCACTTCAACC	14112
Db	31871	CTCGGGCACTTCAACGGCGAGCTGGCGCGCGGCACTGGCGCGGGGTGTCTCGCTGAGC	31930
QY	14113	GAGCGCAACCTTCATCACCAAGCGGCACTCTATGAAACATGCCCCCGGACCC	14172

Dh 31931 GACGCTGACACCTGCTGCGGCGCGGCGGTTCTGTGACAGACCTGCGACCGGCGC 31990  
Qy 14173 ATGACCACTCTGCAACCAACCCCAACCATCAACCACTCAACCCCAACCAAC 14232  
Db 31991 GCGATGCTGCGCTGTGAGACCTTCCGAGACGGAACCTGCGGAACTATATGCGCGGCGAC 32050  
Qy 14233 GACCTCG-----CCATGCGCGCATCAACACCCCACTCCCTGTATGACGCGC 14283  
Db 32051 GTCCGCGACCGGCGGACCATGCGCGGTGTGAACGGAACCCCGGTCTGTGTGTCGCGGT 32110  
Qy 14284 ACCCCCAACCTCTGCAACATCAACCACTCTGCGCAACCAAGCATMAAACAA 14343  
Db 32111 GACCGGAGCGCGGTGTGAGAGGCGTGTGCGCGGAGAGCGGCGGCGAGCGCGC 32170  
Qy 14344 ACCCTCCCAACCAACGACCTTCACTCCCGCAACCAACCCCACTCAACCACTC 14403  
Db 32171 AAGCTGCCATGACGACGCGCGCATCTCGTCCACATGAAACGATCTGCGCGGCTG 32230  
Qy 14404 CACGACACACCAACCAACCTCACTCAACCAACCAACCCCAACCCCACTGATC----- 14454  
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Qy 14455 ACCGCAACACCCCAACCCGACCACTCTCAACCCCACTCTGAGACCAACGCGCGC 14514  
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Qy 14515 AACACCGTGACTAGCGACCAACCAACCCCAACCAACGAGGCTCAACCACTAC 14574  
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Qy 14575 ATCGAATCTGAGACCGGACCAACCACTCTCAACCACTCTCAACCAACCTCCCAAC- 14633  
Db 32411 CTCGAATCGGGGCGCGGCGAGCGCTCATGCGAGTGGCGGAGAGCTGTGGGACCG 32470  
Qy 14634 ----- 14633  
Db 32471 GCGCGGAGTGGCGCTGCTCCCACTCTGACGACGAGCGCGCGGCGCACTTC 32530  
Qy 14634 ----- 14633  
Db 32531 CTGTCCGCGTGGCGGAACCTGCACTGCAACGCGCGTGGCGGTGACCTGGAACCCCGCTC 32590  
Qy 14634 -----CCCAACCAACCTCTCAACCTCTCAACCAACCCCAACCAACCCCAAC 14682  
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Qy 14683 CACTCTCTCAACCACTCTGCGCAAAACCAACCACTCTGAGCAACCCCACTCAACCAAC 14742  
Db 32651 TGGCTGCGCGCGACCGCGGCGACCAACGACCGCGCAACCGGCGGACCGGACCGC 32710  
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Qy 14803 CACCACTAGGCTCTCAACCAACCCGCGCAAGCGGAC----- 14841  
Db 32771 GGCACCTGGCTGTGTGCTGCGCGCGGACGAGCAACGAGGCTACGCGGACGGA 32830  
Qy 14842 ----- 14841  
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Db 33131 GTGACCTGCGCGCGGCTGAGCGCGCTTCTGCGGCTGTGCGGCGGCTGCGC 33190  
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Qy 14864 -----AACAAAC 14871  
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Qy 14872 ACGACCCCATCAACCCCGCTGCGGATGCTCTGTGCGCAAGTCTCCGAGAGAGAGAC 14931  
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Db 34031 GCGCGGACCGGAAACCAACTCTCGAATGTGCGGCGGAGCGCGCGCGGTCTC 34090  
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 QY 16117 GACGTGATGCGGTGAGGCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGAC 16176

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 QY 16597 GGTACCGGCGGAGAGAGAGTGTGCTGCTGCGGAGTGTGAGGAGTGTGAGGCTG 16656  
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 QY 17077 GACCCCAACCAAGAGACCAACCACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 17136  
 Db 36067 -----GACCGAGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 36106  
 QY 17137 CCGTAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 17196  
 Db 36107 GACGTGTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36163  
 QY 17197 GGTACCAATCAACCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 17256

Dh	36164	TCGTAACGGCGGTGGTGGCCCGCGGGTGGCCGGAACCTCGAAGGGGAGATTCGGGGGCGGC	36223
Oy	17257	CACCTCGCGCGCATCCTCAACCTTCAACCGACGCAACCCCTCATCAACCAAGCGCC---	17313
Dh	36224	TGCGTGGCGCGGGGCGCTGTCCCTTGAAGACGCGGCGCGGTGGTCCGCTGGCGCGCCAG	36283
Oy	17314	ACCTTATGCAAAACATATGCCCGGACCATATCAACCTTCCACACACCCCCACAC	17373
Dh	36284	GCGCTTCGCGCGCTCGTCGGCGAGGGGTGGATGTCTCGTCGGCATTCCTTCGCGAG	36343
Oy	17374	ATCAACCCACCACTCAACCGGCCAGAAAAGACTTGGCATTCGCGCGCATCAACACCCC	17433
Dh	36344	GCGGAGCGGTGGCTGCGCGCGCTGGAGACGACAGTCTCGTGGCGGCGCTTCAACGCCCC	36403
Oy	17434	ACCTTCCTCGTCACTCAGCGGCAACCCCGCAACCGTCCAAACATCAACACCTTGGCAA	17493
Dh	36404	TCCGCGGTGGTGTCTCGCGGAGACCGCGCGCTTGGAGGACCTGGTGGCCGCGCGCG	36463
Oy	17494	CAACAGGCACTCAAAACCAAACCTTCCCAACAAAAAGCCTTCCACTTCCCGCACAC	17553
Dh	36464	GACCAAGACGTCCGGGTCCGGCGCATGAGTGACTTACGCTTCGCACTTCGCGCAGGTG	36523
Oy	17554	AACCCCATCTCAACCAACTCAACAGCAACCCCAACCTTCATCAACACCGAACCCAC	17613
Dh	36524	GAGCGGATTCGAGAGCGAGATATGACCGCCCTTGGCCCGGTCCGGCGGGGCGGGACAG	36583
Oy	17614	ACCCCTCATCAACCGCGCAACCCCGCAACCCCAACCTCTCAAC-----CCCGCAC	17664
Dh	36584	ATCCCGTCTTCTTCCACCGTGAACCGCGCATGGACGACCCACCGGCGTCAAGCGCGCG	36643
Oy	17665	TACTGGAACCAAGCGCGCAACCGTGACTAGCGACCAACCAACCAACCTTCAC	17724
Dh	36644	TACTGGTACGCAACTGCGGCAACCGGTCTCTCGAACCCTGCTCAACGCGCGCTGGCG	36703
Oy	17725	CAACAGGCGGTCAACCACTTCACTGGAAGCTGGAGACCGAGCAACCCCTCAACCCCTAC	17784
Dh	36704	GAGCAGGCTTACGACGCTTCTGTGAGGTAGCCCGGACCCGGGTCTGGC-6CGCACT	36762
Oy	17785	CACCAACAACCTCCCAACACCCCGCAACCCCAACCTTCAACCCGACCC-----CCA	17837
Dh	36763	CACCGAAGACCGCGCAACTGGCGCGAGGAGGAAACGGGTGTATAGGGGACCTTGCGCGGA	36822
Oy	17838	CCACCAACCCCAACCAACCTCTCAACCACTTGGCCAAACCAACCAACCAACCTTGGACCC	17897
Dh	36823	CGAAGGCGGTGTGAAGCGCGTACGCAAGGCACTGGCGGAATCTTGAGCGCACGGCGTCCC	36882
Oy	17898	CCACCACTACACCCCAACCAACCAACCAACCCCAACCCCAACCTTGACTTCCCCAC	17957
Dh	36883	CGTGAACGTGACGCGCGCTCTCCCGCGCGACG---GCAACCGGTGAATGCGCGCG	36939
Oy	17958	CTACCCCTTCCAAACAGGACCTACTGTGGCTCGAAGGACACAGCGGGGTGGAGATCCGG	18017
Dh	36940	CTTACCCCTTCCAGGCGACCGGCTTATGGCGGGCGCGCGCGCGCGGCGCTTCAAGGACCC	36999
Oy	18018	TTTCGGATTCCGGTTCCGGGCGGGCGGAGGACTGGCGGCGGAGCGGAGAGGTGAGTCCGG	18077
Dh	37000	GCAAGAGCAGAGGGGTTCGGGAGGCGCGTGAACCAACAGAACCTGCCACCTGGCGGAC	37059
Oy	18078	GTTTCTGGAGCGCGGTGGCGCGCGACGACTTGGAAACGGTGGCGACCAACGCTGCGCGTGC	18137
Dh	37060	GCTGGGCTCGCGCCACCAACAGCGCGTGGCGGAGCTGTACCGGCGCTGTCCGCGCTGGGG	37119
Oy	18138	CCCTTCGCGCGGCGCTTGGACACGGTGGT-----GCCGACACTTCGCGCTGGGACCG	18188
Dh	37120	GCGGACCGCAAGAGCGGGCGCGCGTTCAGTCTTGGCGCTTACCGCATGAGTGGGCGCG	37179
Oy	18189	CCACCAACAGACCAACCGCATCAACCTTGAACCTTACAGAAAACTTGAACCCCT	18248
Dh	37180	GCTGCGCGAGCGGAGGCGGTATGCTGGCCGGGACTTGGCTCTCGTGGTGGCGACCGG	37239
Oy	18249	CACCTTCCCAACCAACCAACCAACCAACCAACCTTGGCTATGGCATCCCGAAACCA	18308
Dh	37240	GACCGGAGCAACGACCAACCGTTTGAACCGGAGCCGGGACCAACGAGCGCGGTGACCGG	37299

QY	18309	GACCCACACACCCCACTACCACTACTCTACCAACTCTACCACTACCAAGGATCAACCC	18386
Db	37300	CGCCACCAACCGGCGGACCGCGGACGACCGCGGTGAACCGCGCGCTACCGCCTCTTGCG	37359
QY	18369	CATCCCCCTCAACCTCAACCAACACCAACCAACCCCAACAACCTCAACCAACCCGACA	18428
Db	37360	GGAACGCGCGGAACAGCTCTGTGGTCTCGCCGTGACACCCCGCTCCGACCCCAACCTT	37419
QY	18429	ACAAGCCCAAAACCAACCAACCGGACCTATCA-----CGGCGTGTCTCTCTCTCT	18479
Db	37420	GGCCACCGCCCTCGGGGGGCGCTCGGGCGGACGAGCGCGCGGTGTGTCTGTGTCAC	37479
QY	18480	CGCCTCTGACGAAACACCCACCCCAACACCCCAACAACCAACCGGACCTCTCTCA	18539
Db	37480	CGGATCGAGGATTCGGCGGACCCCGGAGCGGCGCTGTGTCCGCGGGCGCGGCGCTGAG	37539
QY	18540	CTCAACCTCAACCCAAACCAACCCAAACCAACCCCAACACCCCTCTGTGATGCGCAC	18599
Db	37540	CTTGCGCTCTGTGGGGGCGTGGCCGACCGCGGGGTACCGCGCCTCTGTGTGCTTGAC	37599
QY	18600	CACCAACGCGACACCAACCAACCCCAACGACCCCTCACAACAACCCCAACCCCAAC	18659
Db	37600	CCACGGGCGGTCAACCAACGACGACGCGGACCGGTTCACCCCGGAACAGCGCGCGT	37659
QY	18660	CTGGGAGCTGCGCCGACCAACCTCTCGAACACCCCAACCAACCGCGGAATATGCA	18719
Db	37660	ATGGGCGCTCGGCGGGGTGCGCGCTCGAGTTCCGGGACACTGGGGCGGCGCTGTGCA	37719
QY	18720	CTTCCCAACACCCCAACCCCAACCTTCACCACTTCACCCAAACCTTCAACCAAC	18779
Db	37720	TCGCGCGACCCCTTCACCAACGACGAGCGACGCTTCGCGCGGTGTCTCGCGGCGCT	37779
QY	18780	CCACCAACCAACCAACTCGCATTCGCAACCGGACACCAACCGCGCGCTCAACCC	18839
Db	37780	CGACGGAGGAGACCAAGTGGCGGTGGCGCGGTGTGGCGCGCTGTGGCGCGCTCGTAG	37839
QY	18840	CACCAACCTTACCCCAACCAACCAACCAACCCCAACCCCAACCGAACAACCTCTAT	18899
Db	37840	CGCACCCCGCGGCGCACCGGCGGACAGGGCTGGC---GGCGCGGGACCGTGTCTGT	37899
QY	18900	CACCGGGGAAACGGGCGCCTGGCAACCACTTCACCCCAACCTTACCAACCAACCAAC	18959
Db	37897	GACCGGTGGACCGGACCGCTCGGCGGGCGGGGTGCGCGCTGTGCT---GGCGCGAGGG	37953
QY	18960	CACCAACACCTCTCTCTCAACAGCGGAAACGGGCGCCCAACCCCGCAACCAACCT	19019
Db	37954	CGCGAAACCTCTCTCTCAACAGTGGCGGCGCGCGCTTGACACCGGCGCGGACCGCT	38013
QY	19020	CACCAACCAACTCTCAACAAAGGACATCACTTCACCATTACCACTTGGGACACAGCA	19079
Db	38014	CGTACCGGAATCAACCGGGCTGGCGGTCAAGTCAACCTGTCTCTTGGGACCTGGCGA	38073
QY	19080	CCGACCAACT---CCAACAATCTTCAACACATCCCCCAACAACCCCTCTCAAC	19138
Db	38074	TCCGGCCAGATGACCGGATGGTGGCGGAGCGAGCGGACGCGAGCCGATCGGCGC	38133
QY	19137	CGTATTCACACCGGAGGATCTCTGACGACGCGCAACCTTCAACAACCTTACCCCAACCA	19199
Db	38134	CGTGTCTCAACCGCGGGCGGGCGGGCGCTGGCGCTGTGGCGGAGGCGGGCGCGACGA	38193
QY	19197	ACTCAACAAGTCTCTCGCGCCAAAGCCCAACGCGCACTTCTCTCAACAATTCACCA	19258
Db	38194	CTTGGCGAGGCAATGGCGCCCAAGTGAACCGGACATGGCCACTTGGAAAGCGGCGCTTGA	38258
QY	19257	ACACACCCCTCAACGCGCTTGTCTTACTCTCTCGCGCGGCAACTTGGCGCAAC	19316
Db	38254	CCCGGAACAGTGAAGCGGTGTCTTCTCTCATATAGGCGCTCTGGGGCGCGG	38313
QY	19317	CGGCGAAGCACTACGCGCGGACCAACGCTTACTTGAAGCGCTTGGCCCAACAACGCA	19376
Db	38314	CGACCAAGGCGTCTTACCGCGCGGCAACGGCGGTCTGACAGCCCGTGGCGAGCGCGGAG	38373

19377 CAACCAACGATCTCCCGCCAGCAGATCGCTGGGCACTGGCAAGAAAGCACTGGC 19436  
 Db 38374 CGCGGCGGCGGTGACACCGGTCTCCCTGGGCGCCCTGGGGGGGGGGGATGGC 38433  
 Oy 19437 GACTGTCAAGTACAGGAACATCTCCGCGCGCGGAGATTGTCATGCGCCGAGTT 19496  
 Db 38434 CGACACCGGCGTCTTGACACCTCTCCCGCAAGGGCGTCCCTCATGACCCGGACCT 38493  
 Oy 19437 GCGCGTCAAGCTGTGACGCGGCGATCGCGAGCGGGCGCCGAGTCTCTGTCGCGA 19556  
 Db 38494 GCGCGTCTCGCGCTCGCGCGGTCTCGCGAGGCGAGTCTCGCTGCTGTGCA 38553  
 Oy 19557 TATGCACTGGAAGAAATTGGAGCCGGTCTCTCAAGCAAGTGTGCTGCTGAG-- 19614  
 Db 38554 CGTGAAGTGGAGCGGTTCAACCCCGAGTTACCTTCAGACGGCCCAACCGGCTCTGAC 38613  
 Oy 19615 -GACCTTCCCAAGGCAAGGGAATGAGAGGCGCGAGTACCTTTGACAGACGAGAG 19673  
 Db 38614 CGAATGCGCCGAGCGCGCGCCGAAACCGGCAACGACGACCGCGCCGACCGCGC 38673  
 Oy 19674 CACAAACCTCCGCGCACTCTCATAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19733  
 Db 38674 CTCCCGCTCGCCCAACCGCTGCGCGCACTGACCGGACCCAGCGCACCGCGCTCG 38733  
 Oy 19734 CAGCTCGTCCGATCACTCCGCGAGTGTCTGCGGCGGAGCACTCCAGGCGCATCC 19793  
 Db 38734 CGACTGTGTGGCGGAACAGGCGCGCGCTGACTCGGCGACGCGACGACGCTCTGCA 38793  
 Oy 19794 GCGCGTGTGTGTTCAAGGATCTAGGTTGACTGCTGCGCGGTGGAGCTTTCGAA 19853  
 Db 38794 CCGCGCGCGCGCTCAAGAGACTCGGCTGCACTGCTGCAACCGCGGTGAACTCGCA 38853  
 Oy 19854 CCACCTCGAGACAGAGAGAGCTGCTGCGAGCACTCTGCTTCTGATTAACCCAG 19913  
 Db 38854 CGGCTGAGCAACCGGCGCTGAGCTGCTGCGCGCACTGCTTCTGACCACTCGAC 38913  
 Oy 19914 CCGCAACGATCGGCAATTTCTGCTCTCGAGATCGCGAGTTCCAGCCGCAACTC 19973  
 Db 38914 CATGCGGATCGGCGGATTTCTGCGCGCGCTGACCCCGAGCGCGCTGATCCGGC 38973  
 Oy 19974 AACTCGCTTCGCGAACCCTGGGCAAGAGTCTGATAGCGGATGCGCATGTTGATG 20033  
 Db 38974 CGAACCCTGACCTGCTGACGCTGACCAAGACGACCGATGCGCATGCTGCGATG 39033  
 Oy 20034 CTGTGCTTCCCGCGAGGTGACCTCGCGGAGCACTTCTGAGATCTGATCTCTCGA 20093  
 Db 39034 CTGCGCTACCCCGCGAGCTGCTCGCGGAGACCTGTGCGCGCGCTGCGAGCA 39093  
 Oy 20094 GCAGAGCGGATCGGCGGATTTCCCAAGCAACCGCGCTGGAGCTGACACGCG--TCTA 20150  
 Db 39094 GCGCGACCTGATCAACCGGTTCCCAAGCAACCGCGCTGGCGCTGCGCGCATGCTG 39153  
 Oy 20151 CGAACCCTGACACACCCCGGCACTGCTGACACCGAAGCGCGGATTTCTTACGA 20210  
 Db 39154 GCGCCCGACACCCCGGCAACCGGCGGAGCACTGCTGCGGCAACCGGATTTCTGACG 39213  
 Oy 20211 CGGAGCGCACTTTCGAGCGCGAATTTCTGCGGATGACGCGCGGAGACCTTTCGAG 20270  
 Db 39214 CGCGGCGCACTTTCGAGCGCGGCTTCTTTCGCGATTCGCGCGGAGCGGCAAGCTATG 39273  
 Oy 20271 CCGCGAGCAAGATCTCTCTGAAACGCGCTGGGAAACATCTGAAACGCGCGATGAA 20330  
 Db 39274 CCGCGAGCAAGCGGCTGCTGCTGAAATCTGCTGGAAGCGCTGGAACGCGCGGATG 39333  
 Oy 20331 CCGCGACACCTTCAGCGGACCCCGGAGCTTTCAGCGGACCAACGAGCAGACCA 20390  
 Db 39334 CCGCGAGTGTGCGCGGAGAGACGCGGCTGATGACGCTGACCGACAGGCTGA 39393  
 Oy 20391 CCGCGACACATCTGCTGAGCGCGGAGGATTCGAGGAGATTCGCTGACGCGGAGC 20450  
 Db 39394 CCGGACCGGCTGCGGCTGACGAGCGGATGAGGAGCTACCTGCTG--CAGGCGCTC 39450  
 Oy 20451 CACGACATCGGCTCGGCGGAACTCTCTAATCTCTGCGGTTGAAAGGCGCTGCGGTA 20510

39451 CGCAAGCTGCGCTCCGCGGAGATCTGATCTGCTGCGGCTCCAGGAGCCGCGCTAC 39510  
 Db 20511 CTTGACACAGCGTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 20570  
 Oy 39511 CGTGAACCGGCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39570  
 Db 20571 GTCCGTAATGCAACATGAGCTTGGCGCGGAGGCAACGCTGATGACACCCGATGAC 20630  
 Oy 39571 GAGAGCGAGTGCACCTGAGATGCGGAGGAGTGCACCTGATGCGGACCCACCTC 39630  
 Db 20631 CTTGACCAATTCGCGCGCAACGCTGACCGCGGAGCTGCGCGGAGGCTTTCGAGG 20690  
 Oy 39631 CTTGAGGCTTTCAGCGGAGCGGAGCTGCGCGGAGGAGGCGGCTGCGAGGCTTTC 39690  
 Db 20691 GCGCGCGCTGACGCTGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 20750  
 Oy 39691 GCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 39750  
 Db 20751 CTTGAGCGCGCGCAACGCTGACCGGCTGCTGCGGAGGAGGAGGAGGAGGAGG 20810  
 Oy 39751 GTCCGAGCGCGCGGCTGAGACCGGCTGCTGCGGAGGAGGAGGAGGAGGAGG 39810  
 Db 20811 CCGAGCGGCTGAGCAACGCTGACCGGCGCGCAACGCGGCTTCCAGAGCGGCTCAT 20870  
 Oy 39811 CCGAGCGGCGGCTGCAACGCGGCTGCAACGCGGCTGCAACGCGGCTGCAACG 39870  
 Db 20871 CCGCGAGGCTTCCGCAACGCGGAGCTGACCCCGCGGAGCTGATGCTGAGGAGG 20930  
 Oy 39871 CCGGAGCGGCTGATGCAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 39930  
 Db 20931 CCGGAGCGGCAACTTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20990  
 Oy 39931 CCGTACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 39990  
 Db 20991 ACAGAGCGGCTCCGCAACGCGGCGGCTGCTGCGGCTGCTGCTGCTGCTGCTG 21050  
 Oy 39991 CCAAGAGCGGCGGCGGCGGCGGCGGCTGCGGCTGCGGCTGCTGCTGCTGCTG 40050  
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 Oy 40051 CAGCGAGGCGGCGGCGGCGGCGGCGGAGTATGATGATGATGATGATGATGATG 40110  
 Db 21111 GACACTCCACGACTCTGCAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 21170  
 Oy 40111 ACTGATGCTCCGACCTTGCAGTGAAGCGGCGGAGTCCGACGCTGATGAGTTC 40170  
 Db 21171 TGCGGTGAGTGTGACGAGAGGAGTGCCTGCGCGGCGGAGGAGGAGGAGGAG 21230  
 Oy 40171 GCGGAGTGAATGCTGCGAGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAG 40227  
 Db 21231 GCGAGAGTGTATCATTTGCGGCTGACGCGGAGCAACGCGGCTGATCTCTGAAAG 21290  
 Oy 40228 GCGCGGCTTCTGCGGCTGCGGAGTCAAGCGGAGCAACGCGGCTGATCTCTGAG 40287  
 Db 21291 ACCGCGC-----GACGAGTTCGCGGAGGAGCAACCGCGGAGGAGGAGGAGGAG 21344  
 Oy 40288 ACCGAGACCTTGAAGAGGAGCAACCGAGAGGAGGAGGAGGAGGAGGAGGAGG 40347  
 Db 21345 CGAGAGGCTGCTGCGGAGTCTG--GAGTGTGCGGCTGCTGCTGCTGCTGCTG 21401  
 Oy 40348 CGAGAGGCGCAACGAGAGGAGGAGGAGCAAGAGGAGGAGGAGGAGGAGGAGG 40407  
 Db 40408 GAGAGCGGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 21461  
 Oy 21462 CCGTGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 21515  
 Db 40468 CCGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 40527  
 Oy 21516 CCAAGCGGCAACCTTCAATGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 21575



Db 40528 TCTGCGCACTCTCGGCGCAACCGCGAGCTCTCGACGGGCGGCGTCTGTCG 40587  
Qy 21576 GCGCGCAGCGGAAACCCACCCCGCGGTATCCACAGACGCGCCGAGCGGGAC 21635  
Db 40588 GCGCGACCGGAGCGAACTGCGCGCGGCTTACGGACCTGTCCGGGCGCGTGGCGA 40647  
Qy 21636 GCGGAGCGCGGAGAAAGACCGCATTCATCTGCTCCGACAGGGACCCACCGCGCG 21695  
Db 40648 GGAAGCGCGCGGCGCGGCTGCGCTTCTTCAACCGGCGAGGGCGCGCGACCGG 40707  
Qy 21696 CATGCGCCACGGGCTCTACACACCCACCGCGTCTTCCGCGCGGACCTCAAGCATCTG 21755  
Db 40708 CATGGGCGCGCGCTTACGCGCGCTTCCGCGGTGCGGTGCGCTTCAAGCATCTG 40767  
Qy 21756 CACCGCACTCGACCCCGCACTCGACCAACCGCTCTCCCTCCCTCAACCCAAAGCAAA 21815  
Db 40768 GCGCGCGCTTCAACCGGCACTTCCGCGCGCGCGCGCTGCGCTGCGT-----CGTGT 40815  
Qy 21816 CGACACGACAAAGAGAGCGCGCGCACTGCTTCAGAGACCCGTAAGCGCGCGCG 21875  
Db 40816 GCGCGAGCGCGGCTCGCGGAGCGCGGTATCGACAGACCTCTACACAGCGCGG 40875  
Qy 21876 CCTCTTCCGCTTCCAGGTGCGCTTCCACCGCTCTTCAACGAGGCTACACATACCC 21935  
Db 40876 CCTGTTCCGCTTGAAGGTGCGCTGTTCCGCTGCTG--GAGCATGAGGCGTAAGGCTC 40932  
Qy 21936 CCACTACTACGCGCGACATCCCTCGCGGAAATACCGCGCGCGCACTCGCGCGATCT 21995  
Db 40933 CGAGCGCGGTGCTCGGCACTGATGCGGAGTCCGCGCGCGCGACGTGCGCGGCTG 40992  
Qy 21996 CACCTTCAACGCGCGACCAACCTCTATGACCCAAAGCGCGACCTCATGCAAAACATG 22055  
Db 40993 GTCACCGCGCGCGCGCGCGGTGTACCGCGCGCGCGCGGTGATGAGAACTGCG 41052  
Qy 22056 CCC---CGGACCATGACCACTCTTCAACCAACCCCAACCATCAACCAACTGAC 22112  
Db 41053 CGAGGCGCGCGCATGCTGTGCGCGCGCGCGCGCGAGAGCATGTGCGCGCTGCG 41112  
Qy 22113 GCGCCACGAAAGCATCTGCGCATGCGCGCATCAACCCCGCATCTCGTGTATGAG 22172  
Db 41113 CGAGCGCTTCAAGAGGTGTCTGTGCGCGCATCAACCGCGCGCTGATGTCTGTG 41172  
Qy 22173 GCGGACCCCGCAACCGCTTCAACATGACCAACCTTTCGCAACCAAGGATCAAAAC 22232  
Db 41173 GCGGACGAGAGGCGGTCAAGCGCGCGGCGGTGCGCGGTGCGAGGCGCGCTGCGAC 41232  
Qy 22233 CAAACCTTCCCGCAACCAACGCTTCACTTCCCGCAACCAACCCCATCTCTC----- 22287  
Db 41233 CAAGCGCTCAACCTGAGCGCAACGCTTCACTGCGCGGTGATGAAACGATGCTGCGCG 41292  
Qy 22288 -----AACCAACTCAACGAGCAACCAACCTTCAACCTTCAACCCCAACCGCC 22340  
Db 41293 GTACGAGCGGCACTGCGCGCATGCTTTCGCGAGCGCGCACTGCGGTGTTCGA 41352  
Qy 22341 CCTCATCAACCGCAACACCCCAACCGCACTTCTTCAACCCCGCACTGAGCCCAACA 22400  
Db 41353 GGTGACCGGCAAGCGCGCAACCGGAGAGCTGTGCAACCCCGCTTATGCGCGCGCA 41412  
Qy 22401 AGCGCGCAACCGTTCAGTACGCAACCAACCAACCTTCAACCAACGCGGTGAC 22460  
Db 41413 GGTGCGGCGGAGCGGTGCGGTTCGCGAGCGAGTGAACAGCTGTGCGCGAGAGTAC 41472  
Qy 22461 CACCTATCGAAGTCCGAGCGCGCAACACCTTCAACCCCGCAACCAACCTTCC 22520  
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Qy 22521 CAACACCCCGCAACCACTTCAACCTTCAACCCCGCAACCAACCCCAACCTT 22580  
Db 41530 GCGGCGGCGCGCAACCGGATGCGGTCAAGCGCGCGCAACCGGATGCGGACCT 41589  
Qy 22581 CCTTCAACCTTCCGCAAAACCAACCAACCTTGGACCCCGCAACCTTCAACCAACCA 22640  
Db 41590 GCTTACCGCGCTGCGAGGCTGACGTGCGCAACCGCGCGCGTGTGACTGCGCGCTT 41649

Qy 22641 CAACCAACCCCGCAACCAACCTTCAACCTTCCCAACCTTACCCCTTTCAAACCAACA 22700  
Db 41650 CCAAGGACCGGCGCGCG---CGGAGTGAACCTGCCACGTACCGGTTCCAGCACCGCG 41706  
Qy 22701 CTACTGGCTGCAACTTACCGAGCGCCCAACCA----- 22732  
Db 41707 GTACTGGCTGACCGCGCCCAAGGCGCGGTGAGGCGCTGCGCGCGCGCTGCGCGG 41766  
Qy 22733 ----- 22732  
Db 41767 CACGCGGACCCGCTGCTTCAACGCGCGCGCTGCGCGGTACCGGCGGCTGCTT 41826  
Qy 22733 ----- 22732  
Db 41827 CAGGCGGACCTGCGCGCATTCAGAGAAAGAGCGCGCGCGCTCCGCGCGCATCTCGA 41886  
Qy 22733 ----- 22732  
Db 41887 TCTGATGCTGTGAGCGCGCGCAAGCTGCGTGCAGACCGGATCGCATGATGCC 41946  
Qy 22733 -----GCGCGGTCAAGGCGTTCGCGCGCTCGGCTCA 22767  
Db 41947 GCGCGCGTCCGCGCGGACCGCAAGCGCGCTGCACTGTGAGTGCAGCGCGAGCA 42006  
Qy 22768 G-----ACACCGCGAGTCCGAGTTCTGAGACGCGGTGAAAGAGAAAGA 22811  
Db 42007 GGAAGGCGACCGGGAATTCACCTTCAAGTGGGCGCAAGCATCTCGGTACGCGGGGA 42066  
Qy 22812 CTTCAAGAGCTTCCCGAATCTTCAGCATGACGCTTCTGTGACAGGTGTGCG 22871  
Db 42067 GAGTCTCTGAGACGCGGATTCGCGCACGCGCACGCTGCGCGGTGCGCGCGCGCGGAC 42126  
Qy 22872 GCACTCTCGCGCTGGACCGCGCACCAACAGACCAAGCGCGCATCAACCTGAGACTA 22931  
Db 42127 GCAACCGCGCGCTGCGCGCGCGCGCGCGCAACCGCTGCGCGCGCGAGTGTGCG 42186  
Qy 22932 CCAAG-----AAACTGAAACCCCTCAACCTTCCCGAC 22964  
Db 42187 CCGGCGGAGCAGAGCTTTCGCGGAGCTGTGTCTGACCGAGAGAGCGGCGGACCGGA 42246  
Qy 22965 CACCGCAACCCCAACCAACCTGATTCAGTATCCCGGAAACCGAGCCCAACCGC 23024  
Db 42247 CCGCTTGTGTGACCCCGAGCTGTGCGCGGCGCTGACGAGCTGATCAACGAATGCG 42306  
Qy 23025 CCAATACCAACATCTTCAACCAACCTTCAACCAACGAGGATCAACCCCATCTCCCTAC 23084  
Db 42307 GCGGAGCGGTTCATTTCGCGGAGTACCGGATACCGGACCGGCGCACGAGTGTGCG 42366  
Qy 23085 TGTCAACCAACCGCACCAACCC----- 23108  
Db 42367 GGTTCGGTGAACCGCTTGGCGCGCGCGCGGTGAGCGGTGTGTGAGACGCGGAGG 42426  
Qy 23109 -----CCAACCTTCAACCAACCTTCCACAC 23136  
Db 42427 GAGCGGAGTCTTGTGTGAGCGCGGTGAGGAGCGGACCGGCGCGCGCACGAC 42486  
Qy 23137 ACCGCAACCAAGCCCA----- 23154  
Db 42487 GCGCGCGCGCGCGCGCAACCGGACCTGACTGTCTATGCTGACTGAGACCCGTTGCG 42546  
Qy 23155 -----AACCAACCAAC 23165  
Db 42547 GCGCGGTGCTCCGAACCGCGCGCGCTTGGAGCGGTGTGCGCGGAGCGGCTGCGCA 42606  
Qy 23166 CGAGCCATCAACGCGCTTCTTCTTCTGCGCTTCAAGCAACCCCAACCCCGCAACA 23225  
Db 42607 GCGCGCTGTGCGCACCGAGGCGCGGAAGTGAAGGCCCAACCGGACCTTGTGCTGCG 42666  
Qy 23226 CCGCGCAACCAACCGGACCTTCTTCAACCTTCCCGCAACCCCAACCCCAAC 23285  
Db 42667 CCGCTTCAACGAGACGCGCGCGCGCGCGGTGTGTGTCTGTCTGTGAGACAGGAAC 42726

OY	23286	CCACCCCAACCAACCCCCCTGTGTATCGGCAACACCAAGCCACACCAACCCCAACGA	23345
Db	42172	CGGCGCAACGCTCAAGTCTATCGGCAACACCAACCAACCCCTGAGTGTCAAGGA	42786
OY	23346	CCCCCTCAACACACCCCAACCCAAAGCCCAAACTTGGGGACTGACCAGCAACCACTCTCTGA	23405
Db	42787	ACTGTGTGGGGAAGGCGCGCTGCGCGGAGGCGCGGTTGTCTTGTATCAACCGCGGCGGT	42846
OY	23406	ACACCCCAACCAACCGG-----	23423
Db	42847	GTCCACCGGGGACCGGCAACCCCGGTGACCCGCGCAAGGCGGCGCCCGGGAATGTGTCT	42906
OY	23424	-----CGGATATGACCTTCCACACACCCCCAC	23453
Db	42907	GTCCGCGCAGGCGGAGCAACCCGAGCGGTTGTGTCTGGCCGACCTTGGCGGCGACGC	42966
OY	23454	CCCCCAACCTTCACACACTCAACCAAACTTCACCAACCCCAACCAACCAAACT	23513
Db	42967	GGAAGCGGAATGTGTCCGCGCGCGCGTGGGGAACCGCACTCAACGAAGCGGAACCGAAT	43026
OY	23514	CGCCATTCGCACCAACGGCAACCAACCGCGCGCTTCAACCCCAACCTTCAACCCCAAC	23573
Db	43027	CGCGGTCCGGGACGGGACGAGTGTCTGAGTCCCGGCTTGGCCAGATCAACGAACGGCCAC	43086
OY	23574	ACACCAACCAACCAACCCCAACCC-----CAACGAACCAACCTTCAATCACCGGCGG	23624
Db	43087	CGAGGTGTCCGCGGAAAGCGGCGCCGGGAGGCGAAACAGGACAGTGTGTCTCACCGGCGC	43146
OY	23625	AACCGGCGCCTTCGCACACCAACCTCAACCAACCAACCAACCAACCAACCAACCA	23684
Db	43147	GACCGGGGGCATGGGCAACGAGATCTGTGGGCACTTGGGCAACGGGCGACGGCTGTGGGA	43206
OY	23685	CTTCTCTCTCAACAGCCGAACCGGCGCCCAACACCTCCACGCAACAACCTTCAACCA	23744
Db	43207	CTGTCTGTGTCTGACGAGCGGGGCGCCGACGACCGGCGCGCGCGCAACTGGGCGAGT	43266
OY	23745	ACTCCAAACAAAAGGATCTCACTCACTCACTACCACTTGGGAACTTCAAGAACCAACCA	23804
Db	43267	CTTTGCCGAGCGGGGCGCGACAGCACTTTCACAGGCTTGGGAAACCGCGGACCGGCGCGC	43326
OY	23805	ACTCCAAACAACTCTCAACACCAATCCCGCCCAACAACCCCTCACCACCGTATCCACAC	23864
Db	43327	CTTGGCCGACGCGGTGGCGGACGTACCGGCGGAGCACCCCTGTACCGCGGTGTACACT	43386
OY	23865	CGAGGCGCTAATCTCTTGGCCCCCGTGTGCGAAACCGAGCCGAATCTTCTTTCGT	23924
Db	43387	CGCGGAGTGTGTGACGACGAGAGTCTCACACCTTGAACCCCGACCGGATGACACGCT	43446
OY	23925	TACGGGACGGAAGCAACGGGCGCGGGAATTTCTGATGATTTCTGTGTGAACATGAAC	23984
Db	43447	GCTCGCGGCCAAGGCCGAGGCGGCGGACATCTGCAAGACTGACCGCGAACCTTGC--G	43503
OY	23985	GCTTGAACATCTAATCTCTTCTCGTGGGCGCGCGGCTGTGGGGGAGGGGATCAGTG	24044
Db	43504	GCTGTCCCACTTGTGTGTCTTCTTGGGCGTGGGCACTTGTGGGCGCGGCGCAAGGC	43563
OY	24045	CGCACTACGCGCGCAACGCACTACTGGAACGCGCTTGCAGCACCGCATCTTCAACAATGG	24104
Db	43564	CAACTAAGCGGCGGCAAGCGCTTTCGTGAGGACACTGTGCGCAACCGAGGCGGCGGCGCA	43623
OY	24105	ACTTCCCGGGGCACTGATGCGCTGGGGCCCTTGGGCGCGGAAGGCAATGTGGCGGTGA	24164
Db	43624	CTTGCCTGGGCAACTGTGCTGTGGGGCTGTGTGGAGAACCAACGGCGGCAATGTGGCGCA	43683
OY	24165	TGGGCTCATGTATTACCTGGAAGGCGGCAATTCGCGGATGGAGCAACGATGGCGT	24224
Db	43684	CTTCTCCGAGTGAACCGG-----CGCGGATGGCCAGGCGGCGTCT	43728
OY	24225	CGCGGCAATTCATGTGTGCGGGCGGACGGCGGAATTCACACTGATATCGCGGACAT	24284
Db	43729	CGCTTCAACCCCGGGGAGGAGGTCTCGCGCTGTTCGACGCGGCGTGAATCTCGACCGCAC	43788
OY	24285	CGACTGGAGCGTTTGTTCGCCGCTTTCACCGCTGCAACGCAACGCCGCTCATGAGGA	24344

Db	43789	CACCTTGGTACCCATGCGCCTTCGACAAAGGCCGTATCTGCGGGAAAGCGGCCGAGCGAC	43844
Qy	24345	CATTCCGAGGTTGGCGAAGCGGCTCAGAGCTGGAAGCAGCTGCATCGACCGCAAAAGAC	24404
Db	43849	CCTGCGCGCACCTTCCGGGAGC-----CTGGTCCGGGACCCCTCGCAGAGGCGTCGGCG	43902
Qy	24405	GACCAACAGCTCAGCCGATTTGCGAGCTCTCTCCGTGAGCGATTGGCCCGACTGACGTCCTC	24466
Db	43903	GGCCGGTGGCGGGCGCGCCGGGAGTCTCTTTCGGCAGCAGCTGGCCGAGACAGTCCGAGAG	43962
Qy	24465	AAAGAGAACCAAGGTGTGCTCGGCGCTGATTTCGAGACAGGATCTGCACCGTTTCGGCCT	24522
Db	43963	CGGCGCGGACAGCTGCTGCTGATCTGATCTCACCGGAGGTGGCCCGCTACTGACATTA	44022
Qy	24525	TCGTATTCGGAAGGCATTCGAGGACCAACGAGCCTTCCGAGCCTCGGCTTCGACTCGCT	24584
Db	44023	CGGCGCGGAGCGCCCGGCTCGACGCGAACTCCCTTCGGGAGCTGGATTGACTCGCT	44082
Qy	24585	GACGTCGGCTCAGTTTCAGCAGAACTCGCCAAAGAAACCGGACTGCTCCCTCCCGTC	24644
Db	44083	CACGCGGCTGAGGCTTGCGCAACGCGCTGATCGCCGAGCCGGGCTGCACTCTCCGCGC	44144
Qy	24645	CCTGCTGTTCGACATATCCGACCCCGCAGAAATGTGTCGCCATCT-----	24689
Db	44143	GCTGCTTTCGACTCCCAACGCGGACCGCGCTCGCCGAGCACTTGAAGCAAGTCTCT	44202
Qy	24690	-----GCGCAGACAACTCGTGCATTCAGACGACG	24719
Db	44203	GGGTCGGGTGGCGGGGCTCGGCGCGGGGCTCACCGAGCTGACATCTTGAAAGCGCG	44266
Qy	24720	AGAGAA-----	24725
Db	44263	GCTCGGCACCTCGCACCGGACCGGCGCACCCGCGAAAGCTTCGCGCGCGCTGCGCGG	44322
Qy	24726	-----	24725
Db	44323	GCTGGCTCCGCTCGGAGCGCGGACGAACTCGAAGCCGACGACGCGGACATCACAGCAA	44382
Qy	24726	-----	24725
Db	44383	GCTGGAATTCGCGCTCGGATGAAGAAGCTCTTCGACTTATCAACGCGGAAATTGGAAAGGA	44442
Qy	24726	-----CGCGGCA	24722
Db	44443	CTGAGTCCGATGAGCAACGACGACGAGCTTCGTATCTATCTAAGCGGCTGACGGGAT	44502
Qy	24733	CTTGCGAATGCTCTCCCGCAAGTGGCCCATCGGCGTACCGGTGAGGACGAAACCGATCGCG	24792
Db	44503	CTGCAACGGACGGCGCACGACCTGACCCGAGATCGAGTCCAGGGACACGAGCCGATCGCG	44562
Qy	24793	ATCATCGGTATGGCATGTCCTTCCCGGGCGGAGTACGTTCTTGCCGACGACCTGTGGAA	24852
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Qy	24853	TTGCTTCGCTTCGGGTAAAGACGCTATCGGCTTCCCGACCGACCGCGGCTGGGACCTG	24912
Db	44623	CTGGATCACACGACGACGAGCGGATCGGGCCCTTCCCAACGACCGCGGCTGGGACCTG	44682
Qy	24913	GACACGCTTACGACCCCGACCCCGACACCCCGGAGCCTGTCTACCCGAAAGGGCGGA	24972
Db	44683	GACGCGCTTCACACCCCGACCCCGACACCCCGGAGCCTGTCTACCGGAGGCGGGCGGG	44742
Qy	24973	TTCTCTACGCGGAGGCACTTCGACGCGGAAATTCTTGGGATCAGCCCCGCGAGAGCG	25032
Db	44743	TTTCGTGAGGACATGCTCTTTCGACGCGGCTTCTTGGGATCTCTCCGCGGAGGCGG	44802
Qy	25033	CTCGCCATGAGACCCCGACGACGACTCTCTTCGAAACCGCTGGGAAACCATGAAAC	25092
Db	44803	CAGTCCATGAGACCCCGACGAGCATGCTCTTGGAAGACTCTCTGGGAGGCGCTGGAAAC	44862
Qy	25093	GCGGCAATCAACCCCGACCTTCACGGGACCCCAACCGGAGTCTTGGCGGAAATCAAC	25152

Db	44863	GC	CGGCGCTCGAACATTCACACGGCGCTCGCGGACGCCGTCAGGGGCTTTCGCGGACCTCAAC	44922
Oy	25153	GCT	CAGACGACACCGCCGCGCATATCCGCAAAAGCCGTAATGTGAGACATCGAGGGCTAC	25212
Db	44923	CAG	CAGAGCTACCGGACACCTGCTGGCGCGGCC-----CGAGCGGTCTGGACAGCTAC	44976
Oy	25213	GCC	CTGACCGGCACTTGGGAAATGTGAGCTCCGGCCGGGTGGCTTACACGCTCGGCTC	25272
Db	44977	GG	CTCCACCGGCACTTCAACAGGCTGCTCTCCGGCCGGATCTGTAATGTGCTGGGCTCG	45036
Oy	25273	GAA	GGCCCCCGGGGTGGGAGTAAGGCGGTTCGTCGTCGTTGGTGGCTTTGCAATGG	25332
Db	45037	GAG	GGCCCCCGGCTGACCTGGAGACCGGCTGCTCTCTCGCTGGTGAACCTGACCTC	45096
Oy	25333	GC	CGCAGAGCGGTTCGTCGGCGGGTGAAGTTCATGATGCGCTTGC	25392
Db	45097	GC	CCCGACAGCGGCTCGCGGACCGGGAGTGGGACCTCGCCTGGCCGGCCGGCCGAGACA	45156
Oy	25393	AT	GTGCTCCGGGTAAGTTTGTGAGTCTTCACTGACGCGGGGTCTGGCCCGGACGGG	25452
Db	45157	CT	GTTCACCTTCGCGGCTCCAGTGGCCCTGTCCGGGACAGCGCGCTGGCCCCCGACGCG	45216
Oy	25453	CG	GTGCAAGGCGTATTTGGGGGGGCTGTGAGAGTACCGGCGTGGGCGAGGATGTGGGAATG	25512
Db	45217	CG	CTCAAGGGGTCTTGCGCGGCGGCGGACGGCGGGGCTGGAGCAGAGGACGTCCGCGTC	45276
Oy	25513	CT	GCTGTGATGAGCGGCTCTCCGACGCGCCGTCGACAGTTCACAGTCTCTGCGCGGTGTC	25572
Db	45277	CT	CGCCCGTCAAGCGGCTCTCCGACGCGCCGCGGCTCGTCAACGGGTGCTCGCGGTCTG	45336
Oy	25573	CG	TGTCAGTGGCGGTCAACAGAGACGATGCGAGCAAGTCTGACCGCGCCCAACGGGCCC	25632
Db	45337	CG	CGCGCAGCGCGTCAACAGAGACGAGGCGGTCCACAGGTCTCACCGCGCCCAACGGGCCC	45396
Oy	25633	TC	CCACGACAGCTGATCTCTGACAGGCGCTTGGCCCAATGCGGGAATGACCCCGCCGATGTC	25692
Db	45397	TC	GACAGACGCGGATCTCCGACGCGGCGCTTGGCCCAACGCGGATGTGTGCGCCCGACAGTTC	45456
Oy	25693	GAC	CGCAGTGGAGGCGCACCGGACCGGGACCACTCTGAGGGAGCCGATTCGAGGCCACGACA	25752
Db	45457	GAC	GTGTGTCAAGGCGCACCGGACCGGACCAAGCTCGGCGGACCCGATCAAGCGGACGCG	45516
Oy	25813	AA	ATTCACATCGGGCACGACAGGCGCGCGCGGCGGTGGGCGGATCATCAAGATGTG	25872
Db	45577	AA	GTTCACATCGGGCACAGCGGTGCGCGCGCGGTCTCGCGGTGTGATCAAGATGTG	45636
Oy	25873	AT	GGCCCGCGCAACCGGCGTGTCCACACAACCTCCTCAGTGAAGAGGCCACCCCGAG	25932
Db	45637	CAG	GGCGCTCGGGCACCGGCTGTCTCCAGGACCTGTGACCGCGAGAGCCACCCCGAAC	45696
Oy	25933	GT	CGCAGTGTTCACAGGCGGAGTACAACTCTGACACAACCGGTGCTCTGCGCGCGAC	25992
Db	45697	GT	CGCAGTGTCTCGGGCGCGGTGTGAACTCTCTCAGGAGGCCGCGCCCTGTGGCCGCGC---	45753
Oy	25993	CG	GGCGCGCGCGCACCGCACCGCGCGGTTCATTCATTCGCGGTCAAGCGGACCAACGCGC	26052
Db	45754	---	TCGCAACCCCGCCCTGGCGCGGATGTGCTCTTCGCGCATGACGGGACCAACGCGG	45810
Oy	26053	CAC	ATCATCTCCGAAAGAACCCACCTCCGAGAGAGGATTCGACAGACGAAACCGGCT	26112
Db	45811	CAC	GTGATCTCTGAGACAGGCTCCGAAAGAAACGCGGAAAGACACGAGGAGAAACCCC	45870
Oy	26113	GC	CAACGACACGAGCGCTGCGCCCATCTCTCTTCCCTGCGCGGTCTCGAGAGTCT	26172
Db	45871	GG	AGAGGCGCCCGGGGGGACCGCCCGCACCTCCCTCGTGGGTGCTCTCCGCGCGGT	45930
Oy	26173	GAG	CGGAGTTCGGGCGGACGACAGGCGTGTGCGGACGTAAGTGGACCGCGCGGAC	26232
Db	45931	GAG	CGGCGCTGCGCGGACGAGCCCGTGGCGCGGACGACCTGTGCGCGGTCTCCGCGC	45990

QY	26233	ATGTACCTTCCGACATTTGTGCGGGGTGTGGCCCGCGGCCGCTACTGGAACCGC	26239	ATGTACCTTCCGACATTTGTGCGGGGTGTGGCCCGCGGCCGCTACTGGAACCGC
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QY	26293	GGCGTCAATCCGCGCGCGGAGCCCGCGAGGAACTGGCCGACGGACATGACAGCCCTGGAGCG	26355	GGCGTCAATCCGCGCGCGGAGCCCGCGAGGAACTGGCCGACGGACATGACAGCCCTGGAGCG
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QY	26353	GGCGAACCACCCACCCCGACATCACACAGCGCACACCCGGGGCGGTGACCGCGCGCGCTC	26412	GGCGAACCACCCACCCCGACATCACACAGCGCACACCCGGGGCGGTGACCGCGCGCGCTC
Db	46111	GACCGCCCCCGCGAAGGGGTACTGCGCGGTCAACCCGCGTGG-----ACGGCAAGGTG	46166	GACCGCCCCCGCGAAGGGGTACTGCGCGGTCAACCCGCGTGG-----ACGGCAAGGTG
QY	26413	GTCCTTCGTCCTTCCCGGACAGGGCGGCACTGGGCGCGGATGGAGCTTGACCTTCCTACCC	26472	GTCCTTCGTCCTTCCCGGACAGGGCGGCACTGGGCGCGGATGGAGCTTGACCTTCCTACCC
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Db	46465	GTCGCGGCGGACCTGACCCCTTCAAGAACGCGCGCGCGGTGATCTGCTTGCGCAGCGCATC	46522	GTCGCGGCGGACCTGACCCCTTCAAGAACGCGCGCGCGGTGATCTGCTTGCGCAGCGCATC
QY	26773	CTGGCCG---CCGTACGAGGCGCGGGCGCGCATGGCTCACTGCGCCCTGCGCCGCGACGAC	26828	CTGGCCG---CCGTACGAGGCGCGGGCGCGCATGGCTCACTGCGCCCTGCGCCGCGACGAC
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QY	26830	GTGCAAGACTCATTTCCGAACGGTGGGAAGGCGAGTTGTGGTGCAGGCTTCAACCGC	26888	GTGCAAGACTCATTTCCGAACGGTGGGAAGGCGAGTTGTGGTGCAGGCTTCAACCGC
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Db	46822	ACCGTACCCCTGTACTGACGAGTGAACGGCGCGCGCTGGACACCCCGCATGAGACGCGC	46883	ACCGTACCCCTGTACTGACGAGTGAACGGCGCGCGCTGGACACCCCGCATGAGACGCGC
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QY	28928	ACGATG	CGA	CGA	CTTG	CCCGG	CGCGCGTGT	GGGCTT	2898
Db	48560	GGCGGG	CGTCCG	CTCGCG	GA	GAAC	CA	CTCGCGCG	4861
QY	28988	AGCAC	CCCGA	CCGAT	AC	CGTGTG	ATTT	CGAGCGGG	2904
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## FEATURES

## source

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BASE COUNT 3517 a 10766 c 9529 g 3729 t  
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Query Match 11.2% Score 3443.4; DB 6; Length 27541;  
 Best Local Similarity 52.3%; Pred No.2,3e-279;  
 Matches 11367; Conservative 0; Mismatches 8466; Indels 1914; Gaps 93;

Qy 6241 GAGGCTTGTGACCGAGCGATGCGCATGCTTGCGATGAGCGCTGTGCTTCCCGGCGGA 6300  
 Db 6422 GAGTGGGGGCGCCAGAGAACCGGTGGGCATCGGATGACCTGTGCTACCCGCGCGG 6481  
 Qy 6301 GTGACCTGGGCGGAGAGATTCTGGGATGATCTCTCCGAGACAGAGACCGATCGGCGGA 6360  
 Db 6482 GTCCGCGAGCCCGAGAGACTCTGGGCGCATGTGAGGCGCGGACACCGGCTCTACCCCG 6541  
 Qy 6361 TTCCCGACCGAGCGGGGCTGGGACCTGAGCAGGCTTACGACCCGACCCGACGACCCG 6420  
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 Qy 6421 GGCACCTGTACACCCGAAACCGCGGATTCCTCTACGACGACGACCACTTCGACCGCGA 6480  
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 Qy 6481 TTCTTGGGATAGCCCCCGGAGCCCTGCGCATGAGACCCCGAGCAAGCATCTCTCTC 6540  
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 Db 6698 GAATCCGCTGGGAGGCGTTGAGAGCGCGGCGGATGACCGGACCTGCTGAGAGGAGAC 6757  
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 Db 6758 GCGACCGGAGTCTTATGGGCGCGATGGCGGAGTACCGGCTGGGCGCGCGCGACCGG 6817  
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 Qy 6721 ATCTGTACAGCTTTGGTTTGAAGGCTCTGGGCTGCTGGTGGAGACCGGCTTGTCTCG 6780  
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 Qy 7081 CTGACCGGCGGCGGAGCGGCGCTCCGACAGCGGTCTTCGCGAGGCGCTTCGCAACGGC 7140  
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 Db 8333 GCGGAGTGTGCGGAGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8392  
 Qy 8281 ACCCTGTGCAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8337  
 Db 8393 GCGCTGTGAGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8452



QY 8338 CACATCAACCCACCACTCAACCGCCCAAGAAAGCACTCGCCATCGCCATCAACACC 8397  
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 QY 8398 CCCACTCTCCCTGATCAAGCGGCAACCCCAACACCTGCAACAGATCAACACCTTTCG 8457  
 DB 8513 CCTCCGCGCTGCTGCTGCTCCCGGAGCAAGAGCAAGTGCATGCGCCCTCAACGGC 8572  
 QY 8458 CAACAACAAGGATCAAAACCAAAACCTCCCAACCAACAGCCCTTCACTCCCAAC 8517  
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 QY 8518 ACCAACCCTATCTCAACCACTCAACAGCAACCAACCAACCTTCACTCAACCAAC 8577  
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 DB 8993 GCGGCTGAGTGAACCAACCGCTGCTTCCGCGGCAACCGGCGCCGCGCAACCACTTCC 9052  
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 DB 9053 ACTTACCCCTTCAACCAACCGCGCTACTGAGCCCAAGCCCTCAAGAGGCGCAACCGC 9112  
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 QY 9103 GCTGACCAATGCGCTGAGCGGCAACGAGTGTCTGCTGAGCGCGCAACCTTCTGAGCTG 9162  
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 QY 10333 ACCGAGCTTCAACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10392  
 DB 10480 -----TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10510  
 QY 10393 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10452  
 DB 10511 GCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10570  
 QY 10453 CTGAAGAGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10512

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Db      10571 CTGGTGCAGGCGGCGCTCAACCGAGGT----- 10596
Qy      10513 CGGCGGATCCGAGCGTGCCTGCCAGCGCTCCGGGAGGTGCTCGGCGGTCGTTGAT 10572
Db      10597 -----CGGTGCGGAGTGTGATGACACCGGGAGATGCG 10627
Qy      10573 GATATCGGATCGGAGAGGTGTGCTCGGTGATGTCCGGATGGATCGATGTTGGTGAACGGGTGAG 10632
Db      10628 GTCCGGGATATGGCTCTGTGTGTGTTCTCGGGGTGAAGGATGCGGTCTGTGTCACTGGTGTGT 10687
Qy      10633 AGGGATGTCTGGATTCGGGCGGTGCGCGCATCTGGCTGTGTGTGTGGGTGGGAT 10692
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Qy      10753 CTGGCGCGCTTGGGAGCGGAGGTGCGGATGTTGTCGTGTGATGTGGGAGCGGCGGAG 10812
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Qy      10813 GTGGTCGGGCTGCTGGAGGATGTTCTTCCGCGGATGTCCGCTGACGGGTGTCTGTGATGCG 10872
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Qy      10873 GCTGTGTGTGAGAGATGCGAGTCCGCTCTCTCAACCGCGGAGCGGTGGGCAACGATG 10932
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Qy      10933 TTCCGCGGCAAGATGATGATCCGCTCTTTTGTGTGATGATGATGACGGGAGTATGAGCTG 10992
Db      10976 CTGGCGGCGAAGTGTGATGTCTGTGTGTGATCTAATATGAGGCGACCGCGGCTGTGACCTG 11035
Qy      10993 TCGGGGTTGTGCTGTTCTCTCTCGGCGCGGAGATCTTGGAGTCCGCGGGGAGGAGCAAC 11052
Db      11036 GACGGGTTGTGTGTCTCTCTCTCGCGCGGAGTCTTGGAGATCCCGGAGGAGCAAC 11095
Qy      11053 TACGCGCGGCGCAATGCGGCTGTGACGCGGTGCGCTAACCAGCGGCGGCGGCTGTG 11112
Db      11096 TACGCGCGCGCAACGCTCTCTGTGACGCGGTGTGATGACGCGCGCGCGGAGGAGATG 11155
Qy      11113 CGGGGAGGTGTCTGCTGCGGTGGGAGGTGTGAGAGAGCGAGGAGTGAACGGGACCTG 11172
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Qy      11233 GCACGTGCGCTCTTGTGATGCGGCGCTGTGAGTGTGACCGGCGGCTCTGTGCGCGGAC 11292
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Qy      11293 CTG---CGTCCCGCGCGCGCTGTGCGCGCTGTGACAGACCTCTGCGCGGACCGC 11349
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Qy      11350 CGCGCGACCAACCGGACCACTAACCGGTGTGCGGACCAACGCGCGGCGGCTGTGACGCG 11409
Db      11396 CGCGTCCGAGCGCGGAGCGCGCTGTGCGGCTCGGACCGCGGAGCACTGCCCGAG 11455
Qy      11410 CGGCTGTGCGCGGACAGACAGAGACAGACACCACTCTGTGCGCTGTGCTCGCTCC 11469
Db      11456 GCGCTGTGCGCGCTGTGAGAGAGAGCGCGGAGAGATGTCTGTGAGCTCTGTGCGGAT 11515
Qy      11470 CACATGTGCAACCGTCTGTGGGACACACACCGCGACACCATCCCGCGGACCGCGCTTC 11529
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Qy      11530 CGGACCTGTGGCTTGAATCTCTCAACCGCGGTGAACTAAGCAACCGGCTCTCCGCAAC 11589

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Qy      11698 CCGGTGTGGGAGACTGTGACAAACTGAAATCCGCTCTTCGCGCTGTGACAAACCGAC 11757
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Qy      11758 AGCGACAGAAAGATCACTGTGGGCTGAAG----- 11790
Db      11816 GCGGTACGTCTCCCGAGAGACTGTGGCGGTGTCAACCGAAGGACCGACCGGCTTCG 11875
Qy      11791 -----TCATCATGTTGAGGTGAAACG 11813
Db      11876 GCGTTCGCGACCAACCGGTGTGGGACGTCAATCCCTCTATCACCCGACCTGTACAC 11935
Qy      11814 ACCCGACATCCGACAGCCGAAAGCGCTGATGACGAGAGATT----- 11858
Db      11936 CCGGATACCTCTACACCGCTCGGATGGGTCTGTGATGAGCGGAGATTTCATCCG 11995
Qy      11859 -----CACATCGGCAACAGAGCTGACA 11881
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Qy      12001 GAATATCTTAAGCGGCTCACTGCGGACCTGGAACCGCACTGCGCGCTGTGACGAGTGTG 12060
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Qy      12181 TTCGAGCGACCGGTGTGATGAACTGTGAGAGCTTATACGACCGGACCCGACCGCTCA 12240
Db      12476 TCCAGAGGCGTGTGCGGTGTGTGTGAGAGCGGAGTGTGAGAGCGGATGTGTGAC 12315
Qy      12241 GGAACAGTTTCAAGCGCGAGCGGAGGTTTCTTATGTACGCGGCGACT----- 12289
Db      12536 GAGATTTTGTGTGTGTGCGGGGTTTCCGCGGTCAACGAGATGTGTCTTCAATGTGTTG 12595
Qy      12290 TCGACCGCGCTTCTTGAAGTTGTCAACCGGTGAGGCGCTGTGCAATGTGACCGGACGAGC 12349
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Qy      12350 GCTGTGTCTGTGAACCACTTGTGGAAGGTTGTGAAACAGAGGCGGATGTGACCGGAGTCA 12409
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OY	12410	TTGCGCGAAGCCGGA	CCGGGGTT-----	12432
Db	12716	CCGATTCAGAGCGCAG	GGTGTGTTCGACGATATGGCGGAGTGTGAGCCTTGA	CGGCCG 12775
OY	12433	-----	TTGCTGGGGATCAATCCGAGGACTACACACGGATACA-----	12472
Db	12776	TTGTGTGTGGGTTCCG	TGAAGTGGAACTCTGGGCAATCCGAGGCTGTCTCGGGTGTGGGG	12835
OY	12473	-----	-----	12472
Db	12836	GGCGTTATCAAGATGT	GTTCGATCCGCAATCCGCAATGGCATGTGTGTGTCGCGACGTTTGATGTG	12895
OY	12473	-----	-----	12473
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OY	12520	GGCGCAAGCAATTGCG	TGACGCCGTTA-----	CTCTCAACATTTC 12558
Db	12956	GGCGCTGTGGCCGAG	AGCGGGTCCGGGTGCGCGCGGGGTGTCTCTCTTCGGCAATCAGC	13015
OY	12559	GGGCTCGAAGGCCCCG	TGAGATCACTATGACACCGCGGTGTTCCTCTCGTCTGCTGACCTG	12618
Db	13016	GGTACCAATGTGACAT	GTGATGTTCAGACAGGCGCCGAGCGCCAGGCGAATCCCGCGGC	13075
OY	12619	CATCTGACCTTGCCAG	CGCTCCGATCCG-GTGATGACACCATGGACGCTTCGACAGCGCGC	12677
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OY	12678	CTCCGTCATGGCCACT	CCCCCTTCTGTCTTACCCAGTTCTC-----	12716
Db	13136	GCCTGTGCGGGGCCA	GGCGCGCGCTGTCTGAGACACTTCAGGCGCCGACCGACCGCGGA	13195
OY	12717	-----	TCGCGACGCGGGGCTTGCGCGACAGCGCGCGGTGCACAGCGCTTTTCGCGGCG	12768
Db	13196	CTGCTGCATGTCCGAC	TGTGTGTGGCGACACCGCGGTCCCGCTTCGAGAGGCGGGCCGCGC	13255
OY	12769	CGCGACGCGAACC	CGGTGTGTCCAGAGGTGTGGGATGTCTGTGTGAGCGGCTTTCGAC	12828
Db	13256	GTCTGTGCGGACGAG	CCCGGACCAAGCTGATGCTCTCGGGGGCGGTGCGCGCGCACCGC	13315
OY	12829	GGCGCGCGCAACG	GTACCGGTGCTTGGCGGTGTGTCGCGCGGACCGCGCTCAACAGAGAC	12888
Db	13316	CCCGACCCCGCGCT	GTGTGTGAGAGGCGAGGCGCGCGACGCGCGGTGCTGTTC	13375
OY	12889	GGCGCAAGCAACG	CGCTGACCGGACCCCAAGCTGTTCACAACTCAAGGTCTATCCGCGAG	12948
Db	13376	ACCGGACAGGGCAG	CCAGCGGGCGGCCATCGACGAGGTGACCGGCTGTGTGACCGGCGCTG	13435
OY	12949	GCTTTGGCCCAACG	CAACCTCTCTCCCTGCGGATGTGATGTCCGTGTGAGAGGC-----	12999
Db	13436	TTTCGCGCGGCGTT	CGACGCGGTGTGTGCGCTTTTTCAGCCCGCTGTGTGACCGGCGCTG	13495
OY	13000	CACGCGACGGGGGA	CCACCTCTGGGCGAACCCGATGAGAGGCTCAAGCCCTCTCGCA-AGCCTA	13058
Db	13496	CGCGAGGTGTGTTC	CGCGGAGACGAGAGGAGAGGAGCGGCACTGTGTGACAGACCGGT	13555
OY	13059	CGGTTCAGAGACG	CGCCCCCAAGCGCGCCCTCTTGCGTTCGGAACCTCAAGTCAACATGG	13118
Db	13556	TGAGACGACGCGG	CTGTTCGCGCTGTGAGGTGCGCTGTGAGAGTTGG	13615
OY	13119	GCACTTC-----	-----	ATGGCGGCTGCGGGTGTG 13143
Db	13616	GGTGTCCGTCCGAC	CTTCGTGGCGGCGCATTCATCGGTGAGATCCGCGGCGCGACGTC	13675
OY	13144	GGCGGGGTTCATCA	AGATG-----	TGATGGCGGTGCGGATGTGTGCTG 13188
Db	13676	GC CGGGGTGTGAC	GTGTGAGAGACGCTGCGCTGTGTGTGGCGCGCGCGCGCATGTG	13735
OY	13189	CCGCGACGTTGCAT	GTGTGATGAGCGGTGCGCGCATGTGATCTGTGTGCGCGGGTCCGGT	13248
Db	13736	CAGGCGCTGCGAC	CGCGCGCGGATGTCGATCCAGGCCACGAGGACGAGATTCGG	13795

QY	13249	CAGCTGCTGACGAGAGAGGTGGCTTGCCGCCCGGGGGAGGGGGCGC-----	1329
Db	13796	GCGCACTTCAGACGACAGGTGGGATTCGCCGCTCAACGGGGCGGAGTCCGTGTGATTC	13855
QY	13295	-----TACGGCGGGCAGAGATGTC	13313
Db	13856	TCCGGTACGAGAGAGGCCGCCGAAACGATGGCCGCCACGTTCCGCCGAAACGCCGGGCGCAAG	13915
QY	13314	ATCATTCGGCGCTCAGCGGCAACA-----AC	13338
Db	13916	ACCAAGCGGCTGGGGGTGAGCATTGCTTCACTCCGCCGATGAGACGGAGATGCTGAGAC	13975
QY	13339	GCCCACTGATCTCTCAGAGAGAGACCCGCCCAACAATCCCTCAGACACACCCGCCGAC	13398
Db	13976	GCTTTCGGATGTCTGCGCCAGGGGGCTGACCTTACCGGGCCCGCGCATCCCGCTCTGCTTC	14035
QY	13399	GACGTCCCGGAGAAATCAGCGCGCGACAGAGATGCGGATAGTGGCATGA-----	13448
Db	14036	GACCTTCAACGGCGCGGCGCGCCGACGATGGGAGGTGTGACCGCGGAGTACTTGGGTCCGG	14095
QY	13449	-----	13448
Db	14096	CACGTCCGAGAGGCGCTGCGGTTGCGCGACTGCGTGCGGACGCTGCGGACGCGCGGGGCGC	14155
QY	13449	-----GGCTGCTCGCGGCAATCCAGGGGTGTGGCTGTGCTGTCTC	13499
Db	14156	ACCACTTCTTGAACTGGGCTCCGACGGCTGTCTGACCGCATGGCCAGAGCACCTTTC	14215
QY	13491	GGCCAAATGTC-----GCACCGGCGCTTGCGCGCCAGGCGCCAG	13527
Db	14216	GGTACGACATCAACGACCGCGGACTGTGTGCGATGCTGCGCGCGCCGCCGCGGAGAACTGTG	14275
QY	13528	GCCTTGCACGCCCACTTCAACGACACCCCGGCTTGACCTGCGCGACGTGCGGTAAC-	13586
Db	14276	GCGCGGCGCACCGGCGCTGCGCGCGCTTCAAGGTGCGCGGTGGACGTGACGTGGCGGCGG	14335
QY	13587	--CCTGCGCCACGCGCGCGCGCTTGTGACACAC-----	13618
Db	14336	TACCTTCGCGGACACCGGCGCGCGACGACCGACTTCCGACCTTCCAGACGCGG	14395
QY	13619	-----GGCCACCTCATGCGCGCGCGACCGGCAACCC	13650
Db	14396	TACTACTGGCGCGAGCTGCGGACCCCGGCGCGCGCTTGCAGCGCGCGCATTCGCGCGAC	14455
QY	13651	TTCTTGCAGACACTTCCAGGCACTTCGCGCGGAGCGGAAACCCACCGCGCGCTTACAC--	13707
Db	14456	CAGCAGCTGTGGGCGCGGTGTGAGAGCGCGGAGCGCGCGGAATCGCGCAATTCCTCGCGC	14515
QY	13708	-----AGCAG	13712
Db	14516	CTGGGCGAAGAGACCTCAACGCGCTGTGACTCTCTGCTGCGCGCTTCACTTGTGGCGG	14575
QY	13713	CGCCCGAGGGGGGACCGGGGACCGGGGAGCGCGAGGAAAGACCGGAT-----	13759
Db	14576	CGCGGCAACGAGGAGAAAGCACTTCCTGGAACCTTGCCTTACCGCGGTGAGTGAACGCA	14635
QY	13760	----TCATCTGCTCCGAGACGAGGCAACCAAGCCCGGATGAGCCACAGGCTTACACAC	13815
Db	14636	CTGAGCAAGCGGACCGCGCGCGGTCTCTGAGAGGACCTGTGCTGTGCTCCGACGCGC	14695
QY	13816	ACCCACCCGCTTTCGCGCGCGGCACTTCAACGACATCTGACCCCACTCGACCCCACTTC	13875
Db	14696	ACCGCGGCGGACGACGAGCCCTCTCTGACCGGCTGTGGCGGACGCGCTTCCGCTCGACGCGC	14755
QY	13876	GACCAACCCCTCTTCCCTCTCTTCACTCCAGAACCCCAACCC-----	13918
Db	14756	GCGGAGGTGTGTGCTCTTCTTGAAGCACTCTGTGCGGACCGCGCGGTGTGCGCGAA	14815
QY	13919	-----AGGACACCAACCACTTCGAGAAAGCGCGCGCACTGCTCAGAGACCGGCTAC	13971
Db	14816	CGACTGGCGGAGACCGCGCACTGAGACCGCGGACCACTCAAGTGTGTCTGCTGCGCGCTC	14875
QY	13972	GCCCAAGCCGCGCTTTCGCTTTCAGAGTGTGCGCTTCAACGCGCTCTTCAACGACGAGCTAC	14031

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Db      14876 GACGAGCGGGAGCGCGACGACGCTGACCCGCGGACCTGCGCTGACCGCTGCGG 14935
Oy      14032 CACATCACCCCCCACTACTACGCGGGGACACTCCCTGCGGAAATGACCGCGGCCACCTTC 14091
Db      14936 CTCGCTCGAGGCTCTGCGCGACACCGCGCGCCAGGCGCGCTGTGAGCCGACCGCGGCG 14995
Oy      14092 GCGGCGATCTCTACCCCTCAACGAGCGCACACCTCTCATGACCCAAAGCGC----- 14141
Db      14996 GCGGCTTCACCAACCGCGCGACCGCGGTACCCACCCCGTCCAGGCGCGCTGCGTGGGCG 15055
Oy      14142 ----- 14141
Db      15056 CTGGGCGGGGCGTCCGCTTGAGGACCCACGAGCTGTGGGCGCGCTGTGACCTGCGG 15115
Oy      14142 -----GACCTCATGGAAC 14157
Db      15116 CAGGCTTCGACGAGCGGGCGGACAGCGGCTCGCGGGATCTTGCGCTCAAGAGCGCA 15175
Oy      14158 ATGCCCCCGGACCATGACACACCTCTCAACACCGCCCGACAGATCACCGACACCTTC 14217
Db      15176 CCGGACGGGAGGAGCAGAGGTGGCGTGGGGGCAACGAGTCTCGGGCGCGGCTCGTC 15235
Oy      14218 ACCGCCACGAAAAGACTCGGCATCGCGGCATCAACACCCCACTCTCTCTCAT- 14276
Db      15236 CGGCAACCGTGAAGCGCTGCGCACGCGCGGAGTTTCAACGACCGGCACTGTCTG 15295
Oy      14277 -----CAGCGGCAAC 14286
Db      15296 ATCACTGTGGGACCGGTGGCTTGAGCGCGGAGTGGCGCGGTGGCTGGCGCGCGG 15355
Oy      14287 CCGCACCGCTTCAACATCAACATCAACCTCTGTGCAACAACAGGATCAAAACCAAAAC 14346
Db      15356 GCGGACACCTGTCTGTACGAGCGCGCGCGCGCGGACGCGCGCGCGCGCGGACCTTC 15415
Oy      14347 CTCGCCACCAACAGCCTTCACTCCCCACACCAACCCATCTTAACCACTCAAC 14406
Db      15416 CGGCGGAACTGGAAGGCTACGCGGCGGTGCTGCTGCTGCGCTGCGACGCTCGCGAC 15475
Oy      14407 CAGCACACCAAAACCTCACTCAACCAACCAAC----- 14437
Db      15476 GCGGAGCGGCTTGCGCGCGCTCTTCAACCGACCTGCGCGGAGAACTGCGCTGACCGGTTC 15535
Oy      14438 -CCCAACCGCCCTCATGACCGGCAACACCCGACCGACCACTCTGACCCCGCACTAC 14496
Db      15536 GTGACACCGGAGGCTGCGGCACTACGCGCGCTGAGACACCTGAGACCGGCGGAGTTTC 15595
Oy      14497 TGGACCCAAACAAGCGCGCAACGCTGCACTAGGCAACCAACCAACCTTCGACCA 14556
Db      15596 GCGGCGCTTCAACCGCGCGCAAGCTCGCGGCGCGCGCACCTGACGCGCTGCTCGCGAC 15655
Oy      14557 CAGCGGCTTCAACCTTACATGCACTTGGAGCCCGACCAACCTTCAACACCTTCACCAAC 14616
Db      15656 CGGAACTGGAATTTGTCTCTTCTGCTCTTCTGCTCATGCGGCTGTGGGCGAGTGGCAAC 15715
Oy      14617 GACAACTTCCCAACACCCCGACCAACCTTCAACCTTCAACCCCGACCAACCGC 14676
Db      15716 CAGAGCGCTACGCGCGCGGCAACCGCTTACCTGACGCGCTGCGCTGACCGCGCGC 15775
Oy      14677 CAATCCACCTTCTCAACCACTGCGC----- 14703
Db      15776 GCGGCGCTTGGCGGACCTTCCGCTGCGCTGGGCGCGTGGGCGGAGCGGACCTGCGCGC 15835
Oy      14704 -----AAACACACACCACTTGGACACCCCGACCACTTACCCACCAAC- 14746
Db      15836 GACGATGCGCTTTCGAGACCTTGGCGCGGACGAGGCTTGGCTGTGACCGCGCGCG 15895
Oy      14747 -----ACAACCAACCCAC 14760
Db      15896 GCGATGACGAGCTGCGCGCGCGCTGCTGCGGACGAGACGTACACCTGACCTTCCGCGAC 15955
Oy      14761 ACCCAACCCCACTTGAACCTTCCCACTTACCTTTCACCAACCAACCACTTACCTGCTCA 14820

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Db      15956 GTGACTGGCAGCGCTACGACACCGCTTTTCACTTCGCGCGCGCGGACCGCGCTGATCGC 16015
Oy      14821 CCACCGGCAAGCGGAGGACCGGTCACCGAGCGGAAGGCGGTGAGACAGCAACGACCCCA 14880
Db      16016 GAGCTGCGGAGGTCCGCGCTTGCAGCGGACGACCGACCGGACGAGGACCGCACCGGCG 16075
Oy      14881 TCACCCCGCTGCGATGATCTCTGCTGGCAAGTCTCCGACGAGCGGACGAGAGAGTTC 14940
Db      16076 GCTTCGAGGTGTACACCGCGGTCCGCGCGCTGCGCGGACCGGACCACTGCGCTGCTG 16135
Oy      14941 TTGCGCTGTGGCGGACCAATGCGCGCTGTGCTGCGGACATGCACTCCGAGTATC 15000
Db      16136 ACCGACTGTGTCCGACCGAGTCCGCGCACCTCTCGGCGCACGCTCCGCGACCGCTG 16195
Oy      15001 GTTCCGAACAGGCGCTTCAAGAGGTGGGTTTGAATCTCTCGCGGCAATTGAGTTGT 15060
Db      16196 CCGAGGCGCGGCTTTCGCGAGTCCGCTTTCGACTGTGACCGCGGCTGAGCTTCGCG 16255
Oy      15061 AATCGACTGTGTGACGATGACCTGCGGCTTCCGCGCACGCTGATCTTGGATTACCC 15120
Db      16256 AAGCGCTGGGCGCGGACCGGCGGTCTCTGCGCGACACCATGATCTTGGACTACCG 16315
Oy      15121 ACTCGATGCGCTTGTTCGACTTCTCCGCGCGGAGATGTCGAGCGGACACAGGACG 15180
Db      16316 ACACGCTGGAATCTCGCCAGATACCTGCGGCGGAGAGATCTCGGCGGCTGTG- -AA 16372
Oy      15181 ACGACTGTGTGCGGCTTACCTGCGGTCCTCCCGCGGACGAGCGGATGCGCATGTCGCGCATG 15240
Db      16373 GTGCGGCGCGGTGCGCACCGGCGGCGGCGGACGAGCGGATCGCATATCGGACATG 16432
Oy      15241 GCTGTGCGTACCCCGGATGATGACGAGCGGTCGATGATCTCTGGCAGGTGTCAGTGT 15300
Db      16433 GCTGTGCGCTTCTCCGCGGCGGTGACGTCCTCCCGGACAGCTGTGGAGTCTGTGCTTC 16492
Oy      15301 GCGCATGACGATGCGGCGGATTCGCGAGAACGCTGGGTGGAGCTTGACACGCTGTAC 15360
Db      16493 GGCACCGACGAGTACGAGGATTCGCGTCAACCGCGGCTGGACAGCGGCACTCTTC 16552
Oy      15361 AACCGGACCGGACCAACAGGAAACAGCTTACACCGGAGCGGCGGATTTCTTTACAC 15420
Db      16553 GACCGGACCGGACCGGCGGCGGACCTTACCTTCAACCGGCGGCTTCTTCACGAG 16612
Oy      15421 GCAGGCAATTTGATTCGCACTTCTGCTGATCACTGCGGCTGAGGACTGAGCATGAGC 15480
Db      16613 GCGGACGAGTTCGACCCACCTTCTTGGGATCTGCGCGCGGAGCGCTGTATGAGAC 16672
Oy      15481 CCGGACGAGCGGCTGTGTGAAACAGCGTGGAGAGCATGAAACAGCTGTCAAC 15540
Db      16673 CCGGACGAGCGGCTCTGTGTGAGACCACTGGGAGTCTTTCGAGCGCGGAGTTCGCG 16732
Oy      15541 CCGGACGAGCTCTGTGTGACCAACCGGCGCTTTCGCGGCGTGAACCTTACGAGACTAC 15600
Db      16733 CCGGAAACCTTCGATCCACCTTACCGGACCTTGTGCGCTCCAGCTTACGAGAGTAC 16792
Oy      15601 GCGCGCGCTTTCACAGCTCCGCGAGGTTTCAGAGGAGTATCTCGGCGACGGAAGCGCA 15660
Db      16793 GCGCTGGGCG-----GCGGCGAGCGGACCGAGGCGCACATGTATACCGGACGACG 16843
Oy      15661 GCGAGTATGCGCTGGGCTGTGTGCTGCTGCTTCCGCGCTGGAAGGTCCGCGCTTCA 15720
Db      16844 CCGAGTGTGCTTCCGCGCGACTGTGTACGCTTTCGGTGGAAGGCGCGGCGGTACG 16903
Oy      15721 GTGACACTGCTGTCTCTGTGCTGCTGTGTGCTGTGCACTTGGCTGTGAGGCGTGGG 15780
Db      16904 GTGACACCGCTGTGCTGTCTGCTGTGTGCTGTGACCTGCGCTGCACTGCTGCGC 16963
Oy      15781 TCGCGAGTGTTCATGAGCGCTGCGGAGTGGAGTCAACGAGTATCAACCCCGCGGCG 15840
Db      16964 AACGCGAGAGCAACTGTGCGGCTGCGGCGGCGCGCACGATGATGAGAGCGCCACCG 17023
Oy      15841 TTGCTGAGTTTTCGCGGAGCGGCGGCTGTGCGCTGGAACGCGGCGGTTCCTG 15900
Db      17024 TTGCTGCGTTCAACCGGCGGCGGCTGCGCAAGAGCGGCGCTGCAAGGCTTCTCC 17083

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OY 15901 GCAGCGGCTGACGGGACCGGCTGAGGAGTGTGGAATGCTGTGTGAGGCGCTG 15960  
DB 17084 GACGACGCGGACCGGATGACGCTCGCGGAGGCGTGTGCTGTCTGTGTGAGGCGCTC 17143  
OY 15961 TGGGACGCGGCGGCTGTGTGTGACCGAATCTCTGCGGTGTGTGTGTGTGTGTGTGT 16020  
DB 17144 TCCGACGCGGACCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17203  
OY 16021 CAGACGCGGTGAGGACCGGCTGTGAGGCGGCGGACCGGCGGCTGTGTGTGTGTGTGT 16080  
DB 17204 CAGGACGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17263  
OY 16081 CGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16140  
DB 17264 CGCGAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17323  
OY 16141 GCGACCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16200  
DB 17324 GCGACCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17383  
OY 16201 CAGACCGGCGGCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16260  
DB 17384 CGCGACCGGCGGCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17443  
OY 16261 GCGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16320  
DB 17444 ACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17503  
OY 16321 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16380  
DB 17504 GAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17563  
OY 16381 GCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16440  
DB 17564 AGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17620  
OY 16441 GCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16500  
DB 17621 GCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17680  
OY 16501 CCGGCGGCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16560  
DB 17681 CCGGCGGCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17740  
OY 16561 GACGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16620  
DB 17741 GCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17777  
OY 16621 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16680  
DB 17778 -----CGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17797  
OY 16681 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16740  
DB 17798 GAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17854  
OY 16741 GCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16800  
DB 17855 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17914  
OY 16801 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16860  
DB 17915 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17974  
OY 16861 CACGCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16920  
DB 17975 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18013  
OY 16921 AAGACCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16980  
DB 18014 CGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18073

OY 16981 TACCAACCAACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17040  
DB 18074 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18133  
OY 17041 CACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17100  
DB 18134 TTTACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18181  
OY 17101 ACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17160  
DB 18182 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18240  
OY 17161 GCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17220  
DB 18241 GCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18280  
OY 17221 TACGCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17280  
DB 18281 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18340  
OY 17281 ACCGACCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17334  
DB 18341 CCGGACCGGCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18400  
OY 17335 CCGGACCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17394  
DB 18401 CCGGAGGAGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18460  
OY 17395 CAGGAAACGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17454  
DB 18461 TTTGAGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18520  
OY 17455 ACCGCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17514  
DB 18521 GAGCGCGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18580  
OY 17515 ACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17574  
DB 18581 CCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18640  
OY 17575 CACGAGC-----ACACCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 17625  
DB 18641 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18700  
OY 17626 ACCGCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17685  
DB 18701 ACCGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18760  
OY 17686 AACGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17745  
DB 18761 GAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18820  
OY 17746 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17805  
DB 18821 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18880  
OY 17806 CCC---ACGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17862  
DB 18881 GCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18940  
OY 17863 ACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17922  
DB 18941 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 19000  
OY 17923 CAACCGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17982  
DB 19001 GAGGAGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 19060  
OY 17983 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18042  
DB 19061 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 19104  
OY 18043 GCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18102



Db	19105	-----GAGCAGCGCGGCTTTGGAACCGCGGTTCGAGCGGT	19141
Oy	18103	GACCTGGAAACGGTCGGGACCAAGCTGCAGTGCCTCCGCTCGACCGGCTGGACAGGTC	18162
Db	19142	GAGCTTCGCGGCTGAGACGGCGGCGCTCGG---ACGAGAGGAGCTTCGTCGCGCGCTGG	19198
Oy	18163	GTCGCCGCACTCTTCGCTTGGACCGGCACCAACGACCGACCGGCACTCAACTGG	18222
Db	19199	CTGCCCGCCCTGACTCTCTGGCGCGCGGCGCGGACCGCTCAACCTGGACGCTGG	19258
Oy	18223	ACCTACGAGAACTTGGAAACCTCTCAACCTCCACCAACCAACCCACGAAAC	18282
Db	19259	CGCTACCGCGCTGCGCTTGGAAACCTCTGGGGAC-----CTTGGCGACCTGTC	19309
Oy	18283	TGGCTCATTCGCAATCCCGGAAACCCAGAACCAACCCCACTCAACCAATCTTCAC	18342
Db	19310	CTGACCGGCACTTGGCTGTGTGTACCGCGAGGGATGACGACACGATGTGGAGGG	19359
Oy	18343	AACTTCACCAACGAGCATCAACCCCATCTCCCTCACTCTCAACCAACCAAC	18402
Db	19370	GCGTTGAGAGACTTACGGCGCGAGGTGCGCGGCTGGTCTGTGAGCA-----	19416
Oy	18403	CCCCAACAACCTCCACCAACCTCCGACCAAGCCCAACCAACCAACCGGATCAC	18452
Db	19417	--GGAGTGGCTGACCGCGCGCTCTGCGGGAACGGCTGGCCGCGCGAGGACGTGACC	19474
Oy	18463	GGCTGTGCTCCCTCCTCGCGCTTGAAGAAACAACCCCAACCCCAACCCCAACACC	18522
Db	19475	GGCATCTGCTCTCGCTCTCGCGCGCGGACGAGCGAGTACGGGCACTTCTTG	19534
Oy	18523	AC---CGGCAACCTCTCTCAACTCAACCTCAACCCCAACCCCAACCCCAACCA	18579
Db	19535	GTCGTCGGGCAACCGGCTTGACCGGTGACCTGATCAAGGCTCTGGGACGCGGAATGAC	19594
Oy	18580	ACCCCTCTGTGTACGCAACCAACGCCAACCAACCAACCCCAACGACCCCTCACA	18639
Db	19595	GCTTCGCTATGGGCGATTGACCGCGGCGCGGTCTCAACCGGCGGCGCAAGCTGAC	19654
Oy	18640	CACCCCAACCCGACCAACCTGGGAGCTGCGCGGACCAACCTCTGGAACCCCAAC	18699
Db	19655	GCGCCCTCGAGGACAGGTACCGGAGTATGGGTGAGCGCGGCTGAGACACCGAG	19714
Oy	18700	CACACCGCGGAATCATGACTCCCAACCAACCCCAACCCCAACCTTCACCACTTC	18759
Db	19715	CGCTGGGGCGGCAACCTCGACTGCGCGGCTTGAGGCTCGGGGCGGCGGCGGCTC	19774
Oy	18760	ACCCAAACCTCACCCAAACCC---ACCAACAAACCAACTGCGCATTCGCAACACGGC	18816
Db	19775	GCGCGCGTGTGTTCGCGGCGCTTCGAGCAAGACAGCTGGCTCATTCGCGCTTCGGG	19834
Oy	18817	ACCCACACCGCGCGCTTCAACCCCAACCAACCTCAACCCCAACCAACCAACCCCC	18876
Db	19835	GTTTTCACCGCGCGCATCTGTGCGGCGGAGGCAACCGCGGGGCGCGCGGACCTGG	19894
Oy	18877	ACCCCAACGGAACCACTCTATCAACGCGGGAACCGGCGCTCGGCAACCACTCAC	18936
Db	19895	ACGGCGGGCGGCAACCACTGTGTACCGGGGCTTCGGGCACTTCGCGGCACTTCGCG	19954
Oy	18937	CACCACTCACCAACCAACCAACCAACCACTCTCTCTCAACGCGGAACCGGCGCC	18996
Db	19955	CGCTGGCTGG---CCCAACCGGCGCGAGCACTGGTCTGTATGACGCGGCGGCAAG	20011
Oy	18997	CACACCCCAACGACCAACCTTCAACCAACCACTCAACCAAAAGGATTCACCTCAC	19056
Db	20012	GCGCGCGCGGCGCGCGGCAACTGTGTGCGGAATGGCGAGTGGGACCGAGCGACC	20071
Oy	19057	ATCAACACTTGGACACGAGAACCGAGCACTCAACCACTCTCT---CAACACTATC	19113
Db	20072	GTCGCGCGCTGCAATCAACGACGGAACGGGTGCGCGGCTGTGGCCGACCTCAAG	20131
Oy	19114	CCCCCAACACCCCTCACACCGGTATCACACCGCAGGACTCTTGAAGACGCGCAC	19173

Db	20132	GC	CGACGGGGGACACCGGTCCGACACCGGTGTCACACCGCGGCCACCACTCGAGCTGCACACC	20191
Qy	19174	CT	CAACAACCTCAACCCCCACCACTCAACCAACGTCTCCGCGCCAAAGACCCGACAGCGCC	19233
Db	20192	CT	GGAAGCCGACACACCTTCGGGAGCTTCGACCGGGGTCTGACGCGCAAGGTCAACCGGCGCC	20251
Qy	19234	CA	CTCTCCCAACCACTCAACCCCAACACCCCCCTCAAGGCTTGGTCTTACTCTCC	19293
Db	20352	CAG	GTCTCTCCCGAACCTGCTCGACGACGAAAGACTGGAAGACTTCTCTCTGACTCTCC	20311
Qy	19294	GC	CGCGCCGCACTTTCCGCGGCAACCGGGCAAGGCCATTAAGCGCGACGCAAGCGCTACCTC	19355
Db	20312	AC	CGCCCGCAATGTCGGGACAGCGGGCCACGCGCGCTTAGTGCCTGGCAACGCTACTCTC	20371
Qy	19354	GAC	CCCTCGCCCAACCAACCGCCACACCCAACCACTCCCGGCCACGACTCGCTGGGCG	19413
Db	20372	GC	CGCGCTCGCGGAGCAACCGCGGGGCCAACGACTGTCGCGCTGTGCTGTCTGGGGC	20433
Qy	19414	AC	CTGGCAAGAAACGGACTGGCGACTGGTCAAGTACGGAACATTCCGCGCGCGGG	19473
Db	20432	AT	CTGGGCCCAACGACTCAAACTGGGCGGGGTGATCCCAATGATCCGCGGCGACGCGC	20491
Qy	19474	AT	GTCCCAATGCGCGCGCGGAGTTGGGGTACACGCTGTGAAGCGCGGATTCGCAAGCGGG	19533
Db	20492	CT	GGAATTCATGACCCCGGACTGGGCTCTGAAGCGGCTCGACGCGGCGCTGACGCAAC	20551
Qy	19534	CG	CCCGAGTCTCTCTCGTCCGCGCAATTCGACTGGAAATAATGGGACCGGTTCTCTC----	19589
Db	20552	GAGA	ACGTGCTCCGCGGTCCGCGCACTGGACTGGGAACTTACACCCCGTCTACACTCC	20611
Qy	19590	--	CAGCAATGTCGTCCGCTTGTCTCGAAGACTTCCCAAGCAACAGGAACTGAGAGGGG	19647
Db	20612	GG	CCGACCCACCCCGCTCTTCGACGAGGTGCAGAGATCCGCGCGCTCACCGGCGCGC	20673
Qy	19648	CG	CACTACCGTACGACGACGAGACGACCAAACTCCGGCACTCTCACTAGGTCCGTTA	19707
Db	20672	GAG	CAGAGCGCCCGGAGACCGTGCAGAGGCGAATTTGCGCGCGCTGCGCGCCCTGTCTC	20731
Qy	19708	CG	TTCCAGAGAGAAAGAGAGCTGTCAAGCTGTCTCCGATCACTCCGCGGAGTCTC	19767
Db	20732	GAG	CCCAAGACGACGACCCCTGTGTGAGACCGTTCGACGACGAGGCGGCTTCGTCTCTC	20791
Qy	19768	GG	GGCGCAGCACTTCCGAGGCAATCCGCGCGGTCCGCTTTCAGGAGTTAGAGTTGCAC	19827
Db	20792	GG	GTGTCTTCGCGCGGAGCACTCACGACACAGCGGGGCTTCGCGAGCTTCGAGTTCGAC	20851
Qy	19828	TC	CGTTTCGGCGGTGAGACTTCCCAACCACTTGCAGCACAGACGAGCTGTCTGCGC	19887
Db	20852	TC	GTGACCGCGCTGCGGCTGCGCAACCGGCTGTGCTCTCGTCAACCGGCTGAGCTGCGCC	20911
Qy	19888	AC	CACTCTCGCTTCGATTAACCCGACGCCCAACCACTGGGCCAATTTGTGCTCCGAG	19947
Db	20912	TC	GACATGAGCTTCGACTACCCCAACCGGCGCGCTTCGCGCTTATTCGACGCGGAG	20971
Qy	19948	AT	-----CGCGAGTTTCACGCCCAACTCAACTCCGCTTCGCGCAACCCGCGGCGAG	20001
Db	20972	CT	GGCGGGCGCGCGGTCCGCGCGCGCGCGCGCGCGCGCGCTCCGACCGGCGCCCGAC	21031
Qy	20002	CT	CGATGAGCCGATCCGCACTGTGTGAGTGCCTGTCTCCCGCGGAGTACCTCG	20061
Db	21032	GCC	ACACCCGATCCGAGTGTCTGGCACTGACGTGCGCTACCCCGCGGGGTCCGCTCC	21091
Qy	20062	GG	CGGACGACTTCTGGGATCTGATCTCTCTCGACGACGAGCGGATTCGCCACG	20121
Db	21092	GC	CGAGGACTGTGGCGGATTCGCTTGGAGAGTTCGAGCGGATTCGCGCTTCCCGCC	21151
Qy	20122	GAC	CGCGGCTGGGACCTGACAGCTCTACGACCCCGACCCGACCAACCCCGGACCTGC	20181
Db	21152	GAC	CGCGGCTGGGACCGCGGAGGCGCTCTACGACCCGAGACCCGACCGGCGCGGACAC	21211
Qy	20182	TAC	ACCGGAAACGGCGGATTCCTCTACGACGACGACCACTTCGACGCGGATTCCTTCGCG	20241
Db	21212	TAC	TCCCTTCACGAGCGGATTCCTGCGCGACGTCGCGGATTCGACCCCGGCTTCTTCGCG	21271

20242 ATCAGCCCCCGAAGCCCTCCGCAATGAGACCCCAAGACGATCTCTCTCGAAACCGCC 20301  
21272 ATCTGCGCGCGAGAGCGCTGTGATGAGACCGGACAGCGGCTCTGTGTGAGACCGCC 21331  
20302 TGGGAACCATGAAACAGCGCGCATCAACCCCAACCTTCCACGAGCAACCCCAACGGA 20361  
21332 TGGGAGGGTTCGACAGCGCCGCAATCAACCGGTTCGACAGCGGCGGACCGGACCGGC 21391  
20362 GTCTTACCGGACCAAGCAAGAGACCAAGGAGCAACATCTGTCAGGCCCCGAGCGGT 20421  
21392 ACCTTGTGAGCGCCAGCTACAGAGACTAGCTTCGAGGTGCTCCCAACAGCGAG--GAC 21448  
20422 ACCGAGGATTCGTCTGACCGGAGCAGCAACAGATCTGCTCCGAGCGAATCTCTAC 20481  
21449 TCCGAAGGCAATGATACCGGCAACGCTCTCAATGTGTCTGTCCGGCGGGTGTCTAC 21508  
20482 ATCTCTGGGTGGAAGGCGCTGCGGTCACTCTGACACAGCGTGTCTCTCTGCTGCTC 20541  
21509 CTCTTGGCTTCGAGGGCCCGCGCTCAAGCTGACACCGCTCTCTCTCTCTGCTC 21568  
20542 GCCCTGACCTGCGCTGCAAGTCCCTCAGGTCCGAGTCCGATGACATGAGCGCTTGGCGGC 20601  
21569 GCGATGACCTTGGCTTGGCTGAGTCCCTGCGCAACGAGGAGAGCTCGCTGAGCTTGGCGGC 21628  
20602 GAGGCGACGCTATGACCAACCCGATCACTTCAACGAAATTCGCGCAACGCGAGCTC 20661  
21629 GAGGTCAACATATGTCACACCCGATGTGTTGTTGTTGCTTCAAGCGGAGCGCCCTC 21668  
20662 GCGCCGACGCGCGTTCGAAAGCGCTTTCGCGCGCGCTGACGAGTACCGAGCTGGGTAG 20721  
21689 GCGGAGAGCGCGCTGCAAGGCGCTGACGCGCGCGCAAGGAGTACCTCTCCCGAG 21748  
20722 GGTGTGGGATGCTGTGTGAGAGCGCTCTCCAGCGCGCGCGCAAGGTCACCGTTC 20781  
21749 GAGCTGCGCTGTGTGTCTGTGTGAGCGCTGTGCGACCGCGCGCAAGGAGACCAAGTGT 21808  
20782 CTGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 20841  
21809 CTGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21868  
20842 CCGCAACGCGCGCTTCCAGAGAGCGGTCACTCGGCGCGCTGTGCGCAACGCGAGCTGAC 20901  
21869 CCGCAACGCGCGCTTCCAGAGAGCGGTCACTCGGCGCGCTGTGCGCAACGCGAGTGTG 21928  
20902 CCGCGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 20961  
21929 CCGCGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21988  
20962 GAGGCGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21021  
21989 GAGGCGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22048  
21022 CTGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21081  
22049 CTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22108  
21082 ATCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21141  
22109 ATCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22168  
21142 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21201  
22169 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22228  
21202 TGGCGCGCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21261  
22229 TGGCGCGCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22285  
21262 ACCAAGCGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21321  
22286 ACCAAGCGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22328

21322 GCGAGAGATGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21381  
22329 --CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22386  
21382 TGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21441  
22387 CGGCG-----AGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22429  
21442 CACCTACCGACCAACCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21501  
22430 TTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22489  
21502 GCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21561  
22490 GCGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22549  
21562 GCACTTCAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21621  
22550 GCGCTGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22609  
21622 GCGGAGACCGGAGACCGGAGAGCGCGCAAGAACCGGATTCATCTGTGTGTGTGTGTGTGT 21681  
22610 CGC-----GCGCGAGCGCGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22645  
21682 ACCCAACCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21741  
22646 AGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22705  
21742 CTCAACGACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21801  
22706 CTGACGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22765  
21802 ACCCAAAACGACCAACGACCAAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21861  
22766 TT-----GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22813  
21862 TACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21921  
22814 TAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22873  
21922 TACCAATACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21981  
22874 GCGC---TGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22930  
21982 CTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22041  
22931 GTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22990  
22042 ATGCAACCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22098  
22991 ATGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23050  
22099 ACCCAACCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22158  
23051 CTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23110  
22159 TCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22218  
23111 TCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22370  
22219 CAAGGATCAAAACCAAAACCTTCCACCAACCAACCGCTTCCACTCTCCCAACCAAC 22278  
23171 GAGGAGGCGCGAGCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22330  
22279 CCGATCTTCAACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22338  
23231 GCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22390  
22239 CC-----CGCATCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22386  
23291 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 22350  
22387 TACTGACCAACCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22443

Db	23351	TACTGGGTGGGACAGTCCCGCGCGGTCCGTTCCGCGACGGATTCAGCTGGCTCGCC	23410
Oy	22444	CACCAACGCGCGTACCACTTACATGAACTGGAACCGGACAAACCTTCAACAACCTTC	22503
Db	23411	ACCACGAGGCGCAGTCTCAACCTTCTGGAGCTCGGCGCGGACGGCTGTCTAGCGCAGT	23470
Oy	22504	ACCACCAACAACCTTCCCAACACCCCAACAACCTTCAACCTTCAACCCCAAC	22563
Db	23471	GCCGGGGAGACCTTCAACGACCCGTCCCGACGGCACTGTGCGGACCTTGGCGCGGAC	23530
Oy	22564	CACCCCAAAACCCACCTCTCAACCACTTGGCAAAACAACAACAACCTTGGACCCCAAC	22623
Db	23511	CGGCCGAGGAACTTGCCCTGTGTACACGCGGTGCGCGGCGCCACCGACGACGCGCGCC	23590
Oy	22624	CATTACACCCACCAACAACAACCCACACCAACCCACCTTCGACCTTCCCACTTAC	22683
Db	23591	GTGCACGTGAGACGGGTACTTTGCGGACACAGGGCGCGCGCGACACAGCTGTGCACCTAC	23650
Oy	22684	CCCTTCCAAACAACAACACTACTGTGTGAATTAACCAAGCGCCAAACAGCCCGGTCA	22743
Db	23651	GCGTTTCAACACGAGCGGTACTGTGGCCGACACACACGCGCGCCACGAGC-----	23698
Oy	22744	AGGGGTTCGCGCGCTGGCTCCAGAACCGCGGAGTTCGGAATTTTGGAGCGCGGTGAAC	22803
Db	23699	-----GCCCAACAGCCCGGATTCGCTTCCGACCGCAGTTCGTGGCGCGCGTCCGAG	23749
Oy	22804	GAGGAAGACCTCCAGACCTTCGCGGAAACCTTGACATCGACGCTCTGTCTGGAACAG	22863
Db	23750	CGGAGCAAGCTGCGCGCCCTTGGCGGCTCTCTTGAACCTTGAACAACGACCTTCAACGCG	23809
Oy	22864	GTGTGCGCGGACCTCTCGCGCTGGCACCGCACCAACAACAACGACCGGACATCAACCC	22923
Db	23810	ATGTGCCCCGGGCTCAACGACTGGCGCGCGCGCGGAGGACACCGAATGAGCTTCC	23869
Oy	22924	TGGAACCTTACAGAGAAACCTTGAAAACCTTCAACCTTCCCAACCAACCAACCCCAAC	22993
Db	23870	TGGGCTTACCGCGTCACTTGAAGCCGCGGAGGCGGACACGCAACCGCGCGCTTCAAC	23929
Oy	22994	ACCTGGCTCATTCGCTATCCCGGAAACCCACACCAACCAACCCCAATCAACAATCTTC	23043
Db	23930	GCGCGCTGGCTGTGTCTCTGTCCTCGGACGACCAACGAACTGTGAGACGACGGACGCG	23989
Oy	23044	ACCAACCTTCAACAACAACGAGATCAACCCCATCCCTTCACTGTCAACAACAACAACCC	23103
Db	23990	GCTTGGGAGCGGACGCTGAGAACCGGCTTGGGACCAACAACCGTCCGGGTGAGCGTCAAC	24049
Oy	23104	AAACCCCAACACTTCAACAACAACCTTCAACAACCCGACCAACGCAACGCAAAACAACCC	23163
Db	24050	ACCAACGACGCGCGCGGCTTGGCCGCGGATCAACGAAACGCGCGGCA-----C	24100
Oy	23164	ACCGGACCCATCAACCGGCGCTGTCTCTCTCTCTGCGCTTGAAGAAACACCCACCCCAAC	23223
Db	24101	CAGGCGCCGTTCACAGGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	24157
Oy	23224	CACCCCAACAACAACAACGAGAACCTTCAACCTTCAACCTTCCCAAAACCAACCAACCA	23283
Db	24158	CACCCCGGTGCGCGCGCGGCTTCACTTCAACAACAACGCGCTTCAAGGCTTCTGAGCAG	24217
Oy	23284	ACCCACCAACAACCCCGCTTGTGTAGCAACAACAACGCAACAACAACAACAACAACAACA	23343
Db	24218	GCGGCAATCGACGCGCGGTGTGGAAGTCAACCGGCGGCGCGTGGCGGTGCGCGCGCG	24277
Oy	23344	GACCCCTTCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA	23403
Db	24278	GAAACAAGTCAACGCGCGCGGCAACGCGCGGTCTTGGGCGCTTGGGCGCGCGCTGCGCTG	24337
Oy	23404	GAAACAACCAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA	23463
Db	24338	GAACTGCGGCGCGGCTTGGGCGGACCTTGAACCTTGGCGGCAACCTTGAACGCGCGGCT	24397
Oy	23464	CTTCAACAACCTTCAACCAACCTTCAACCAACCCACACCAACCAACCAACCTTGGCTCGC	23523

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OY 24601 AGCAAGAACTGCGCAAGAAACCGGACTGCACTCCCGGCTCTGTTCTTCACTAT 24660  
 DB 25499 CGGAAGCCCTCAACCGCCGCAACCGGCTGAGCTTCCCGCACTTGGTCTACGACTG 25558  
 OY 24661 CCCACCCGCAAGAAATGCTGCTCCATCTGCGCAACAACCTGTGCACTTAAGCAAGAA 24720  
 DB 25559 CCCACCCCGGCAAGAAATGCTGCTCCATCTGCGCAACAACCTGTGCACTTGGCCACC 25618  
 OY 24721 GAGGAGCGGCGC-----ACTGTGAATGCTCTCCCGAAG-----TGCGCCAT 24762  
 DB 25619 GACACCGCGGCAACCGTCCGCAAGCAAGCGCTCCCGCAAGCTCTCAAGCTTCTGCAAG 25678  
 OY 24763 CGGCGTACCGTGAAGAGCAACCGATCGCATCATCGATGATGATGCTGCTCCCGG 24822  
 DB 25679 GCGGGAATCCCTTTCGACCAACCGATCGCATCATCGATGATGATGCTGCTCCCGG 25738  
 OY 24823 GCGGTAAGTTCGCGCAACCTGTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 24882  
 DB 25739 GCGGTAAGTTCGCGCAACCTGTGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25798  
 OY 24883 GCTTTCGCGCAACCGTCCGCGCTGGAACCTGCAAGCTCTAAGACCCCGCAACCCGCAAC 24942  
 DB 25799 CGCTTCCCGCAAGCAACCGGCTGGAACCTGCGCGCTGCGCG----- 25841  
 OY 24943 CCCGCACTGCTGCAACCGCAACCGGATTCCTCTAAGCGCAAGCGCACTTTCGACG 25002  
 DB 25842 -CCGCGCTTCCGCAACCGTGAAGGCGGCTTCTGACCGGCTGCGCACTTTCGACG 25900  
 OY 25003 GAATTCCTGCGATCAAGCCCGCGAAGCTTTCGCGCAAGCGCACTTTCGACG 25062  
 DB 25901 CGGTTCTTTCGCGATCAAGCCCGCGAAGCTTTCGCGCAAGCGCACTTTCGACG 25960  
 OY 25063 CTGGAACCGCTGGAACCAACCGCAACCGGATCAACCCCGCAACCCCGCAACCG 25122  
 DB 25961 CTGGAACCGCTGGAACCAACCGGATCAACCCCGCAACCCCGCAACCG 26020  
 OY 25123 ACCCGCACTGCTGCAACCGCAACCGGATTCCTCTAAGCGCAAGCGCACTTTCGACG 25182  
 DB 26021 TCCACCAACCGGCTTTCGCGCAACCGGATTCCTCTAAGCGCAAGCGCACTTTCGACG 26075  
 OY 25183 AGCGGTATGTAAGCAACCTGCAAGCGGCTTTCGCGCAAGCGCACTTTCGACG 25242  
 DB 26076 -GCGGTATGTAAGCAACCTGCAAGCGGCTTTCGCGCAAGCGCACTTTCGACG 26134  
 OY 25243 TCCGCGCGGCTGCAACCGGATTCCTCTAAGCGCAAGCGCACTTTCGACG 25302  
 DB 26135 TCCGCGCGGCTGCAACCGGATTCCTCTAAGCGCAAGCGCACTTTCGACG 26194  
 OY 25303 TGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25362  
 DB 26195 TGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26254  
 OY 25363 TCGATGCGCTTTCGCGGCGGCTGCAAGCGGCTTTCGCGCAAGCGCACTTTCGACG 25422  
 DB 26255 GACCTGATGCGGCTTTCGCGGCGGCTGCAAGCGGCTTTCGCGCAAGCGCACTTTCGACG 26314  
 OY 25423 TCGATGCGGCTTTCGCGGCGGCTGCAAGCGGCTTTCGCGCAAGCGCACTTTCGACG 25482  
 DB 26315 TCGATGCGGCTTTCGCGGCGGCTGCAAGCGGCTTTCGCGCAAGCGCACTTTCGACG 26374  
 OY 25483 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25542  
 DB 26375 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26434  
 OY 25543 CGCAACCGTGAACCGGCTTTCGCGGCGGCTTTCGCGCAAGCGCACTTTCGACG 25602  
 DB 26435 CGCAACCGTGAACCGGCTTTCGCGGCGGCTTTCGCGCAAGCGCACTTTCGACG 26494  
 OY 25603 AGCAACCGTGAACCGGCTTTCGCGGCGGCTTTCGCGCAAGCGCACTTTCGACG 25662  
 DB 26495 TCCAAACCGTGAACCGGCTTTCGCGGCGGCTTTCGCGCAAGCGCACTTTCGACG 26554

OY 25663 GCCAATGCGGCACTGACCCCGGCGGCTGATGCAAGCGGCTGAGGCGCAAGCGCAAC 25722  
 DB 26555 GCGCAACCGGCGGCTGCGGCGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAGCGCAAC 26614  
 OY 25723 ACTTGGGCGGCAACCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAGCGCAAC 25782  
 DB 26615 ACCCTGCGGCAACCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAGCGCAAC 26674  
 OY 25783 CACCAACCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAGCGCAAC 25842  
 DB 26675 GCGCAACCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAGCGCAAC 26734  
 OY 25843 GCGGCGGCTGAGGCGGCTGATGCAAGCGGCTGAGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 25902  
 DB 26735 GCGGCGGCTGAGGCGGCTGATGCAAGCGGCTGAGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26794  
 OY 25903 ACCCTGCAACGTAAGCAACCGGCTGAGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 25962  
 DB 26795 ACCCTGCAACGTAAGCAACCGGCTGAGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26854  
 OY 25963 CTGACCAACCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26022  
 DB 26855 CTGACCAACCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26082  
 OY 26023 TCAATTCGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26082  
 DB 26909 TCCGCTTTCGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26959  
 OY 26083 CAGGACCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26142  
 DB 26960 CAGGACCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27019  
 OY 26143 CCGTTCGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26202  
 DB 27020 GTCGCTTTCGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27079  
 OY 26203 TCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26262  
 DB 27080 TCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27139  
 OY 26263 GCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26322  
 DB 27140 GCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27199  
 OY 26323 CTGCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26382  
 DB 27200 CTGCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27225  
 OY 26383 CACACCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26442  
 DB 27226 CACACCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27274  
 OY 26443 TGGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26502  
 DB 27275 CACGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27334  
 OY 26503 GCATGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26555  
 DB 27335 ACCGCTGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27394  
 OY 26556 --GACCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26613  
 DB 27395 GCGGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27454  
 OY 26614 TCCGCTGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26673  
 DB 27455 TCCGCTGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27514  
 OY 26674 GTCCTGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 26700  
 DB 27515 GTCCTGCGGCTGAGGCGGCGGCTGATGCAAGCGGCTGAGGCGCAAG 27541







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Db	7054	-----GAGCCGGTCCGTGCCCC	7070
Qy	2868	GGTCCGGATGCCGGTTCCTGTCGCCGATCGCATAGCTAGAGCTGGGTTGCCGCGCA	2927
Db	7071	GGAACTCCGGATGGTCCCTCTGTGTGTCTGGCCGGCGAGCAACGAGTGTGTCTGTCCGGCA	7130
Qy	2928	GGCGAGGCGCTTGGCTCAGTACTGTGCAGTCCGGCCGGACGTTTCTGCTTGGCCGATGTGGG	2988
Db	7131	GGCCGAGGCGCTGGCGCTCCCTCTCCGAAG-----GGGACATCTCCGACGACCGAGTGGC	7184
Qy	2988	TGCCGGTCTGGCCTGTGGGCGGGCGTGTCTGTGAGAGCATGTGCGGGTCGCTGGCCGCGGA	3047
Db	7185	CGGGGCGCTGGTGTCCGCGCGGGGAGTCTGTGAGAGCGGGCCGTCGTGTGTGGCCGATTCC	7244
Qy	3048	CCGTGAGAGCTGTGTGCAAGGATTTGGGGCGCTGTGCGCGGGGTGAGCGCATCGCGCGGAT	3107
Db	7245	GCGGAGGAAACCGTGAACCGGGCTGTGGGGCGCTGAACACGCGCGGTTTCGGGAGAGCC---	7301
Qy	3108	GACCACGGCTATGGCGCGGGTGTGACCGGGGCGGTGTGCTTTCGTGTTTCCCGACA	3167
Db	7302	-----GGGCAAGTCTGTGTGGGTGTTCGCGGAGCA	7331
Qy	3168	GGGTGAGCAGTGGGCGGGGATGGATGTGCTGTGCGCTTCCTCCGGGTTCGCGCC	3227
Db	7332	GGGACGAGTGGGCGGGGATGGGCGCGTGAAGCTGTGTGCGCAATGCCGGGTGTCCGGA	7391
Qy	3228	GCGATGCGAGCGTGTGCGAGAGGCTGTGCGCGCGCTGTGGATGTGATGTGTGTGTGATCAT	3287
Db	7392	GCGATGCCCGAGTGTGCGGCGCGCGGTGGCGCCCGTGAATGACATGTGTGCTGTGTGAGT	7451
Qy	3288	CTTGGCGCGGAGACGCGGGGATGCGGTGTGGAGCGGGCGGATGTGTCAAGCTGTGCT	3347
Db	7452	CCTGGCG-----GGCGAGGCGAGCATGGGTCTGGGTTCGATGTGTGCGACGCGGCTGTG	7502
Qy	3348	GTTACAGCTCATGTGTCTTTTGGCTGTCTGTGTGCGCTTCTTACGATATGCAACCGAGGC	3407
Db	7503	TTTGGCGTATGTGTGGCTGTGGCTGTGCGCTGTGTGGAGTCTGTGGGGGTCCGAGCGAGCGC	7563
Qy	3408	GGTCTTGTGGCATTTCCACGAGCGAGATGTGCGGCGCGCATGTGTGTGGGCGCTGTGAGCT	3467
Db	7563	CGTCTGTGGGAGCTGTGCAAGGATGAGATGTGCGGCTGTCTGTGCTTTCGGGGCGGTGTCCCT	7622
Qy	3468	GAAAGACGCGCGGAGAACTGTTTGGCTGTGCGAGCGCGGGCGCTGGCGCGCTGTGTGCGGAGCG	3527
Db	7623	CGAGGACGCGCGGAGAGTGTGTGCGCTGTGCGAGCGAGGCATTCGCGGCGGAACTGTCCGG	7682
Qy	3528	GGGCGCGATGGCTCAGTGTGCGGCTGTGCCCAGAGAGTGTGAGCAGCTCATTTGTGTGAGCG	3588
Db	7683	CCGCGCG-----GGATGTGGGTGTGTGCGCTGTGGCGAGGACGAGCTGTTCGG	7733
Qy	3588	GTTGGGCGGGGCGGTTGTGTGTGTGTGCGCGAGCTCAACGCGCCCGCTGTCAACCGCGCTGTGCGG	3647
Db	7734	GCTGTGTGACGGGGTCCAGATGTGCGCGCGCTGTCAACGCGCCGTCGTGTGTGTGTGTGTGCGCG	7799
Qy	3648	GGATGTCCGAGCGGTTGTGACGAGGTGTGCGGCTGTGTGCTGTGTGCGGACACCGGGATGTGCGGCGCG	3707
Db	7794	GGATGTCCCATGCTCTGTGACCGGACCTGTGGAATCTTGTGCGGGGAGGCAATCCGGGTTCTG	7853
Qy	3708	GCGGATCCCGGTCTGACTGTGTCTGTGCGACTGTGCCCATGTGTGAGCCCTGTGCGGAGAGACTT	3767
Db	7854	GCGGGTGTGCGGTGTGACTTACGCTGTGTGACACCCGGGCAATGTGTGAGGACATCTCCGACACTCT	7913
Qy	3768	GCTGGAGCTGTGCGGGGACATCACGCGCGAGCGGTCGCGGCGGTGTGCGGTTCTTCTTCCAGGAT	3827
Db	7914	TGCGGAAACTTGGGCGCGGATCAGTGTGCGAGGCGCGCGCTGTGTGCTTCTTCTTCCAGCT	7973
Qy	3828	GGAGGGACCTTGGCTG-----GACACACAAACCTTGTGACGCGCGCTTACTGTGTACGCGCACT	3884
Db	7974	CACAGGAGAGTGTGGGTGCGGACGCGGGGGTGTGTGACGCGGCTTACTGTGTACCGGAACCT	8033
Qy	3885	GCACGAGCGGCTCCGTTTCAAGCATGTGCTGTCAAGCCCTGTGCGGATGTGACGACACCGCT	3944
Db	8034	GCGCAACAGGATCCGTTTCCGAGGCGGCGCGACGCGCTGTGTGTGTGAGCAGGGCCACACCGT	8093

Oy 3945 CTTGCTGGAAGTCAGACCCCAACC---CACCTCTCCCGCATCGAAGACACCAACCGA 4001  
 Db 8094 GTTGCTGAGAGTCATGCGCAACCCGGTGAAGCTTGAAGCTGACGCTCACCAGGGA 8153  
 Oy 4002 AGACACCGCCGGAAGCTCAGCCGATGCGAGCTCCGCGCGGCGAACAACGACACCG 4061  
 Db 8154 CGCGATCCGGGACATTTGCGCGCTGGAAGACGGTGGCTGGCGCGGTCTGCTTCATGGG 8213  
 Oy 4062 CCGCTTCCGACCGCGCTCGGCCACACCCATTCACCGGCAATCGGCAACCCACACCTG 4121  
 Db 8214 TGAGCTGTTCTGTCGCGGATGATGATGAGCTGACCGGATGTTGCCGCGGCGCTG 8273  
 Oy 4122 GCACCAACCTACACCAACCAACCAACCCACCCCAACGCACTTGAACCTG 4181  
 Db 8274 GGTGACCTTGGCGACTAGCGGTTGAAACCGGCACTAGTGGCTGAGCCCGCGAACC 8333  
 Oy 4182 CACTTACCTTCCAAACAGCACTAGCTGCTGAGAGCTC-ACAGCCGGTTCGGAT 4240  
 Db 8334 CGCTTCGGCGGAGACCGCTGCTGGGCAAGTCTGACACTCCCGGTTGGGACCGACT 8393  
 Oy 4241 CCGGTTCCGGTCCGGTCCGGTCCGGTCCGGTCCGGTCCGGTCCGGTCCGGTCCGG 4300  
 Db 8394 CACCCGCTGCGCAGTGGTGGCGCGCGCGCAGCCCTGGGGGCTGGAACGGCTGGTCC 8453  
 Oy 4301 GGACCGCAGAGGTGAGTCCGCTTCTGGGAGCGCGGTGGCCGCGCAG----- 4347  
 Db 8454 GAACCGCGCCCTGCTGAGGCGGCGCATCCGGCTCGGCACTGGCGGCAACCCCGCTGT 8513  
 Oy 4348 ----GACTGGAAACGGTGGGCAACACTGCGCGTCCCGCTCCGCGGCTGGAGAC 4403  
 Db 8514 CGGCGACATGTCGTGACGCGCCGCTGGTCTGGCGGCGCGCAGCCGCGAGGTCCA 8573  
 Oy 4404 GGTGGTGCCTGACTCTCCGCTGGCAACCGCAACCAACCAAGCC----- 4452  
 Db 8574 GCTGATCGTCCGCGAGCCCGGCGAGCGGCGGCTCGATGAGGTCTTTTCCGGA 8633  
 Oy 4453 -CGCATCAACCTGGAACCTACAGAAACCTGAAACCCCTCAACCTCCACACCA 4511  
 Db 8634 AGCGAGCGAGCGTGGAGCGCGGCAACCGCAACCTCGTCCGCGCGCTGGCGGT 8693  
 Oy 4512 CCAACCCCAACCACTGCTCATGCGATCCCGAAACCGAGACCAACCCCACT 4571  
 Db 8694 GCGAGAAACCGGCGGCGGAGAGCGACCGACTGCTGGCGCGGCTGGCGGAGCG 8753  
 Oy 4572 CACCAACATCTCAACACTCCACCAACCGGATTCACCCCACTCCCTCAACCTCAA 4631  
 Db 8754 GGAACGGATTCACCCCGCTGAGACCGCGCTGCGGCGGCTGGCGGAGCGA 8813  
 Oy 4632 CCACACCC-----ACACCAACCCCAACCTCAACCAACCTCCACAC 4677  
 Db 8814 CGACTGCTCCCGTGGGTGGAGCGGGGTGCTCTGCTGGCTCCGGGGCCACCGCGT 8873  
 Oy 4678 ACCCGCAACCAACCCCAACCAACCGAGCCATTCACCGGCT-----TCT 4727  
 Db 8874 GACCTGTAGCGCGAGCGGCGGCTGCGGTGACCGACCGGCGCGGAGCGCGTCT 8933  
 Oy 4728 CTCCCTCTCCCGCTCGAGAAACACCCCAACCCCAACCCCAACCGGAGAC 4787  
 Db 8934 GACCGTCAATCCGTGGCGGACCGCGTTCGTGCTCGAGAGGAGACCAACGAGCGCT 8993  
 Oy 4788 CTTCTCAACCTCAACCTCAACCAACCAACCAACCAACCAACCAACCCCTCTG 4847  
 Db 8994 CTTCCGCTGCACTGGCGGAAATCCCGTCCCAACCGCGAAACCGGAGCTTCTCTCC 9053  
 Oy 4848 GTACGCAACCAACCGCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 4907  
 Db 9054 GTACGAAACCAAGTGGCGAGGAGCACTCTCCGCTCCAGGCTGGCTGGAGAGACC 9113  
 Oy 4908 AGCCCAACCTGGGAGCTGCGCGCAACCACTCTGAAACCAACCAACCAACCGCGG 4967  
 Db 9114 CGCGGAAACCGGCTGGCGGTGTCACCGGGGAGTGCACCGAAACCGCGCGCGCGAT 9173

Oy 4968 AATCATGACCTTCCCAACCAACCCCAACCCCAACCTTCAGCACTTCAACCAACCT 5027  
 Db 9174 CTGGGCGCTGGTGGCTCGGCGCAGTCCGAACACCCCGCGGATGCTGGCGCACT 9233  
 Oy 5028 CACCAACCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 5076  
 Db 9234 CGAGACCCCGCTGTGCTGCGCGCGGTGGCGAGCGGCAACCGAGGTGGGCTGG 9293  
 Oy 5077 CAGACCGCGCTCAACCC-----ACACCTCAACCCCAACCAACCAACCAAC 5129  
 Db 9294 CAAAGGCTGGCTCGGTGGCGGCTTGAACCCGGGTTACTCCGGGAGAGAGCGCGCC 9353  
 Oy 5130 CCCCCCCCCCAAGAAACCAACCTCATACCGGAGAAACCGGCGCTTCGCAACCT 5189  
 Db 9354 GCTGACCCCGAGGAGCAACCGCTGATCAACCGGAGGACCGGCGAGCTGGTGGCTGAC 9413  
 Oy 5190 CACCAACCTTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 5249  
 Db 9414 CGCCGGCACTCTGTCACCGGACCGGCTGCGGCACTGGTGTGATGAGCTCGCGG 9473  
 Oy 5250 CCCCCAACCCCGCAGCAACACACTCAACCAACCAACCAACCAACCAACCAACCA 5309  
 Db 9474 TGAGGCTCCGAGCTGAGAGAACTGACCGACTG-----GGGATCTCGT 9521  
 Oy 5310 CACCATCAACACTGCGAACACCAACCAACCAACCAACCAACCAACCTTCAACCA 5369  
 Db 9522 CGCATGCGCGCTGCGACGTTGGCAGACCGGCGCAGCTGAAACCGCTTGGCGGAT 9581  
 Oy 5370 CCCCCCAACACCCCTTCAACCAACCTGATCAACCGGAGCACTCTTCAACCGCGCAC 5429  
 Db 9582 CCGGCGAGACCGCTGTCACCGCGGTGATCAACCGGAGGCTCTGACGAGCGGT 9641  
 Oy 5430 CCTCAACCACTCAACCCCAACCAACCAACCAACCAACCAACCAACCAACCAAC 5489  
 Db 9642 GCTACAGAGTGAACCCCGAGCGGCTGCGCAACCTGCGGCGGCGGAGGTCAGCGCGC 9701  
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 Db 9702 CCGGCTCTTGAACAGCTCAACCCGGAGCGGATCTGCGCGCTTGTGCTTCTCTC 9761  
 Oy 5550 CGCGCGGCACTTGGCGGCAACCGGCAACCAACCAACCAACCAACCAACCAACCA 5609  
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 Oy 5610 CGAGCCCTCGCCCAACCGGCAACCAACCAACCAACCAACCAACCAACCAACCAAC 5669  
 Db 9822 GGATGCTTGGCGGCGGCAAGGAAACAGCTGACCTGCGGCTGCTCATCGATGGG 9881  
 Oy 5670 CACTGCAAGAAACGACTCGCTGATTGGAACAGGCGCGCATATCTGACCGCG 5729  
 Db 9882 CTACTGGGCGAGCGGTCAAGCGGATGACCGAGCACTGGGCGAGCGCACTGGCGCA 9941  
 Oy 5730 CGGCTTTCGACCATGTCACCCGAGTTGGCTCAGGCGAGCGGTACCGAGCGATCGGGA 5789  
 Db 9942 CCAACGATCGCAATGTCGCGCTTCCCGCGAGAGGAGGAGCTGCTGAGCGCGC 10001  
 Oy 5790 CA---CGAAGCGGCTGATGCTGATGCTGCAATGAGCATGAGAGCAAGTCAACAC 5846  
 Db 10002 CATGCGCAACCGGTGAGCGCTGCTGGCGGCAAGTTGACCTGCGCGCGCGGAGAC 10061  
 Oy 5847 CTTCAGACAGCACTGTGAGCGGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 5905  
 Db 10062 GCGGAGGCGGCGCGCGCGGCGCGGCGGCTGCTGCGCGCGCGCGCGCG 10121  
 Oy 5906 -----CACTTCACCGCGGAGTTGCAACAAACCTGCGCATAGAGCTGCGGAC 5960  
 Db 10122 GCGCGCGGCAAGACCGCGTCTGAGCAACGCTTGGCGGCGGCGGAGCGAGCA 10181  
 Oy 5961 ACGGCGGCAATGCTGAGCTGAGAGAGCAATGAGCGGCAAGTCTGCGGCGAGCGGA 6020  
 Db 10182 GCGCGCGGCTGCTGACCTGCTGAGCTGCGGAGGAGCGCGGAGGCTGCGGAGCA 10241  
 Oy 6021 CCGGAAAGCATCGCGCGGCGGAGGAGTTCGCTGCACTGGCTTCAATTCACGAGC 6080

Db 10242 CGCCCAATCCGCTCATTGAGACGAGACGTCGAGGACGCGCTTCCGACTGACGCG 10301  
 QY GGTGAGTTCGGAACCTGTCTGATTCAGGACACAGAGATCCGCTTCTGTCTGCTGAT 6140  
 Db 10302 GGTGAGTTCGGAACCTGTCTGATTCAGGACACAGAGATCCGCTTCTGTCTGCTGAT 10351  
 QY 6141 GTTGCACCAACCGACCCCTGTCGAACTGCGCTGACCTGACGAAACCACTGCGGGGAC 6200  
 Db 10352 GTTGCACCAACCGACCCCTGTCGAACTGCGCTGACCTGACGAAACCACTGCGGGGAC 10421  
 QY 6201 AGCAACGAGTGGCTCTTACGAGCGACGCTTACCGCCGAGGCTTCTGTACCGAGCC 6260  
 Db 10422 GCGCGCGA-----CGCGCGCGCGAGATCGGACCGCGCGCGCGAGAGAC 10469  
 QY 6261 GATGCGCATCGTTGGACGAGCTGTGTTTCCCGCGCGAGTACCTGCGCGAGACGAT 6320  
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 QY 6321 CTGGGATCTGATCTCTCGAGACGAGACGATCGCGCGAGTTCCCGACCGACCGCGCTG 6380  
 Db 10530 GTGGCGGCTGTGCGCGAGCGCGCGCGCGCTGACCGAGTTCCCGCGCGAGCGCGCTG 10589  
 QY 6381 GGAAGCTGACAGCTCTGACAGACCGCGACCGCGACCGCGCTGACCGCGAA 6440  
 Db 10590 GGAAGCTGACAGCTCTGACAGACCGCGACCGCGACCGCGCTGACCGCGAA 10649  
 QY 6441 CGGCGGATTCCTCTGACAGCGAGCGCGCTGACCGCGAGTTCTTCCGAGTACGCGCGCG 6500  
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 QY 6501 CGAAGCCCTCGGACATGAGACCGCGACGAAAGATCTCTCTGAAACCGCTGCGAAACAT 6560  
 Db 10710 CGAAGCCCTCGGACATGAGACCGCGACGAAAGATCTCTCTGAAACCGCTGCGAAACAT 10769  
 QY 6561 CGAAGCCCTCGGACATGAGACCGCGACGAAAGATCTCTCTGAAACCGCTGCGAAACAT 6620  
 Db 10770 CGAAGCCCTCGGACATGAGACCGCGACGAAAGATCTCTCTGAAACCGCTGCGAAACAT 10829  
 QY 6621 CACCAACGAGACGAGCTACGCACTTCCGCTGCAACCGCGCGCGAGTCAACCGAGTGT 6680  
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 Db 10887 CGCACTGACCGGACCGCGAGCGCTCATCTCGGCTGATCTGTAACCTTGTGTT 10946  
 QY 6741 TGAGGCTCTGCGGCTGCGGAGACAGCGCTTGTCTTCTGCTGTTGAGTGTGATCT 6800  
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 QY 6801 GCGCTGTGAGCGGCTGCGGAGAGTGTCTGATGAGGCTTCCGCGGGGAGTGTACGCT 6860  
 Db 11007 GCGCTGTGAGCGGCTGCGGAGAGTGTCTGATGAGGCTTCCGCGGGGAGTGTACGCT 11066  
 QY 6861 GATGTCGTCTCGGAGCTTCTGTAAGTTTTCGCGGACGCGGAGCTTGGCGCGAGACG 6920  
 Db 11067 GATGTCGTCTCGGAGCTTCTGTAAGTTTTCGCGGACGCGGAGCTTGGCGCGAGACG 11126  
 QY 6921 GATGTCGTCTCGGAGCTTCTGTAAGTTTTCGCGGACGCGGAGCTTGGCGCGAGACG 6980  
 Db 11127 GATGTCGTCTCGGAGCTTCTGTAAGTTTTCGCGGACGCGGAGCTTGGCGCGAGACG 11186  
 QY 6981 GATGTCGTCTCGGAGCTTCTGTAAGTTTTCGCGGACGCGGAGCTTGGCGCGAGACG 7040  
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 QY 7041 GATGTCGTCTCGGAGCTTCTGTAAGTTTTCGCGGACGCGGAGCTTGGCGCGAGACG 7100  
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 QY 7101 GATGTCGTCTCGGAGCTTCTGTAAGTTTTCGCGGACGCGGAGCTTGGCGCGAGACG 7160

Db 11307 GTCCAGACGCGGCTGATCCGAAAGACATGCGCGCGCGCGAGCTGTTCACATCGAGCT 11366  
 QY 7161 CGAGCGGCTGAGAGCCGACCGGACCGGACCGATTTGGGCGACCGGATCGAGCGCGAGCG 7220  
 Db 11367 CGAGCGGCTGAGAGCCGACCGGACCGGACCGGATTTGGGCGACCGGATCGAGCGCGAGCG 11426  
 QY 7221 CCTCTGCGACCTTACCGAGACGAGACCGGCGAGGAGCGCGTGTGCTGAGCTGCT 7280  
 Db 11427 GCTGCTGCGACCTTACCGGACCGGACCGGATTTGGGCGACCGGATCGAGCGCGAGCG 11480  
 QY 7281 CAAGTCGAATCGGTCACACAGGCGCGCGCGCGCGCGCGCGCGGATCAAGATGCT 7340  
 Db 11481 CAAGTCGAATCGGTCACACAGGCGCGCGCGCGCGCGCGCGCGGATCAAGATGCT 11540  
 QY 7341 GATGCGCTGCGGAGATGCTGCTGCGCGGAGCGCTTGCATGATGAGCGCTGCGCGCA 7400  
 Db 11541 GATGCGCTGCGGAGATGCTGCTGCGCGGAGCGCTTGCATGATGAGCGCTGCGCGCA 11600  
 QY 7401 TGTGACTGTTCGCGGAGTGTGCGGAGCTGCTGAGCGAGACGCTGCGCGCGCGCG 7460  
 Db 11601 TGTGACTGTTCGCGGAGTGTGCGGAGCTGCTGAGCGAGACGCTGCGCGCGCGCG 11657  
 QY 7461 GAGAGGCGGCTGAGCGGCGGAGAGTGTCTATCTGCGGCTGACGCGGACCGACCGCA 7520  
 Db 11658 GAGAGGCGGCTGAGCGGCGGAGAGTGTCTATCTGCGGCTGACGCGGACCGACCGCA 11717  
 QY 7521 GGTCTCTCTGAGAGACCGCGCGAGCGGAGCGTTCCGCGGAGGACCGCGCGCGAGAG 7580  
 Db 11718 GGTCTCTCTGAGAGACCGCGCGAGCGGAGCGTTCCGCGGAGGACCGCGCGCGAGAG 11775  
 QY 7581 TGAAGCGGAGCGAGCGATGAGGCTGCTGCGGAGCTGCGGAGTGTGAGCGGCTGCT 7640  
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 QY 7641 GTGCGGCAAGTGTGAGCGGCGGCTTGCAGCGGCGGCGGCGGCGGCGGCGGCGGCTGAC 7700  
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 QY 7701 CGAGCACCGGCGGCTGAGCTGCGGAGTGTGAGTATACCGCTGCGGCGGCGGCGGCT 7760  
 Db 11856 CGAGCACCGGCGGCTGAGCTGCGGAGTGTGAGTATACCGCTGCGGCGGCGGCGGCT 11915  
 QY 7761 GTTGCACCAACCGCGGCGGCTGATGCGGAGCGGAGCGGAGCGGCTTCTGCAAGCACTGCA 7820  
 Db 11916 GTTGCACCAACCGCGGCGGCTGATGCGGAGCGGAGCGGAGCGGCTTCTGCAAGCACTGCA 11975  
 QY 7821 GGCACCTGCGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 7880  
 Db 11976 GGCACCTGCGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 11999  
 QY 7881 CGGAGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7940  
 Db 12000 CGGAGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12056  
 QY 7941 CGGAGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 8000  
 Db 12057 CGGAGCGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12116  
 QY 8001 CATCTGACCGACCTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8060  
 Db 12117 CATCTGACCGACCTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 12176  
 QY 8061 CGACACGAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 8120  
 Db 12177 CGACACGAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12218  
 QY 8121 CTTCTTCTGCTTCCAGGCTGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAG 8180  
 Db 12219 CTTCTTCTGCTTCCAGGCTGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAG 12275  
 QY 8181 CCACTTACGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 8240  
 Db 12276 GAGTCTCTTCCAGGCTGAGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12335

QY	8241	CACCTTCAACGAGCGCCACACCTCTATCCACCAACGCGCCACCTCATGTGAAACAATGCC	8300
Db	12336	GAACCTGGCCCAACCGGCGAGCGTGTGTGCGCGCGCGCGCGCGCTATGACAGCCCTGGCC	12395
QY	8301	CCC---GGGACAAGATGACCAACCTTCCGACACCAACCCCCCAACATGACCCACACCTCAC	8357
Db	12336	CGCGGCGGCGCGCATGTGTGCGCGTTCAGGGGACCGAGAGAGAAAGTGGCGCCCTGTCTGCA	12455
QY	8358	CGCCACGAAACGACCTTCGCATTCGCGGCATCAACCCCCACCTCCCTCGTATCAG	8417
Db	12456	CGGACCG-----TGTGCGTGTGCGCGGATCAAGGTCCGAGCTGTGTGTGTCTC	12506
QY	8418	CGGCAACCCCAACACCTGTCAACATCACCACCTTCTGCAACAAAGGATCAAAAC	8477
Db	12507	CGGACACGAAAGCCCGGTGTCTGCGCGTGTGAGATGAACTGTGTGTGTGTGTAAAGC	12566
QY	8478	CAAAACCTCCCGCAACCAACGCGCTTCCACTCCCGCCACCAACCCCATCCTCAACA	8537
Db	12567	CGAAGCTGGCGCTGTGAGCAACGCTTTCACCTGCGCTATGAAACGATGTGACGA	12626
QY	8538	ACTCCACAGACACCAACCAACCTCACTTCAACCAACCCCAACCCCGCTATCAACGAG	8597
Db	12627	CTTCCGCGCGGTGCCCGAAGCGCTGACGTACCGGCGCGGTGTGCTGCCGTGTCTCGAC	12686
QY	8598	CAACACC---CCACCGGACCAACTCTCACCCCCCACTATGAGCCCAACAAAGCCCGCA	8654
Db	12687	GCTACCGGGGAACTCCGCGCGCTCGACACCCGAGACTCTGGGTGGGCAAGTGGCA	12746
QY	8655	CACCGTGACTACGCCACACCAACCCCAACCCCTTCACCAACAGGGGTCAACCACTACAT	8714
Db	12747	CGCGGTGGGTTCAGCGACGCGCTCACCGGCTGGGCGCCCAAGGCGGTGACGTTCT	12806
QY	8715	CGAACTGGGACCCGACAAACACCTTCAACCACTTCAACCAACCAACTCCCAACCCGCC	8774
Db	12807	CGACTGTGCGCGCGCGGTGTGCTGCGCGGATGGGTGGGTGTGGCGCTGGGGGACCGGA	12866
QY	8775	CACCAACAACCTTCAACCCCAACCCCAACCAACCCCAACCCCAACCTTCTTCAACCA	8834
Db	12867	GCAGAGCTGGGTGGCAACCTTGGCAAGAAAGGCGCGGAGGTGCCGAGTCTTCAACGCG	12926
QY	8835	CTTGGCCAAAACCAACCAACCTTGGACCCCAACCACTACCAACCAACCAACCAAC	8894
Db	12927	GCTGCGGAACCTGACGCTCGGCGCGGTGGCGGTGACGTGACGACGCTGTGAGAAC	12986
QY	8895	CCAACCCCAACCCCAACCTTCCCAACCTTCCCTTCAACCAACCAACCAACCTTCT	8954
Db	12987	GGCCACGCGCGGTGGGACCGTCTTGGCCACTTACGCTTCAAGCAACACGCTTCTGGGT	13046
QY	8955	CGAAAGCAACAGCGCGCGGTCCGGAACGTTGTACGAGCGCGGACCTTCAACCCCAAC	9014
Db	13047	CGAGTGTGAGGAAACAGCGGCGCGTCAAGGTCAACCCGCGCGCGGAGAACCATGTGTGA	13106
QY	9015	CCCCCTTCTGGGCGCAATTGGAATGTGCACTGACGTTGAGGCGCTTCTTGCAGGGCG	9074
Db	13107	CCGCGCGGTGAGGACGTGTGAGGCTGTGTCGAGAGAGCGCGCGGTGTGTCTCGGCA	13166
QY	9075	CTTGTCTTTTGAAGTCGATCCGTGTGCGGTGTGACATGTGCGGTGTGAGAGCGGTCTCT	9134
Db	13167	CC-----GGAGCGCGGCAAGTTTCACTTGAACGAGTCTTCA	13205
QY	9135	GTCCGGGCGCACTTCTCGAACTCGCGCTTCAATGCGGCAACATAGTGGGTGGACCG	9194
Db	13206	GGACCAAGGCTTGAACCTGCTACGCGCGGTGCAAGCTGTGCGCAACGCTGTGCGGACTTAC	13265
QY	9195	AGTGAATGAGCTGACGCTGCATGCGCGCTGTGTGTTCTTGTGAATGGGAGTGTGAGTGT	9254
Db	13266	CGGCGTGAAGCTG---CCAGCAACCTGATCTTGCATACCGAAACCGGCGGTCTCGCGG	13324
QY	9255	GCAGGTGGGTGTGCGGTGTGCGATGGGAGAGGGGCGGCTTGTGTGAGTGTATGCGCG	9314
Db	13325	ACCACTGTGCGGCGAACTGTCTGCGGAGGCGCCGCGCGCGCGCGCGCGCGCGTGAAGAGG	13384

[illegible]



Db 14384 AGCGGAAACAGCCGTTGGCTCGGCTCGTGAAGTCAACCTCGGGACACGCGGCGG 14443  
 Qy 10452 CCTGAAGACTGTGATCATCCGGTGAATTCACAGCCGAGCGGTCCGGTGAACACGAGC 10511  
 Db 14444 CGCGCGGGGTCTGGGCGGTGATCAAGATGATCATG----- 14478  
 Qy 10512 CGGCGGTCCGACGTGCTGCCACGGCTCCGGTGGCGTCTGCTCGGCGGTGGTGA 10571  
 Db 14479 -----GCCATGCGCCACGGCGCTCATGCCGCGCACGCTGCAAGTGA 14519  
 Qy 10572 TGTATCGAGTCGGAGGTGTTCCTGTGTGTGGGTGGGTGCTGTGTGTGAAGGTTGG 10631  
 Db 14520 CG---AGCGACAGACCAAGTGAAGTGGCGGGCGAGATGAGAGTGTAC----- 14570  
 Qy 10632 GACGGGTGTGCTGGGTGGCGGGTGGCGGGATCTGGCTGGTGTGTGTGGGTGGGGA 10691  
 Db 14571 ---CGAGCGCGGAGTGGCGCGCACCGACGTCCGCGCGGGCCGGGGTGTCTCT 14626  
 Qy 10692 TCTGCTGTGTGAGCGCGCGGTGTCCGATGCTCCGGGTGGAGGGTCTGCGGGCGGA 10751  
 Db 14627 TCGGCGCAAGCGGACCAACGGCGACCTGATCATC----- 14681  
 Qy 10752 GCTGCGCGGTTGGGGCGGAGGTGCGGATTGTGCTGTGAATGTGGGAGACGGCGGGA 10811  
 Db 14682 -----GAGGAAGGTCCGCGCGAAGAGGCGGTGAGACGAAGAGTGGCTC 14705  
 Qy 10812 GGTGCTCCGGCTGTGAGAGGGTGTCTGCGGGGTGTCCGCTGAGAGGGTGTGTGATGC 10871  
 Db 14706 CGTGTGTCCGCTGTGCTGTCTCCGCGCGACGCGCGGTGTGCTGGCGG----- 14753  
 Qy 10872 GAGCTGTGTGTGAGAGTGAAGCATGCGATCGCTCTCTACAGCGCGGCTGGGCGAGT 10931  
 Db 14754 -----GCAAGCGCGGCGCGCTGTGGCGGGTCTTCAAGAACGAATGCTTGGCGGGGT 14804  
 Qy 10932 GTTTCGCGGCAAGTGAATGCCGCTTTTGTGTGATGACTGACGCGGGATGAGACT 10991  
 Db 14805 GAGCGGTGCTCGGTGCTTCCGGCGCGCGACGCTGAACGAGCGCGGTGTGATCG---- 14860  
 Qy 10992 GTCCGCTTCTGCTGTCTCTCGGCGCGGGAGATCTGGGGTGGCGCGGCGAGGCGAA 11051  
 Db 14861 -----CGGGCTC 14867  
 Qy 11052 CTACGCGCGGCAATGCGGCTGTGAAGCGGCTGGAGTACCGGCGGCGGCGGGGTCT 11111  
 Db 14868 CGGCAAGAGGCTCAAGAGGCTGTGAAGCACTGGCGCGGCGAGAACGCGCGGCGT 14927  
 Qy 11112 GCCGGGGTGTCTGCTGGCGGTGGGGCTGTGGAGAGGCGAGCGGATGACCGGCGACT 11171  
 Db 14928 CGTGAACGGGAGCG-----GCGGGCAAGCGGGCAAGTGTGTGGGTCTTCCGGCGAG 14982  
 Qy 11172 GCGCGGCAACCGACCGGCGCATATCGGTTCCGGTCTGCAATCCCATGTGCAACCCCGGA 11231  
 Db 14983 GGCCTGCAAGTGAATGGGATGGGCGGGGACCTCTGTGAAGTCTCTCCCGGTTTCCCGG 15042  
 Qy 11232 CGCACTGGGCGCTTCTGATGGGCGGCTGGCTGTGAACGGGCGGCGGTCTGTGCGGCGGA 11291  
 Db 15043 CGGA-TCAAGGAATGGCTGGCGGCACTGGAGACATGGAGCCGATGCTGCTGAGAGT 15101  
 Qy 11292 CTTGCTCCCGCGCGCGCGCTGCGCGCTGTGTGAGAGACTTCTGTCGCGCACCGCGCG 11351  
 Db 15102 GCTGGCGGGCGAGCGCGAGCTGTGGAACGGGTGCAAGTGTGTGAGCGGCGCA----- 15154  
 Qy 11352 CGGACACCGCGACCAACCACTAACGGGTGTGGAGCAAGGCGCGCGAGCTGACGCGCG 11411  
 Db 15155 -----GCTTTCGAGATGATGTGG 15173  
 Qy 11412 GCTGGCGGGCGAGACACGAACACGACACCAACCTCTGCGCGGTGTGCGCTCCCA 11471  
 Db 15174 GCTTGGCGGGGTGTGAAGCTTCTGCTGGGGTGAACCCCGAGTGGGTGCTGCGGCACTTCCA 15233  
 Qy 11472 CATTCGACCGTCTGTGGGCAACCAACCCCGAGACCATCCCGCGAGCGCGGCTTCG 11531

Db 15234 GGGGAGATCGCCCGG-----GTGCGTGTCCGGCGCGGTGTGCTGTGAAGACGCGGCGAA 15290  
 Qy 11532 CGACTCGGCTTGCATCTCCCTCACCGCGGTGAACTACGAACCGGCTCTCCGACACAC 11591  
 Db 15291 GGTGTGCGCTTGGCGAGCCAGCGGATTCGGGGAGCTGGCGGCGCGCGGGAGTGGC 15350  
 Qy 11592 CGGACTCGGCTTCCCAACCAACCTTCCGCTTGAACCAACCAACCAACCAACCAACCA 11651  
 Db 15351 GTCGGTGCACTGAAGCGAAGAGAGCAGTGTGGCGGCTGACGCG----- 15395  
 Qy 11652 CCACCTCCACACACACTCCAGCCACAAACCGGACAGCTGTCCGCCCCGTGTGGCGGA 11711  
 Db 15396 -----GTGGCGAAACCGGCTGAGGTGCGCGGTCAACAGCCCTTC 15437  
 Qy 11712 GCTGACAAACTGCATTCGCGCTCTCCGCGCTGACAAACCGACAGCGCGAGGAAG 11771  
 Db 15438 CTCGAGTGCATTCGCGGAGAGCGGACAGGCGCTGACGAACCTTCGAAGCTTGGCCGG 15497  
 Qy 11772 AGTCAACCTTGGCGGTGAAGTCACTCATGTGTGAGGTGAACGACACCCAGCATCCGACAGC 11831  
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 Qy 11832 CGAAAGCGCTGTATGACGACGAGAGTTCAATCGGCAACAGAGCTGATTTCAATT 11891  
 Db 15558 GCGCATGCGCGAAACCTTGGCGAAAGCTTGGCGGGATCGACGC----- 15602  
 Qy 11892 CATTGACAAAGACCTCGGCGCTGTCTGAAACCGGACGCTGCGCATCGCGCGGTATCGGCT 11951  
 Db 15603 -----GCGGGTTCCGGGATTCGTTTATTCACCC 15633  
 Qy 11952 GGGCCTGTCTAGGACGTGAATGCAATTGGCGAATGAAGCAAGGCTCTGAATACCTCA 12011  
 Db 15634 G----- 15634  
 Qy 12012 GCGGCTCATCTGCGAAGCTGAGCCGCACTCGCGCTGTGACGAGGTGTGAGAGCTGA 12071  
 Db 15635 -----TCTTGGGACGTTGATTCAGAGAGCGCTGTGTGACGCGGCTATCTGTACCGGA 15688  
 Qy 12072 GCAGAGGCCATTCGCGATTGTGGGGATGGCGCTGTGTTAACCAAGCGGGGGAGAGCTAAC 12131  
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 Qy 12132 CACGCGACTGTGGATCTCGTCAAGTCCACAGAGGACGCTATCGGGAGATTCCGACCGGA 12191  
 Db 15749 C-----GCTGTCTGTGAGATCAGGCGCCA 15773  
 Qy 12192 CCGTGAATGAAGCTTGAAGAGCTCTACGACCCGGAACCGGACCGCTCAGGAACCAATT 12251  
 Db 15774 CCGGCTGTGTGACAGCGCTG----- 15795  
 Qy 12252 CACGCGCAGGAGGTTTCTATAGAGCGGGGAGCTTGAAGCCCGGCTTCTTGAGATT 12311  
 Db 15796 -----AGGAAATACGACACAGCGGAGTGAACCGGGTTC 15830  
 Qy 12312 GTCAACGGGTGAGGCGCTGCAATGAGACCCGACAGCGCTGTGCTCGAAACCACTTG 12371  
 Db 15831 GCTGCGGGGGA-----GAGCGGGAGATGGGGGCGCTGTGCGGTGCGCGCG 15878  
 Qy 12372 GAAACGTTTGAAAGAGGCGGAATGACCCGAGGTCAATGCGCGGAACCGGAGCGGGGT 12431  
 Db 15879 CGAATGTGACGTCCGGGCG-----GT 15899  
 Qy 12432 TTTTGTGGGATCAATCCGAGAGTACACCAACCGGATACACATGAGCCCTCAAGAG 12491  
 Db 15900 GGGCGTGAATGAGACGGGCGGCGGTGCGCGCGCGGCTGGGTGAACCTGCGGACGTAGC 15959  
 Qy 12492 AGTGAAGGCTAACCTGTCACTGTGACAGCGCGCAAGCATTGTGTCAGGCGGTATCTCTTA 12551  
 Db 15960 CTTGACGCGCGCG----- 15973  
 Qy 12552 CAACCTTGGGCTGAAAGGCGCTGCGAGTACATATGACACGCGGTGTCTCTCGCTCGT 12611  
 Db 15974 --ACTTCTGTGCTGACGAAGCGGAGACCGCGCGAAGCGCGCGAGGG----- 16016

QY 12612 CGCCTGCATCTGGCTGCGCAAGCGCTCCGCTCCGATGATGACACCATGGCGCTCGCAGG 12671  
Db 16017 -----CATGACCGCGAGTTCTGACCGGCAATGCA-- 16047  
QY 12672 CGGCGCTTCGATGAGCCACTCCCTTGTCTTCAACGATTTCTCTCGCAGCGGGGCT 12731  
Db 16048 ----CAGTCCGATGAGCAGCTTGGCCGAGCTGCTCGAGCTGTGTCGAGCAGCGCGG 16103  
QY 12732 GGGCCGACAGCGGCGCGGTGCAAGCGCTTTTCGGCGCGCGCGAGACCGGCTGTCCGA 12791  
Db 16104 GCGCTCAGACACCTGTGTCGCTGTGCGCAGATGGCGGACCGCGCGCGGACCGCTC 16163  
QY 12792 GGGTGTGGGATGCTGTGTGAGAGCGCTCTCCAGCGCCCGCAACGATCACTGT 12851  
Db 16164 GACCGCGAGAGAGCTGCTGCTACAGGTACCTGGCAGCCCTTGGAGCGGAGACCGCGG 16223  
QY 12852 CCGTGCCTGTGCTCGCGGAGCGCGCTCAACAGAGCGGCGGACGAGCGCTGACCGC 12911  
Db 16224 CGTGCCTGGCGCGGCGCTGCGCTGCTCGTCCGGCGGCAACACCGAGCGCT----- 16277  
QY 12912 ACCCAACGCTCGTTCAAGTACAGTATCCGCGAGGCTTGGCGCAACGACACTCTC 12971  
Db 16278 ----- 16277  
QY 12972 CCCTGCGATGTCATGCGGTGAGAGGCCACGCGACCGGAGACACCTTGGCGAGCCGAT 13031  
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QY 13032 CGAGGCTCAGCGCTCTGTGAGAGCTTACGATGAGAGCGCGCCAAACCGCGCGCTCTG 13091  
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QY 13092 GCTTGGAGACCTCAAGTCCAAATATGGGAGCTTCCATGGCGCGCTGGCGGTGTGGGGGT 13151  
Db 16371 CTTGCGAGAGCAGACCTTACCGGCGTGTGCTGTGCTGTCTGACAGGCGGCGCGC 16430  
QY 13152 CATCAAGATGTGATGAGCGCTCGGAGATGTCTGTGCGCGGAGCGTTGATGATGATGA 13211  
Db 16431 GAGCGCGCGGAGATAC-----CGGTGAGCGCTCGCGCTGTGCA 16472  
QY 13212 GCGCTGCGCATGTGAGCTGTGCTCGCGGAGCGGTGACGCTGACGAGACGCTGCTC 13271  
Db 16473 GCGCTGCGGAGACACACACACGCTCGCGCGCTGTGTGTCCTCACTTCGCGGCGGTGA 16532  
QY 13272 CTGGCGCGCGGAGGCGCGCTACGCGGCGGAGAGATGTATATTCGCGGTGACGGG 13331  
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QY 13332 CACCAACGCCACGTCATCTCGAGAGAGACACCGCCCAACATCCGTCAGACACAC 13391  
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QY 13392 GCGCGACGAGCTCGCGGAGAAATCAGCGCGCAGCAGAGATGCGGTAGTGATGAGGC 13451  
Db 16653 GAGCGCGCGACCGGCTCAGGCGCTGCGCGCTGCTGAAACGCGCGCGCGGAGAGA--- 16709  
QY 13452 TGTGCGCGGATCCAGGGGTGTGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13511  
Db 16710 -CGACTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16766  
QY 13512 GCGCGCGGAGCGGCGGCTTGCAGCCACTTCAACGACACCGCGGCTGACCTGCG 13571  
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QY 13572 CGACGTGCGGTACACCTTGCAGCGCAGCGCGCTGTGTGTGTGTGTGTGTGTGTGT 13631  
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QY 13632 GCGCGCGAGCGGAGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13691  
Db 16887 CGTACCGGAGCGGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16946

QY 13692 CCGCGCGCTCATTCACAGCAGCGGCCAGAGCGGAGACCGGAGAGCGCGAGAAA 13751  
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QY 13752 GACCGATTATCTGTCTCGGAGCAGGGGCAACCAACCGCCCGGATGCGCCACGCGCTCTA 13811  
Db 17000 ----- 16999  
QY 13812 CCACACCCACCGCTTTCGCGCGCGGACATGACAGACATCTGACACCCACTGACCCCA 13871  
Db 17000 -----ACTGAGAGTACCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17051  
QY 13872 CCGTGCAGCAGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 13931  
Db 17052 CGTGCAGACACCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17109  
QY 13932 CTTGAGAGAGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13991  
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QY 13992 CTTCCAGGTGCGCGCTTCCACCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 14051  
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QY 14052 GCGCGACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 14111  
Db 17220 GAGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 17279  
QY 14112 CGAGCGCACACCTCATCTACCTCAACGCGGCAACCTCTATGCAAAACATGCTCCCGGAC 14171  
Db 17280 GATGCGCTGGGCGCGCTGTGACAGATGCGATGCGATGAGACAGAGCGCGCTCTGCGCCA 17339  
QY 14172 CATGACACCTCTCAACACACACACACACACACACACACACACACACACACACACAC 14231  
Db 17340 GCTGCGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17393  
QY 14232 CGACTCGCATCTGCGCGCATCAACACCGCCACTCTCTCTCTCTCTCTCTCTCTCTCT 14291  
Db 17394 GGTGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17453  
QY 14292 CACGTTCACATCAACACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 14351  
Db 17454 CTTTATCTCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17483  
QY 14352 CACCAACAGCGCTTTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 14411  
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QY 14412 CACCAACCTCTCACTTACACACCGCCACACCGCCCTCTCTCTCTCTCTCTCTCTCT 14471  
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QY 14472 CGACCACTCTTACACCGCCCACTACTGTGACCAACAGCGCGCAACCGTGTGACTTAC 14531  
Db 17604 CGACAGAGACCGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17663  
QY 14532 CACCAACCGCAACCGCTTCAACAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 14591  
Db 17664 CAGGCGCGCGAGAGCATGCGCGCGCGCGCGCGCGCTTCAAGAGGTGTGTGTGTGTGT 17723  
QY 14592 CACACCTCTCAACCTTCAACAGACACCTTCCAGACACCGCCCAACCGCCACTCTAC 14651  
Db 17724 GCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17783  
QY 14652 CTTTACCAACCGCCACACACCGCCCAACCGCCCAACCGCTTCTCAACCTGTGTGTGTGT 14711  
Db 17784 GCTGTATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17838  
QY 14712 CACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 14771  
Db 17839 -----CTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17888  
QY 14772 CTTGACCTTCCCACTTACCGCTTCAACACCACTTACTGTGTGTGTGTGTGTGTGTGTGT 14831

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Db      17889 GCGAGTCTCGCGCGCGCTGCTC-----GCCGATTCAAGAGCGCGGCTGTGAC 17943
Qy      14832 GCGGAGGACCCGTCACCGAGCGAAGGCGTGAAGCCACGACCCCATCAACCCGCT 14891
Db      17944 ACCTGCTCGGCTTCGCGGACCGGACCGAACCGGCGACGAGCGCGAGACCAAGGAA 18003
Qy      14892 GCGTATGTCTCTGTGGGCAAGTCTCGCAGAGCGAGACGAAAGCTGTTCGCTGTGT 14951
Db      18004 GC-----GCGCCGCGCGCGAGAGCGACAACTGATCGAGCGACT 18044
Qy      14952 GCGGACCAATGCGGCGCGCTGTGTGGGCAATGCCATCTCCGAGTATCGTTCCGAACAA 15011
Db      18045 GGAATC-----TCGGTCTCGTGAACGAGCCCTCGGCGAGACGAGCTGACCGCGAT 18098
Qy      15012 GGCCTTCAAGAGGTGGGTTTGAATCTCTGCGCCAAATTCAGCTTGATGACAGTGT 15071
Db      18099 GGGCAACCAATCGTAGAGAAAGAACATGTCCGCGCCGAACGAGC----- 18142
Qy      15072 TGCTGACGTTGACCTGCGCTTCGCGGCAAGCTGATCTTCGATTACCCCACTCCGATGAC 15131
Db      18143 -----AGATGTTAAGCACTGCGCGCTGCTGAGAGAAAGTCCGGCTTCAGCAGGA 18197
Qy      15132 GCTTTCGCAAGTTCCTCGGCGCGCGATGTCGAGCGGACACAGGACCACTCGTCT 15191
Db      18198 GAACAGCGCGCTC----- 18210
Qy      15192 GCGGCTAATGCGGATCCCGCGGACAGACCGAATGCCATCTCGGCAATGCGCTGTGCTA 15251
Db      18211 -----GCCGCGCGCGCGCGGAGCCGCTGCGCATGCTCTCAATGGCTCCGCTA 18260
Qy      15252 CCGCGGTGATGATGAGCAGCGGTGATGATCTGTGGCAGGTGTGATGAGTGTGACATGACG 15311
Db      18261 CGCGGCGGGAATCCGCGGCGCGGAGACTTCTGGCGGAGTGTGAGAAAGCGCGACGT 18320
Qy      15312 GATGCGGATTCCTCGAGAACCGTGGGTGGACCTTGACAAGCTGTAAACAACCCGAGACC 15371
Db      18321 CTACACGCGCTTCCCGAGAGCCGCGGTGGAGATGAGAGGCTCTTACACCCGAGACC 18380
Qy      15372 GGAACCAACAAGGACCAAGTACACCCGAGGAGGAGATTCCTTTAACAGAGAGCAATTT 15431
Db      18381 CGAACACCCCGGACGAGATGATGAGGAGGAGGCGCTTCTTGACAGAGCGCGGCTCAGTT 18440
Qy      15432 CGATCCGCACTTCTTCGGATCAGTCCGCTGAGGACATGAGGACATGAGACCCGAGACG 15491
Db      18441 CGAGCGCGGATTCTTCGACATCTCGCGCGCGAGGCGCTGACATGAAACCCCGAGACG 18500
Qy      15492 GCTGCTGTGAAAACAGCGTGGAGAGATGAAACAGCGCTGATCAACCCCGACAGCT 15551
Db      18501 GCACTCTGTGAGGTGCTGTGAGAGACTTGGAACCTTGGAACGCGGCAATCGACTCGGT 18560
Qy      15552 CCGTGGACACCAACCGGCGCTTTCGCGGAGCTGACCTAACAGACTACGCGCGCGCTT 15611
Db      18561 GCGGGGAGCAACATCGCGCTTACGCGCGGAGTGTGACACAGAGACTACGCGCGGACT 18620
Qy      15612 TCCCAAGCTCCGAGGAGTTCAGAGGATCTCGGAGCAGGAAGCGAGGAGATGCTG 15671
Db      18621 CAGCGGTTCCAGAGCTTATGAGCTGAGACGCGGCTTGAGGACCGCGGCGGTTGCTG 18680
Qy      15672 CTCGGGTGCTGCTGACCTGCTGCGCTGAGGAGAGTCCGCGCTTACAGTCACTGCTG 15731
Db      18681 CTCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 18740
Qy      15732 CTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 15791
Db      18741 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 18800
Qy      15792 TTTCATGAGCTCTGCGGAGTGTGCTGACGAGTATGAAACCCCGCGGAGTGTGAGATTT 15851
Db      18801 CTCATGAGCTCTGCGGAGTGTGCTGACGAGTATGAAACCCCGCGGAGTGTGAGATTT 18860
Qy      15852 TTTCGCGGAGGAGGCTGAGCTGAGAGGAGGCTGCAAGGCTTCTTCGAGCGGCTGA 15911

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Db      18861 CGGCGCTCAGCGGCGGTTGGCTTCGACGCGGCGCTGCAAGTCTTACGCGCGCGCGCGA 18920
Qy      15912 CGGCAACGAGCTGAGGATGAGGATGCAATGCTGCTGAGAGCGCTGTGACGCGG 15971
Db      18921 CGGTTCCGCTGAGGCGGAGGCGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 18980
Qy      15972 GCGGCTGCTGCTGCAATCTCTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16031
Db      18981 CGAGCGGAGCACCAAGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19040
Qy      16032 GAGCAACGAGCTGACCGCGCGGCAACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16091
Db      19041 TTCCAAAGGCTTACCGCGGCAACGAGCGCGGAGCAACGAGGATCTTCGCAAGGACT 19100
Qy      16092 GGCCAACGCGGACCTGACCCCGCGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16151
Db      19101 GCGGAGCGCGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19160
Qy      16152 CACTTGGGCGACCCGATCGAGGCGCGGCGCTTCTGCGCACTTACGAGACGAGCGCC 16211
Db      19161 GGTCTCGGCGACCCGATCGAGGTCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19220
Qy      16212 GCGCAACGAACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16271
Db      19221 CCGCAGCAACCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19280
Qy      16272 CGGAGTGTGAGGCGGAGTCAACGAATGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 16331
Db      19281 ATCCGATGTGCGGCGCTGATCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19340
Qy      16332 GACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 16391
Db      19341 GATCCAGCAAGTGAACGCGCGCAACGCGGCAAGTGAATGATGATGATGATGATGATGATG 19400
Qy      16392 GCTGACGAGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16451
Db      19401 GCTGACGAGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19457
Qy      16452 ATGCTTGGGCTGAGCGGCGCAACGCGCGCAAGTATCTGCAAGAACACCGCGCGCA 16511
Db      19458 GTGCTTGGGCGCAAGCGGCGCAACGCGCGCAAGTATCTGCAAGAACGCGCGCGCA 19517
Qy      16512 CATCCGTCAGACACACCCGCGGACGAGCGCGCGGAGAAAGCGCGCGCAAGTGTTC 16571
Db      19518 GCGGCTGACCGAAGCGCGCGGCG-----CGAGGATGTGATCGCTGATGTGTGCGG 19571
Qy      16572 GGGGAAAGCGCGCGGCGCAACGCGCGGATCCGCGGAGAAAGCACTGATCTGCTGCGG 16631
Db      19572 GCGGACCGCTGCTTCCCTGCGCGCGCGCGCGCTGCGCGGAGGTCGAGCTGCTC 19631
Qy      16632 CAGTCCAGGAGTGTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16688
Db      19632 CTGAGCGATGTGCGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19691
Qy      16689 ----CGAGGCGCGGCGCTGACGCGCGCTACCGCAACCCCGCGCTGCACTGCGCGA 16745
Db      19692 GCTGTGCGCGGCTTCCAGAAAGCGCTGACCGGCTGCGCGGCGCTGCGCGGCGG 19751
Qy      16746 GCTGAGTACACCTGCGCAACGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 16805
Db      19752 GAGGCGCGCGGCTGCTTCCGCGCGCGCTGCGGAGTCCCGGCAAGGCTGTGAGGT 19811
Qy      16806 GCGCAACCGGAGCACTTCTGCAAGACTGCAAGGCACTGCGCGGAGCAACCCGACCC 16865
Db      19812 GTTCCCGGCGAGGAGCGAGATGAGGCGGAGCTGAGGCTGCTGCTGCTGCTGCTGCTG 19871
Qy      16866 GCGCGTATCAACAGCAGCGCGCGGAGCGGAGCGGAGCGGAGCGCGGAGGAGGAGGAGG 16925
Db      19872 GGTGTGCGCGCGGAGATGCGGAGTGCAGAGACCGCGCTGCGGCGGTGTGCTGCTGCTG 19931
Qy      16926 CGCATTCATTCCTCGGAGAGGAGCAACCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 16985
Db      19932 GCTGACCGAGCTGCTGCGGCGGAGGCGGAGCTGCTGAGACCGGAGTCACTGCTGCAACC 19991

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QY 16986 CACCCACCCCGTCTTTCGCGCGCACTACAGACATCTGCAACCCACTGACCCCT 17045  
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QY 17046 CGACCAACCCCTCTCTCCCTCTCTCAACAGAGACCCCAACCCAGACACCA 17101  
Db 20052 CGAGGCTGTGAGGCACTCGCAGAGGAGATCCGCGCGCATCGTCTCGAGGCACT 20111  
QY 17102 ---CCCTCGAAGAGGCGCGCACTGCTCAGACAGCCCGTACGCGCCGCGCTCTT 17159  
Db 20112 GTCTCTGAGAGAGCGGCGAGAGGTGATGCTTGCGCAGCGAGATCGCGCTCGCT 20171  
QY 17160 CGCCTTTCAGGTGCGCTTCAACCGCTCTCTCAACGAGGATACCAATACCCCACTA 17219  
Db 20172 GAGCGGCGGCGGCGCATGAGGCTGAGTGTGAGCGTGAAGAGAGAGAGAGCGCGGCT 20231  
QY 17220 CTACGCGGAGCACTCTCTGCGGAATACCGCGCGCAC 17259  
Db 20232 CGAGCGTGGGCGGCGCGCGTGAAGTGGCGCGCTCAACGAGCGCGAGCTCGTGTAT 20291  
QY 17260 -----CTGCGCGGATCTCTCAACCTCAACCGAGCGCACACCTCTAT 17300  
Db 20292 CGCGGAGGAGCGCGAGCGCTGAGAGACCTTCAAGCGCTTCAAGAGAGGCTCG 20351  
QY 17301 CACCCACGCGCAACCTCATGCAAAACCATGCGCGCGCAACATGACACCTCTCAAC 17360  
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QY 17361 CACCCCAACCAATCAACCCCACTCAACGCGCGCAAGAAAGCATCTGCGCATGCGCG 17420  
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QY 17421 CATCAACACCCCACTCTCTGTATGATGAGGCGACCGCGCAACCGTCAACATCAAC 17480  
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QY 17481 CACCTCTGCAACCAAGGATCAAAACCA 17528  
Db 20532 GACCTCGCGGTGATGAGTGGGTTGCGCGCGGTGCGCACTGATGAGAGGCGCA 20591  
QY 17529 AAAGCGCTTCACTGCGCGCAACCAACCTCACTCAACCACTCAACAGACACCA 17588  
Db 20592 CGGATGTGTGATGAGTCAAGCGCGCATCGGTGTGATCAAGATCAAGACTGT 20651  
QY 17589 AACCTGACCTAACCAACCCCAACCCCTTATACCGCGCAACCCCAACCCGACCA 17648  
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Db 20712 CTTGTGCGCTTGGGCGCGAGCTTGTGTGCGCGGTGAGCGTGAAGTGTGCGGT 20771  
QY 17709 CACCAAAACCTTCAACCAAGCGGTCAACCACTGATGAACTGGAACCGGACAC 17768  
Db 20772 GCTGCAACGTCGCGCGCGGTGAGCTGAGCTGAGCTTCAACCAAGCTACTG 20831  
QY 17769 CCT-----CACCAACCTCAACCAACCAACCTTCCCAACCCCGAC 17810  
Db 20832 GCTGCAATGAGCGGCGGTGCGCAACGAGCGGTGTGCTGAGCGCTGCGCGCGGACCA 20891  
QY 17811 CACCAACCTCAACCTCAACCAACCCCAACCAACCCCAACCTCTACAC---AA 17867  
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QY 17868 CTTGCGCAAAACCAACCAACCTTGAACCCCACTTACCAACCAACCAACCAAC 17927  
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QY 17988 C-----GAAAGCAACAGCGGCTCGGA 18012  
Db 21072 CCTGAAAGAGCTCGTATTCAGAGCACCGCTGTGAGGAGAGCGCGGCTTCGCGT 21131  
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Db 21312 GGTGAAACCTTCAACCGACCTTACCGAGCGGAGTACGCTTACAGCGCGCTTCA 21371  
QY 18219 -----CTGACCTTACAGAAACCTGAAACCTCTCAACCTCCGACAC 18263  
Db 21372 GGGATGCGGCGGCTTGGCGGCGCGGTGAGAGAGTCTTGGCGAGGCTCGCTCTGA 21431  
QY 18264 CCACCAACCCCAACCAACCTTGTATGATGATGATGATGATGATGATGATGATGATGAT 18323  
Db 21432 CGACCAACCGAGAGAGCGCGGCAAGTTCGCGCTTCAACCGCGCTCTCTGAGCGCTCT 21491  
QY 18324 CATCAACCAATCTTCAACCAACCTTCAACCAACCAACCAACCAACCAACCAAC 18371  
Db 21492 GCACAGAACCGCTTCCGAGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 21551  
QY 18372 CCGCTCAACCTTCAACCAACCAACCAACCAACCAACCAACCAACCAACCTCTC 18415  
Db 21552 CGGCTGTGCTTGAACCGCGCTGAGCGCGGTGAGAGAGTCTTGGCGAGGCTGCGCG 21611  
QY 18416 -----ACCAACCGGAGCAAGCGGCAACCAACCAACCAACCAACCAACCAAC 18470  
Db 21612 TCCGAGCGCGGTGAGTTCAGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 21671  
QY 18471 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18503  
Db 21672 TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 21731  
QY 18504 CCACCAACCCCAACCAACCGGCAACCTCTCTCAACCTCAACCTCAACCTCAACCTCAAC 18563  
Db 21732 GACTCTGCTTTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 21791  
QY 18564 CCAAAACCAACCAACCCCTCTGTGTAGCGCAACCAACCGCAACCAACCAACCC 18623  
Db 21792 GCAAGCGAGAGTGTGAGAGCTTTCGCGAGGAGCGCGCTGAGCTGAGCAACCGAGT 21851  
QY 18624 CAAGAGCGG-----CTCAACCAACCAACCAACCAACCAACCAACCAACCAACCT 18671  
Db 21852 GCTGAGAGCGGTGAGTCTGAGTCTGAGCGGAGCGGAGAGAGAGAGAGAGAGAG 21911  
QY 18672 CCGGACCAACCTCTCTCAACCAACCCCAACCAACCGCGGAGTATCTG----- 18718  
Db 21912 GACTGTGAGCGCTGAGCGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 21971  
QY 18719 -----ACCTCCCAACCAACCCCAACCCCAACCCCAACCCCTCAACCACT 18758  
Db 21972 GCGAGCGCGCGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 22031  
QY 18759 CACCAAAACCTTCAACCCCAACCAACCAACCAACCAACCAACCTGAGTCTGAGCAAC 18818  
Db 22032 CCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 22091  
QY 18819 CCAACCGCGCGCTCAACCCCAACCAACCTCAACCCCAACCAACCAACCAACCAAC 18878  
Db 22092 CTCTGTCTCGCGCTCTCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 22151  
QY 18879 CCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 18938

Db	22152	TTGGGAAGGGAACGGTCTTGCTCAACGGGCGACCGGCTCGCTGGCGGCTTGCTGGCCAA	22211
Qy	18939	CGACTTCACCAACCCACCAACCCCAACCAACCTCTCTTACAGCGCAACCGGCCCA	18998
Db	22212	GCACCTGGTTGGCCCGGACCGGGCTCGGGGGGCTGGTGCTCGCAGCCG-----CG	22262
Qy	18999	CACCCCCACGCAACAACTTCAACCAACCACTTCAACAAAGGATCCACTCAACAT	19058
Db	22263	AGGGTGGCCGCGGAAGACTTGGTCAACCGAGCTGACCGAGCGAGGGCGGACGGTGGCT	22322
Qy	19059	CACCACTTGGGACACCAAGCAACCCCAACCACTTCCAAACAATCTTCAACCAATCCCC	19118
Db	22323	GGTGGCTTGGAGGATCTCTCCAGCGGACCA-----GGTGGCGGCTTCTGGC	22370
Qy	19119	ACAACACCCCTTCAACCAACGTCATCCACACCGGAGGATCTCTGACGACGCAACCTTAC	19178
Db	22371	CGAACCCTGGCCGACCGGACTCTGGTCACTCGGCGGGCTCTGGAGACGAGGGTATCGG	22430
Qy	19179	CAACTTCACCCCAACCCMACTCAACAGCTCTTCGCGCCAAAGCCACAGGCGCCACT	19238
Db	22431	AGCCCTGAACCGGAGAGGCTGGCCGGGGGGTTCGCGCCCAAGTGAATGGCTGACGA	22490
Qy	19239	CTTCCACCAACTCAACCCCAACACACCCCTTCAACGCTTCTGTCTTACTTCTTCCGCGC	19298
Db	22491	CTTCGAGAACTGACCCGCAACCTCGGCTCGACGGGTTCTGTGTCTGTCTGTCTGTCCGACG	22550
Qy	19299	CGGCACTTGGGGGCAACCGGGCAAGCACTAAGCGGAGCAAGCAAGCTTACTTGAAGC	19358
Db	22551	CGGCTATAGGAGCTCGCCCGGCGAGGGACTAAGCGGCGCCAAAGCTTCTTGAACG	22610
Qy	19359	CTTGCGCCACACCGGACCAACCAACCACTTCCCGGCAACAGGATCGCTGGGGCACTTG	19418
Db	22611	CTTGAATGGCCGGGGCGCGCGGGGGGGGCTGGCAGAGGCTGTCTGTGGCTGGGGCTGG	22670
Qy	19419	GCAGAAGAACGGAAGCTGGCGACTGGTCAAGTCAAGCAATCTTC-----GCCG	19466
Db	22671	GGAGCAGGCGGAGCGGCTTGACCCGCAACTCAAGCGCAACGACGACGACGACGCGATGAGCG	22730
Qy	19467	CCGGGGGATGTGGCCATGCGCGGCCAGTGGGGGGTCAACAGCTGTGAAGGGGCGATGCG	19526
Db	22731	CGGGGGGCTGTGGCAGTGAACCCGCGGAGGCTTGACATTTGACATGAGCTGGC	22790
Qy	19527	GAGGGGCGCCCGAGTCTCTCGTGGCGCATATTCGACTGGAGAAATTTGGACCGGTTCT	19586
Db	22791	CGCGGAGCAGGCGCTGTGGTCCCGATCAAGCTTGAATCTGGACGACCTGCGGCCAGGC	22850
Qy	19587	CTTCAGCAAGTCTGCGTCTTGTCTGAGAACCTTCCCAAGCAACAGGAACTGAGAGGC	19646
Db	22851	CACGCGGGGGGAGAGGTGCGGACCTGCGGGGCTGTGTCTGGCGAGCGCGCGCT	22910
Qy	19647	GGCGAGTACCGTTTGAAGACAGAGAGACAAACCTTCGCGCACTCTCATGGGTGGTCT	19706
Db	22911	GACCCGCAACGGCTGCGCGGAGTGGCGGGTGGCTGTGTCTCAACACTGCGCGGGGCGC	22970
Qy	19707	ACGTTCCGAGAGGAAGAGAGCTGACGCTGTGTCGATCATCTCGCGGAGTGTCT	19766
Db	22971	AGCCGAAGAGAGGAAAGCTGTGCTGCTGGGCACTGTCTAGGCGGAGCGGCGGGTCT	23030
Qy	19767	CGGGCGGCGACTCCAGGCGCATCCCGCCGGTGGCTGGCTGTTCAGGAGATCAAGGTTTCA	19826
Db	23031	CGGCTTCAAGCGCCCGAGGCTGGCCAGAGGACCCCGGGGTTCAAGGACCTTGGGCTTCA	23090
Qy	19827	CTGGCTTGGCGGGGTGAAGCTTGGCAACCACTTCGACGACAGAGCGAGTGGCTTGGC	19886
Db	23091	CTCCCTGACCGCGGTTCAGGCTGCGGAACCGGCTGAAGCGCGACACCGGGGTCAAAATTGC	23150
Qy	19887	GACGACTCTGTCTTCAATTAACCCAGCGCCACCAAGCTGGCCCAATTTCTGTCTCCGA	19946
Db	23151	CGCCACGCTGTCTTCACTAACCCGAGCGGGTGGGCTGCGCCGCACTTGGCGAAGA	23210
Qy	19947	GATGCGGAGTTCCAGCGCCGACCACTCACTCGCTTCCGCGACCCCGGCGAAGTCTCA	20006

Db	23211	GCTGGGCGAAGCGGTGGCGGGTGGCCGGGCAACGCGGTGAAGACCGTTCGCCGACGCGGG	232170
Qy	20007	TGAGCCGATGCGCATCGTTGGACATGAGCTGTGCTTTCCCGGCGAGTGACTCCGACGGA	20066
Db	23271	CGAGCCGATGCGCATCGTGGGACATGGAGGTGCGGCTTCGCCGGGCGGGTATAGAGCCGGA	23330
Qy	20067	CGACTTGTGGAAATCTGATCTCTCCGAGCAGAGCGGATGGGCGGATTTCCCAACGACCG	20126
Db	23331	CGACTCTGGCGGATGGTTCGCGAGGGGCGCGATGGGAATGTCGCCGTTCCCGAGAGCCG	23390
Qy	20127	CGGCTGGGACCTTGAGCAACGCTTACAGACCCGACCCCGACACGCCCGGACCTGTACAC	20186
Db	23391	CGGCTGGGACCTTGAGCGGCTGTTCATCTGAGCCCGAGCGCGCGGACCGGACCGCTTACAT	23450
Qy	20187	CCGAAAGGCGGGAATTCCTCTACAGACGACGACCTTTCGAGCGCGAATTTCTCGGATCAG	20246
Db	23451	CCGGCAAGGGGCGCTTCTGTGACAGAGGCGGCGCTTTCAGACCGGGGCTTTGGGATCTC	23510
Qy	20247	CCCCCGGAAAGCCCTTGCCATGGAGCCCGGACGACGACTTCTTCCTGAAACGACTGGGA	20306
Db	23511	GC CGCGGAAAGCCCTGGCCATGGAGCCCGAGCAGCGGCTGTGCTGAGAGCTTCCTGGGA	23570
Qy	20307	AACCATGGAACAGCGCGGATTCACCCCGACACCTTCACAGGCAACCCCAACCGGAGTCTT	20366
Db	23571	AGCCTTAGAACCGCGCGGACATGACCCGACCAAGGCGCGCGGAGAGCGCTGTGGGCTTT	23630
Qy	20367	CACCGGACCAAGAGACAGAGACGACGCGGACATCTCGCTAGGCGCCGAGCGGTACGA	20426
Db	23631	CTCGGGGCTTCCATCTCAGCATCTACTCGAGTCTCTGAGCACAATGCCCCGGAAGTCCA	23690
Qy	20427	GGGATGTCCTGACCGGGGCAcCAACAGCATGCGCTTCGCGGAAATCTCTACATCT	20486
Db	23691	AGGCTTCGTCAACAGGCGCACGCGCGGAGAGCGTCCGCTCGGGCGGGGTCTCTACACTT	23750
Qy	20487	CGGGTGGAAAGGCGCTTGGCTACCTTCAGACAGAGGTCTCTCTCGCTGTGCGCT	20546
Db	23751	CGGGTGTGAAGGCGCGCGGCTACAGGTGACAGAGGCTGTCTGTCTCTGTGTGCGAT	23810
Qy	20547	GCACCTCGCGCTGCGAGTCCCTCAGGTTCGGGTGAATGCACATAGGCTTTGAGCGGCGGCG	20606
Db	23811	CCACTTGGCGCACAGGCACTGGCGGAGGGCGAGTGCAGATGAGCCCTTGGCCGGGT	23870
Qy	20607	CACGATCATGACACCCCGATCACTTACCCGAATTCGCGCGGCAACGCGGACTCGCCC	20666
Db	23871	CGCGGTATGGGCGTCCGCGATCGGATGATTCGCGCATGTGCGGCGAGCGCGCATGGCGGA	23930
Qy	20667	CGACGGGCGTTGCAAGGCGTTCTTCGCGCGCGCTGACGATCCGCTGGGGTGAAGGT	20726
Db	23931	GGAAGGCGGGGTCAAGCGTTCGCCCAAGCGCGCGGACCGCACCGTCTCTCCGAAGCGT	23990
Qy	20727	GGGATGCTGTGTGTGAGGGGCTTCCAGCGCGCGCGGACAGGTCACTGTCTCTGGC	20786
Db	23991	CGGATGCTGTCTCTCGAACGGCTTTGTGTGGCCCGGAAACGGGGCACCGGGTGTCTCG	24050
Qy	20787	CGTGTGCGTGGCGAGTGGCTTCAACAGGACGCTGTGAGCAACGATCTGACCGCGCCAA	20846
Db	24051	CGTCTCCGCGGAGCGCGGCTCAACAGAGACGGCGTTTGAACAGGCTACCGCGCCAA	24110
Qy	20847	CGGGCCCTCCAGCAGCGGCTCATTCGCGCAGGCGCTTCGCCAACGCGGAACCTGACCCCG	20906
Db	24111	CGGGCGGTGAGCAGCGGGGTGATTCGCAACGCGCTGCGCGGGCGCGGACTGCAACCTGTC	24170
Qy	20907	CGAGTGTGATCCGTTGAGGCGCAACGCGCACCTGTTGGGGAGACCGATCGAGGCG	20966
Db	24171	CGAAGTGACGCTGTCAGGCGGACCGGCAACCGGACCGCGCTGGGGAGACCCGATTCAGGCG	24230
Qy	20967	CGAGGCAATCTCGCGACTACAGGACGAGACCGTCCCGGCAACGCGCGCTTGTGTGGCG	21026
Db	24231	CGAGGCGCTGTGGCACACTACGGAAGAGCC-----GCGAGAGCGCGTGTGTGCTGGG	24286
Qy	21027	CTCGCTCAAGTCCAGCTCGAACAACAGGCGCGGGCGGGCGTGGCGGAGTATCA	21086
Db	24285	GTCCCTGAAGTCAAACTCGGCGCACCCAGGGCGGCGCGGCGGTGGCGCGCTGATTCAA	24346



OY	21087	GATGATGATGAGCCCTTCGCGCACCGGACATCTCCACCGACTCTCCAGCGGATGAGCCGCT	21146
Db	24345	GATGATCCAGGAGCGCTGCGGACAGCACCTTCGCGCCACCTCCACGATGAGGAAACCCAC	24404
OY	21147	GCCGATGTGACTGATGTCGCGGAGTGGGATGAGCTCTGACGAGACGGATGCGCTGGCC	21206
Db	24405	CAAGAGAGTGGACTGTGTCCGCGGATGGGTGTGATGACTCTCAACGAAGCCGGAGATGGGC	24464
OY	21207	CGGCGGAGGAGGGGCGCGCGCGGCGAGAGTGTATCATTTGGGCTCAGCGGCACCAA	21266
Db	24465	CCGC---AACCGCCACC CGCGCCCGGCGCGGATGTCCTGTCGTTGGGATACGCGGCACAA	24521
OY	21267	CGCCACGTCATCTCTCGAAGAAAGACCCGCGACG--ACGTCGCGGGGGGACACCGCGCC	21324
Db	24522	CGCGACCTCATCTCTGAGAAAGAGGCGCCGCGACAGACCGCGGAGCGGACGTGCCGA	24581
OY	21325	GACGAGATGCGCGTATGTCGCGAGAGCTGTCCCGGCACTGCGGG-----	21373
Db	24582	CGCGGTGGTGCCTCGTGATCTCCGCGCGGACACCGGATCCCTGGCGGGCCAGGCGGG	24641
OY	21374	-----TGCGCGGTGGCTGTGTGTGGGCGCAAGTGCAAGCGGACCTGCGGCCAGGCCCA	21428
Db	24642	ACGCTGGCGGCGTTCTTCAGCGAGACGTCCGCTGACCCGCGTGGCGGTGCCCTGT	24701
OY	21429	GCGCCTGACCGCCACCTCAACCAACCAACCCCGGCTTCGACTGCGCGAGCGTGCATACAC	21488
Db	24702	GTCCAGCCCGGCGAGCGGTACCGACCGGCGCGTGTGTGTGGGGGCTCGGCGAGGAGGC	24761
OY	21489	CC-----TCGCCACCGCGCGCGCGGTTCGACAC-----GCGCCACCTTC	21531
Db	24762	CCGGGCGGGGCTGACCGCGCTGGGCCCGCGGCGAGCGAGCGGCTTGTGACCGGTAC	24821
OY	21532	ATCCCGCGCGACCGCGACACCTTCCTGACAGCACTCCAGGACATCCGCGGAGCGCAACC	21591
Db	24822	CGCAGGATGCTCGGCGAGACAGCGGTCTGGGTTCCTCCGCGCAGGAGACGACATGGGCGGG	24881
OY	21592	CACCCCGCGTCATCCACAGACGCGGCCAGGCG-----GGACCGGAGACGGAGGA	21641
Db	24882	CATGGGCGGGAGGCTCTCCAAAGGTGCCCGGTTTCGCGGAGCGGATTCAGGAATGCGC	24941
OY	21642	GGCGCGAGAAAGACCGGATTCATCTGTCTCGGACAGGGGACCGAAC---GCCCGGCACT	21698
Db	24942	GGCGCGCTGACGCGGTGATCGATCTGTGTCTGTGACTGAGAGTCTCCGTGGGCGAAGTGA	25001
OY	21699	GCGCCAGGCGCTTCACACCAACCCCGCTTCCTGCGCGCGCATCCACAGCATCTGCAC	21758
Db	25002	GCTGGATCGGATCGACGTGCTGCAGCCGGCGTTCCTCGGATGATGTGTGGGCTGGCGCG	25061
OY	21759	CCACTTGACCTCCCACTCGACCAACCCCTTCCTCCCTCTCTACCCAAAGACACACGA	21818
Db	25062	CGTCTGGGCTCTGGATCGGCTGTGCGCGGACGCGGCTCTGGGCACTCCACAGGCGAGAT	25121
OY	21819	CAACGACACAGAGGACCGGCGCGCATCTGCTACAGACACCGGTAAGCCAGCGGCGCT	21878
Db	25122	TGCGCGCGCTCGCTGTGTGGGTGACGTGTCCCTTCAGAGACGACCAAGTGTGTGGCT	25181
OY	21879	CTTGCGCTTCAGGTGCGCTTCACCGGCTCTTCACCGAGCGTACACATCACATCCGCCA	21938
Db	25182	GCGCAGCGCGGATTCGCGCGGAGCTGTGGGCGCGCGGGGATAGGCTGATCAAGCT	25241
OY	21939	CTACTGACGCGGACATCTCCCTCGGCGGAAATCAACGCGCGCACTGTGCGGAGATCTTAC	21998
Db	25242	GAGCCACAGAGGTGGCTGTCCGGCTCTCGCGCTGGGGGGGGCGCGGTGAGATGCGCGC	25301
OY	21999	CCTCACGACGCGCACCTCTCATCAACCAACGCGCACCTTCATGCAACATGATGCCCC	22058
Db	25302	CGTACACGATCCGCGCTCGGTGTGATTCGCGGTGACGCGGAAGCGTCAACCGAAGCGT	25361
OY	22059	CGGACCATGACCACTCTCACACACACCCACACACATATCACCTCACCTCACCGCCA	22118
Db	25362	CGAAGTCTCGCGGCTGGGGGGGTGGGTGATCATAGGTCTCCACACCGGCAAGTGA	25421

QY	22119	CGAAACGACCTGGCCATC-----GGCGCATCAACACCCCACTCCCTCGT	22166
Db	25422	GGAATCTCAGAGACACTCTCCCGAGA CTCTGGCCGGGATCGACGCGACGGCCCCGTGAT	25491
QY	22167	CATCAGCGGACCCCCACACCGTCCAAACATCAACCACTCTGTGCAACAAAGGCAT	22286
Db	25492	GCCCTTCTACTCCACGGTCCGCCGAGTGAATCAACGATGCCGGGGTGTGACGGCCGG	25541
QY	22227	CAAAACCAAAACCTTCCCAACCAACGCTTTCATCTCCCCCAACCAACCCATCCT	22286
Db	25542	GTACTGGTATCCGGAACTCTGGCAACACGAGTCCGCTTTCGCGCGCGCGTGGACGCTGAT	25601
QY	22287	CAACCACTCCACAGACACACCAACCTCACTCACTCAACCAACCCCAACCCCTCAT	22346
Db	25602	CGACCAAGGGACGGGGGTGTTCTGAGAGTCAATGCGCATCCGGTGTGTGACGCTGAT	25661
QY	22347	CACGGCCAAACCCCAACCCGACCAACTCCCACTCCCACTC-----CCCCACTATCTGAGCCA	22397
Db	25662	CAGGAGACTCAACGATGCGGTCTCTACCGGAGCTTGGCGGCGGACGACGGTGGGTGG	25721
QY	22398	ACAAAGCCCGCAACCGTTCAGTACGCAACCAACCAACCCCAACCTTCAACCAACGCGGT	22457
Db	25722	GCGGCTGTGACCTCGATGGCCGAACTGTTGTCGCGGGGTGTCGGGTGATCGGAGCCAC	25781
QY	22458	CACCACTATATGAACTGGAGACCCGACCAACCTCTCAACCTTCAACCTTCAACCACT	22517
Db	25782	GATGGCCCGCGCGCGCGCTCAGGTGCGACCTTACGGCTTTCGACCAACCACTTCTCG	25841
QY	22518	CCCCCAACCCCAACCAACCTTCAACCTTCAACCCCAACCAACCCCAACCAACCCCA	22577
Db	25842	GCTCAGCCCGCGCGCTGGCGGACCGCGCCCGGCTTGGGCTGGCGGCGGACCAACC	25901
QY	22578	CTTCTTCAACCACTTCGCGCAAAACCAACCACTTGGCAACCCCAACCACTACCCACCA	22637
Db	25902	GCTGCTGGGGGCGGTTCTCCGCTGGCGGAGTCCAGCGGCTGAGTTCACCTCCGCGCT	25961
QY	22638	CCACCAACCAACCCCAACCAACCTTCAACCTTCAACCTTCAACCTTCAACCAACCA	22697
Db	25962	GTCGGTCCGACGCGATCCGTGGCTGGCCGACCGCGCTCCCGCGCGCTTGTGTGAAGT	26021
QY	22698	CAACTACTG-----GCTGGAACCTACCAAGGCGCCAAACAGGCCCGGTCAAA	22744
Db	26022	GCGCTGCGGGCGGGTACGAAACCGGTTGCCGGTCTTCCGCACTTACCGTGGAAAA	26081
QY	22745	GCGCTTTCGCGCGCTCGGCTCCAGACACCGCGAGTCCGAGTCTTGGAGCGGCTGAAC-	22803
Db	26082	GCTGCTGTCTCGCGGACGAGCGGTGGCGCTGCGCGTCCAGGTGATCTGTAAGGGGAGGG	26141
QY	22804	-----GAGGAGACTCTCAGAGCTTCGCCAAACCT	22835
Db	26142	CACGGTCAAGGTATTTTCGAGCTCGAAGGCGCGGAAGATCGGAATCCGGAAGCGCACGG	26201
QY	22836	CGACATTCGAGGCTTCTGTCGCAACGAGTGGCCCGCACTCTCCGCTGGCAACGCCA	22895
Db	26202	GCACTGTTCGCAACGCTTCGCGGACGAGGCTTTCGCTTACCGCTTCGCGCGCGC	26261
QY	22896	CCAACGACCAAGCCCGCATCAACCTTGAACCTTACGAGAAACCTGGAAACCCCTCAC	22955
Db	26262	CGAGCCCAAGAGTGAACGGCTCTTGGGGCGGCGGCGACAGATCTTCCGGAAGTGGC	26321
QY	22956	CTTCCCAACCAACCCCAACCCCAACCAACCTTGGCTCATGCTATCCCGAAACCCAGAC	23015
Db	26322	CTTCCGAGAGACTGGAACGCGCGGCGGTTCCGGAATCCACCCCTTCTGTGAGCGGCG	26381
QY	23016	CCACCAACCCCAACATCAACCAATC-----CTCACCAACCTTCAACCAACGGGATCAC	23069
Db	26382	CTGCAACCGGTCTTCGCGGACGACGAGCAGCGCGGAGTGGCCAGCTGTGTCTTCA	26441
QY	23070	CCCCATCCCCCTCATCTGTCAACCAACCCCAACCAACCCCAACCTTCAACCAACCT	23129
Db	26442	CGCGCGGGGTCTTCGGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	26501
QY	23130	CCACCAACCCCAACCAACCAAGCCCAACCAACCAACCAACCCCAACCAACCCCAACCT	23189

Db 26502 GGACGAACCGCGCGGCTGGTCTCTACGGCGGATTCGGTGGCAGCGCCGGGAACCTCTCGGC 26561  
Qy 23190 CCTCTGGCCCTCGACGAACACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCCT 23249  
Db 26562 CGGGAAGACCGCGCGCGGATCGTGTACCGGGTGCATGGAGCGAAGTGTCCATTGACGA 26621  
Qy 23250 CCTCAACCTCACCTCCGCCAAACCCACACCCAAACCCACCCACCCACCCCTCTGGTA 23309  
Db 26622 CAGTCGGGTGCGGCGCAACATCGAGTGGTGGAGCCCTTCGAAGCCCTTCGGTGAAGAGCCCT---GGA 26678  
Qy 23310 CGCCACCAACCAAGCCACCAACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC 23369  
Db 26679 ACTACCGCGCGGCTCTGGAGGTGTGACAGCTTGGTCTGCTACCGCGCGCGATGC 26738  
Qy 23370 CCAAACTGGGGACTCGCGCCACACACCTCTCTGAAACACCCACCCACCCACCCACCCGCG--- 23425  
Db 26739 GCGGCTGGTGTGGTGTGACCGCGGCGCGTGGCGAGTGACGACCCCGCGCGGTGGCG 26798  
Qy 23426 -----GAATCATGACCTCCCAACACCCACCCACCCACCCACCCCTCACAACCTCACCCA 23480  
Db 26799 CGTGGGGCTGGTTCGAGCGCGGAGGAGAAACCCGCTCGCATCTTCTGATCGA 26858  
Qy 23481 AACCTTACCACCCACCAACCAACCCAACTCGCCATCGGACCCGACCCGACCCACAC 23540  
Db 26859 CACCGACGGGAGATCCCGGCCCTGACCGGTGACGAGCCGAGATCGCGGTGCGCGGCGG 26918  
Qy 23541 CCGCGCTCACCCACACCTCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCC 23600  
Db 26919 GAAGTTCTTGTGCGCGCATCTCGCGCGGAGCGGAGCGGCGCGGTGTTCGCGCC 26978  
Qy 23601 CGGAACCACTCATCACCGGGAACCGGCGCCCTCGCCACCCACCTCACCCACCCACCT 23660  
Db 26979 GGACGGGACAGTGTGATCTCGGCGCGGGTGGCTCGGTGGCTGTGGTGGCGCGTCT 27038  
Qy 23661 CACCACCAACCAACCAACCACTCTCTCTACAGCGGAGACCGGCGCCCAACCC 23720  
Db 27039 CGTGAACCGCACCGCGGTGCGGAAGCTGTGTCTGCGGTGCGCGCGCGCGCGGACGCGGA 27098  
Qy 23721 CCAGCGAACACCTCACACCCCAACTCCAACAAAAGGATCCACCTCACCATCACAC 23780  
Db 27099 CGGCGTGGGACCTGTGGCGGACCT-----GGCGGGAGCTGTCCGTGGTGGC 27149  
Qy 23781 CTGCGACACCAAGCAACCCAGACCAACTCCAACAACTCTCAACACCAATCCCGCCCAACA 23840  
Db 27150 TTGGAGCTCTCCGATCGCGCCAGGTGGCGGCTGTCTGAC-----GAGCA 27197  
Qy 23841 CCCCTCACCAACCGTATCCACCGCAGGCGTCAATCTTTCGCGCCCGGTGTGCGAAGC 23900  
Db 27198 CCGGCCGACCCGCTGTGCAACCGCGCGGTTCATCGACCGGCGGTGATCGAGACGCT 27257  
Qy 23901 CGATGCGGAATCTTCTCTCGTTACGGCAGCGAAGCAACGGCGCGGCGGATTCGCA 23960  
Db 27258 GGACCGGACCGGCTGGCCACCGGTTCGCGCCGAAGGTTCAGCGCGTGGCGACCTCGA 27317  
Qy 23961 TGAGTTGCTGGACCATGAACGCTTGAACACTTCAATCTCTCTCTGTCGCGCGCGG 24020  
Db 27318 CGAGCTGACCGCGACCGCGA---CCTCGACGCTTCTGTCTACTCTCTCGGTCTCGGC 27374  
Qy 24021 CGCTTGGGCGAGCGGAATCAGTGGCATACTCGCGCGCAACCGCATACCTTGGACGCGCT 24080  
Db 27375 CGTGTTCATGGCGCGGCGAGCGGAGTTAGCGCGCGCGAAGCGCTTCTTGGACGCGCT 27434  
Qy 24081 CGCAGCGATCTCAGACACATGACTTCCCGGGCATCGATCGCTGGGCGCCCTGGG- 24139  
Db 27435 GATGGGACCGCGGGGGCGGCTTCCGGGCTGTCTGCTGGCGTGGGCGCTGTGGGA 27494  
Qy 24140 -----CCGGAAGGGCATGTGGCGGCTGATCGGCTCATGTTTACCTGGAAGACG 24191  
Db 27495 CCAGAGCACCGGTATGGCCCGCGGACCGACGAGGCGCACCGGGCGCGGATGAGCCGCG 27554  
Qy 24192 CGGATTTCTGCGATGAGACCAACGATGGCGCTCGCGCATTTCCATCGTGGCGGGCGCA 24251

Db 27555 CGGTGGCTGCGAGATCATGACGACGAGCGGCGATGGACCTGTTCAGCGCGCGCTGTC 27614  
Qy 24252 GCGGCCGAATTCCAAACCTGATCATCGGGACATCGACTGGGAGCGCTTCGTCCCGCCTT 24311  
Db 27615 GTCGCCGAGTGTCTGTGGTGGCCGCAAGCTCGACTGCGTGGGTGCGCGCGGACGC 27674  
Qy 24312 CACCGCTCGACGCCACAGCCGCTCATCGAGGACATTCGCGAGGTTCGCGAAGCGGCTCA 24371  
Db 27675 CGCGCGGGGGGTGTGCGCGACAT-----GCTGCTGGCTGTGTCGCGGGGCG 27728  
Qy 24372 GGAGCTGGAAGCAGCTGCGTTCGAGCGGCAAGACACACAGCTCAGCGGATTCGACGTC 24431  
Db 27729 GGCGACGCGCGCGCGGTCCACTG-----TGGACAACGG 27764  
Qy 24432 TCTCCGTGAGCGATTGGCCCGACTGAGGTCTCTAAAGCAGAACACAGGTGCTGCTCGGCT 24491  
Db 27765 GCTGGCCGAGCGGTGCGCGGCTCGCCCGGCGACAGCTCAGCTGCTCTCTGGACT 27824  
Qy 24492 GATTTCGACAGGACATTCGACCGTTCGCGCTTCGTAATCCGGAAGCATCGAGGACCA 24551  
Db 27825 GGTCCGGCGCAGGTGCGCGCGTGTCTGGGACCGCGACCGCGAGCGCTCGCGTGA 27884  
Qy 24552 ACGAGCTTCGCGACCTCGGCTTCGACTCGCTGACGCTCGGCTCAGTTCAGTAAGGAAC 24611  
Db 27885 CACGCGCTTCAAGGACCGCGCTTCGACTCGCTGACCGGTCGAGCTGCGCAACCGCAT 27944  
Qy 24612 CGCCAAAGAAACCGGACTGCGACTCCCGCTCTGCTCTTCGACTATCCACCCCGCA 24671  
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Qy 24672 GGAATGTGTGCCCATCTGCGCACACAACTGTCGACTAGACGACGAAGAGGACGGC 24731  
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13892 CCTCTCTCAACGAGACCGGCAACCGCAGGACACCAACCGCTCGAAGAAG-----CGG 13945  
48798 CCGCGGTTCTGCTGTTGGTTCGAGTATGTCGGCGCGAAGAGTTCGAGGTTGGATCCCTGC 48857  
13946 CCGCACTCTCCAGAGACCGCTACGCGCGCGCGCTCTTCGCTTCAGGTTCCAGGTCGCCC 14005  
48858 GTCGCGCGCGCAAGAGTCGACCTCCGATCTGCTGGCTCTCTGTCGAGTCTGTTGGTGG 48917  
14006 TCCACCGCTCTCTCA-----CGACCGGCTACCAACATCACCCCGCA 14045  
48918 ACAGCGGTTTCGCGAATCCGATCTGCTGGTGGTCGTCAGCGGTGTCAGGCTGTCGCGGACT 48977  
14046 CTAATACCGCGACACTCTCTCGCGAATCACCGCGCGCCACCTCGCGCGGATCTCTCAC 14105  
48978 CCGAATTCGAGCTCGCGACCTGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 49037  
14106 CTTACCGA-----CGCCACCGCTCATACCCNAACCGGCGCACCTCATGCAACCC 14157  
49038 AGTCGGAAGACCCCGGTCGCTTCTGCTGGTGGAGCTGGACGCGCACCTGAGTCTGTCG 49097



Db 51258 GCGTGGTATCCGATCGAGGCGCAGGCGTTGATCGCTACGTACGGCCGGGATCGTGATC 51317  
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Db 51318 CCGGTGGCGGTTGTGGCTGGGTCGGTGAAGTCGAATATGTTGTCACACCGAGGCGCGG 51377  
Qy 16274 CAGGTGTGGCGGGTCTATCAAGATGTGTATGGCGCTGGGAATGGTCTGTGCGCGGA 16333  
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Qy 16394 CGTTCATGTGTATGAGCGCTGCGCGCATGTGCACTGTGTCCGCGGGCGGTGCAAGCTGC 16393  
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Qy 16394 TGACGAGACGCTGCTGTGCGCGCGGAGGCGGTGCGGCGGCGAGGATGTAT 16453  
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Qy 16454 CGTTCCGGGTGAGCGGCACCAAGCCACGTCATCTCTGAAAGAGCACCGGCCACAA 16513  
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Qy 16514 TCCCGTCAGACACACCGCGCAGCAGCGCCCGGAGAGCAGCGCCGACGATGTTCCGG 16573  
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Qy 16574 GGGAAAGCGCGCGGAGCAGCGCGGTACCGCGGGGAAAGCAGTGTCTGTGCGGCA 16633  
Db 51608 GAGTCGACGCTCAACAGAGCGGATTCGG-----GTTCTGTCCGG 51650  
Qy 16634 GTCCAGGGGTGTGGCGGTGTGTGTGCGCCAAAGTCGAGCGCGGCTGTGCGGCCAGG 16693  
Db 51651 ATTTTCCGGTGTGCGGTGTGTGTGCGGCAAAACACCCGAAGCGCTATCCGCCAGG 51710  
Qy 16694 CCCAGCGCTGACGCGCACCTCACGACACCCCGCGCTCGACCTCGCGGAGCTCGGT 16753  
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Qy 16754 ACACCTTCGCCACACCGCGCGGTGTGTGACACCGCGGCCACCTCATCGCGCGGACC 16813  
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Qy 16934 TCTGTCGGGACAGGCGACCCAAACGCGCGGATGGCGCCACCGGCTCTACCAACCCACC 16993  
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Db 52047 TGGCCGGGTACAGATGTTGTC-----CGGTTCGG 52079  
Qy 17114 CGGCGCACTGTCTCAGAGACCCCGGTAGCCCGAGCCCGGCTCTTCGCTTCCAGGTTCG 17173  
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Qy 17174 CCCTCACGCGCTCTCACCGAGCGGTACCAATCACCCCGCACTACTACGCGGACACT 17233  
Db 52140 GACT---CTGGGAGTGTGTGGGTTGTGGGGTGTCCGGCCCGCTGTGTGTGGGCCACT 52196  
Qy 17234 CCCTCGGCGAATACCGCGCGCCACTTCGCGGGATCTCTACCTCTACCGAGCCACA 17293  
Db 52197 CGGTGCGTGTGCGGCGCGGTTTCGCGGTGGAGTGTGTGCTTTCAGAGATGCGGCTC 52256

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Qy 17351 CCCTCCACACACCCCGCCACCATCAGCCAGCAGCTCACCGCCACGAAACGACCTCG 17410  
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Qy 17411 CCATCGCGCGCATCAACACCCCGCCACCTCCCTCGTCATCAGCGGACCCCGCCACACCGTCC 17470  
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Qy 17531 AGCGCTTCACTCCCGCCACCAACCCCATCTCTCAACCAACTCCACGAGACACCCAAA 17590  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2003, 01:00:44 ; Search time 3837 Seconds  
(without alignments)  
18012.465 Million cell updates/sec

Title: US-09-914-286-1  
Perfect score: 30690  
Sequence: 1 gtcagaggatggacggcgg.....acgaagtgagacagcgtga 30690

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

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24: /SID52/gcgdata/geneq/geneq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	30690	100.0	30690 22	AAH79277 Streptomyces averm
2	30672.4	99.9	30690 21	AAA92301 S. avermitilis ave
3	11914.4	38.8	11916 22	AAH79279 Streptomyces averm
4	11548	37.6	12381 21	AAZ58381 Streptomyces averm
5	6437.2	21.0	31422 21	AAA92302 S. avermitilis ave
6	6437.2	21.0	31422 22	AAH79278 Streptomyces averm
7	4347.6	14.2	125401 22	AAD17186 Streptomyces nours
8	3786.2	12.3	65140 22	AAD17184 Streptomyces nours
9	3443.4	11.2	27541 22	AAD17185 Streptomyces nours

10	3399.8	11.1	53789	19	AAV21187	Amvcolatopsis medi
11	3194.8	10.4	49377	19	AAV05287	The soraphen biosy
12	3142	10.2	50000	22	AAF88313	S. spinosa DNA fra
13	3142	10.2	50000	22	AAF88316	S. spinosa DNA fra
14	3142	10.2	80161	20	AAZ21501	DNA fragment of Sa
15	3140.6	10.2	28958	18	AAH89956	Sorangium cellulose
16	3140.6	10.2	28958	21	AAH75299	DNA sequence of So
17	3071.8	10.0	28598	17	AAAT6769	Sorangium cellulose
18	2956.6	9.6	38506	21	AAA75633	Nucleotide sequenc
19	2956.6	9.6	38506	21	AAZ56001	Recombinant codmid
20	2951.8	9.6	37948	21	AAZ87285	S. venezuelae pik
21	2951.8	9.6	37948	21	AAZ87285	S. venezuelae pik
22	2939.8	9.6	36778	21	AAZ87318	Tylosin synthase
23	2847.2	9.3	20394	22	AAE24892	Pimaricin biosynth
24	2663	8.7	44377	18	AAH78508	Platanolide syntha
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26	2545	8.3	77536	21	AAH14651	Nucleotide sequenc
27	2340	7.6	13842	21	AAZ87297	S. venezuelae macr
28	2304.2	7.5	50937	21	AAQ9469	Streptococcus olea
29	2270	7.4	29879	14	AAQ46806	eryA region of S.
30	2188.4	7.1	15872	21	AAZ87283	S. venezuelae vep
31	2180.4	7.1	15872	18	AAH6715	Streptomyces venez
32	2179.4	7.1	47981	22	AAE30757	Micromonospora meg
33	2140.6	7.0	11220	21	AAZ87298	S. venezuelae macr
34	2000.8	6.5	77536	21	AAH14651	Nucleotide sequenc
35	1854.8	6.0	9513	22	AAH88337	S. spinosa DNA fra
36	1852.8	6.0	13987	18	AAH80415	Hybrid armg/tylg O
37	1800.8	5.9	33529	23	AAH17367	DNA sequence of S.
38	1706.4	5.6	14775	22	AAH88338	S. spinosa DNA fra
39	1698	5.5	16767	22	AAH88339	S. spinosa DNA fra
40	1071	3.5	12249	21	AAH55840	Complete Mitomycin
41	1071	3.5	18331	21	AAH55857	Type I polyketide
42	1010.2	3.3	3978	21	AAH55785	Complete nucleotid
43	1007	3.3	71989	21	AAA29349	Sorangium cellulose
44	1004.4	3.3	4041	21	AAZ87300	S. venezuelae macr
45	1004.4	3.3	4818	21	AAH14669	Nucleotide sequenc

ALIGNMENTS

RESULT 1  
AAH79277  
ID AAH79277 standard; DNA; 30690 BP.  
AC AAH79277;  
XX  
XX  
DT 04-DEC-2001 (first entry)  
XX Streptomyces avermitilis coding sequences SEQ ID NO: 1.  
DE  
XX  
XX  
KW Avermectin aglycone synthase; AAS; avermectin derivative;  
drug production; veterinary drug; pesticide; ds.  
XX Streptomyces avermitilis.  
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XX  
XX Key Location/Qualifiers  
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FT /partial  
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XX 30-AUG-2001.  
XX  
XX 23-FEB-2001; 2001WO-JP01381.  
XX  
XX 24-FEB-2000; 2000JP-0047405.  
XX





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QY 8281 ACCCTCATGCAAAACCATGCGCCCGGCAACATGACCCCTTCACACACCGCCCGCAC 8340

Db	8281	ACCCTCATGAAACCATGCCCCCGGACCATGACCAACCTCCACACACACCCCCACCAAC	8340
Qy	8341	ATCACCCACCACTCACCGCCACAGAAAGACACTCGCCATCGCGCGCATCAACACCCCC	8400
Db	8341		8400
Qy	8401	ACCTCCCTCGTCAATCAGCGGCAACCCGCCACACCGTCCAAACATCACCACCCCTCTGCCAA	8460
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Qy	8461	CAACAAAGGATCAAAACCAAAACCTCCGCCACACCGTCCAAACATCACCACCCCTCTGCCAA	8520
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Qy	8521	AACCCCATCCTCAACCAACTCCACGACACACCCCAACCCCTCACCTACCAACCCACCCAC	8580
Db	8521		8580
Qy	8581	ACCCCTCATCACCGCCAAACCCCAACCCGACCAACTCCTCACCCCCCACTACTGGACC	8640
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Qy	8641	CAACAAAGCCGCAACACCGTCACTAGCGCAACACCCCAACCCCTCAACCAACCGGC	8700
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Qy	8701	GTACCACTACATCGAACTCGGACCCGACACACCCCTCACACCCCTCACCCACCAAC	8760
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Qy	8761	CTCCCAACCCCCCAACCAACCTCACCTCACCCCAACCCCAACCCCAACCCCAACCC	8820
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Qy	8821	CACCTCTCAACAACTCGCCAAACCAACCACTGGCAACCCCAACCCCAACCACTA	8880
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Qy	8881	CACGACAAACCCCAACCAACCAACCACTCGACCTCCCAACCTCCCAACCACTCC	8940
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Qy	8941	CACCACTACTGCTCGAAAGCACACAGCCCGTGGCGCAACCTGACGAGCCGGA	9000
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Qy	9001	GACCCCAACCAACCCCAACCAACCACTCGGCGCAACCTGGCAACCTGGCAACCT	9060
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Qy	9061	CTTCTTGAGGGCGCTGTCTTTGAGGTGCGATCCGCTGGCTGACCATGCGCTCGGC	9120
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Qy	9121	GGCAGGTGCTGCTGTCGGGCGCAACCTTCCTCGAACTCGCCCTTCATCGCGGCA	9180
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Qy	9181	GTGGGCTGCGACGAGTGAGCTGACGCTGCAATGCGCGCTCGGTGCTCTGTGGAT	9240
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Qy	9241	GGGGGTGTGAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT	9300
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Qy	9301	AGTGTGTATCGCGGGGTGGAGTGTCTGTGTGTGGGGTGTGTGTGTGTGTGTGT	9360
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Qy	9361	AGTGTGTATCGCGGGGTGGAGTGTCTGTGTGTGGGGTGTGTGTGTGTGTGTGT	9420
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Qy	9481	CGTTTGGCTGCGGGCTGTGTGTGTTTGGGGCCGCTGTTTTCGGGGCTGCGTGC	9540
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Qy	9541	CGTATGCGGGGATTTGCTGGCTGAGGTGTCTGCGGAGGAGGCGTGGGTGATGCG	9600
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Qy	9601	GCTGTTTGGGCTGCACTCCGGCGTCTGCTGATGCTGTGCTGCTGCTGCTGCTG	9660
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Qy	9661	CTTCCGGGTGGGACGGGGTTTGGGGAGGGGCTGCGGGAGGGTGTTCGGGTGCG	9720
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Qy	9721	GCTGTGTGGGTGTGTGTGCTGCTTACCGGGCGGGTGTGACCGGTGTGCGGGTGTG	9780
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Qy	9781	TCGGCTGTGCGGGCGGGCGGGCTGAGGCGGTGTGCGGTGCTGCTGCTGCGGGATG	9840
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Qy	9841	GGTGTGCGGTGGCGTGGGTGAGTTCGAGTTCGGGCTGCGGCTGCGGATGAGGTG	9900
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Qy	9961	GTGGCTCTGTGCGGTGTGCGGCGGTGGCGCTGGGACGAGGACGCTGGGTGAGAGC	10020
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Qy	10321	ACCGACACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGAC	10380
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Qy	10381	CGTGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG	10440
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QY 16141 GGCACCGGACCACTTTTGGGCGACCCGATCGAGGCCCAAGGCCCTCTCGCCACCTACGGA 16200  
DB 16141 GGCACCGGACCACTTTTGGGCGACCCGATCGAGGCCCAAGGCCCTCTCGCCACCTACGGA 16200  
QY 16201 CAGGACCGCCCGCGCAACCGCTGTGGCTGGGCTCGATGMACTGMAAGTGCNAATCGGCCAC 16260  
DB 16201 CAGGACCGCCCGCGCAACCGCTGTGGCTGGGCTCGATGMAAGTGCNAATCGGCCAC 16260  
QY 16261 GCGCAGGCTGCGCAGAGTGTGGCGGGTTCATCAAGATGGTGTGAGTGGCGTTCGGAATGCT 16320  
DB 16261 GCGCAGGCTGCGCAGAGTGTGGCGGGTTCATCAAGATGGTGTGAGTGGCGTTCGGAATGCT 16320  
QY 16321 CTGCTGCGCGGACGTTGCTGATGTGATGAGCGGTGCGGCTGCTGGAATGCTGCGCGGG 16380  
DB 16321 CTGCTGCGCGGACGTTGCTGATGTGATGAGCGGTGCGGCTGCTGGAATGCTGCGCGGG 16380  
QY 16381 GCGGTGACGCTGCTGACGAGACGCTGCGCCCGCGGGAGGGGCGGCTGCGGGCG 16440  
DB 16381 GCGGTGACGCTGCTGACGAGACGCTGCGCCCTGCGCGGGAGGGGCGGCTGCGGGCG 16440  
QY 16441 GCAGAGTGTCTATCGTTTCGGGCTCAGCGGCAACCGCCACGCTCATCTCGAAGAAGCA 16500  
DB 16441 GCAGAGTGTCTATCGTTTCGGGCTCAGCGGCAACCGCCACGCTCATCTCGAAGAAGCA 16500  
QY 16501 CCGCGCCACAACATCCGCTCAGACACACCCCGCGAGAGCGCCCGGAGAGAGCAGCGCC 16560  
DB 16501 CCGCGCCACAACATCCGCTCAGACACACCCCGCGAGAGCGCCCGGAGAGAGCAGCGCC 16560  
QY 16561 GACGATGTTTCGGGGAGAGCGCGGACGACGCGGTACCGGGGGAGAGCAGCTGCT 16620  
DB 16561 GACGATGTTTCGGGGAGAGCGCGGACGACGCGGTACCGGGGGAGAGCAGCTGCT 16620  
QY 16621 CTTGTCGCGGAGCTCAGAGGGTGTGGCGGTGTGCTGGCCAACTCGCAGCGCGCC 16680  
DB 16621 CTTGTCGCGGAGCTCAGAGGGTGTGGCGGTGTGCTGGCCAACTCGCAGCGCGCC 16680  
QY 16681 CTGCGCGCCAGGCGCCAGGCGCTTGCAACCGCACTTACCGGCTCGACCTC 16740  
DB 16681 CTGCGCGCCAGGCGCCAGGCGCTTGCAACCGCACTTACCGGCTCGACCTC 16740  
QY 16741 GCGAGCTGCGGTTACCCCTCGCCACCGCGCGCTGTCGACACCGCGGCGCCCTC 16800  
DB 16741 GCGAGCTGCGGTTACCCCTCGCCACCGCGCGCTGTCGACACCGCGGCGCCCTC 16800  
QY 16801 ATCGCGCGGAGCGGACACCTTCTGCAAGCACTTCCAGGCACTCGCGGAGGCGAAGCC 16860  
DB 16801 ATCGCGCGGAGCGGAGACCTTCTGCAAGCACTTCCAGGCACTCGCGGAGGCGAAGCC 16860  
QY 16861 CACCCGCGCTCATCAACAGAGCGCCCAAGCGGAGCGGAGCGGAGGCGCGAGGA 16920  
DB 16861 CACCCGCGCTCATCAACAGAGCGCCCAAGCGGAGCGGAGCGGAGGCGCGAGGA 16920  
QY 16921 AAGACCGATTTCTGCTGCTGCGGAGAGGCGCCCAAGCGCGGCTGCGGCGCGGCTC 16980  
DB 16921 AAGACCGATTTCTGCTGCTGCGGAGAGGCGCCCAAGCGCGGCTGCGGCGCGGCTC 16980  
QY 16981 TACACACCGGCTGCTGCGCGCGGCTTCAACAGCATCTGACACCTTCAACCTCAGCC 17040  
DB 16981 TACACACCGGCTGCTGCGCGCGGCTTCAACAGCATCTGACACCTTCAACCTCAGCC 17040  
QY 17041 CACCTCGACACCGGCTGCTGCGCGGCTTCAACAGGAGCGGCGGAGCGGAGCGGAGCGG 17100





Db	21421	CAGGCCAGGCGCTGTGACGCCCACTCACCGACACCGCGGCTCGA	21480	QY	22561	CACCAACCCCAACCCACCTCTCACCAACCTCGCAAAACACCA	22620
QY	21481	GGATACACCTCGCCAGCGCGCGGTGTGACCAACCGCGGCA	21540	Db	22561	CACCAACCCCAACCCACCTCTCACCAACCTCGCAAAACACCA	22620
Db	21481	GGATACACCTCGCCAGCGCGCGGTGTGACCAACCGCGGCA	21540	QY	22621	CACCACTACACCCACCAACCAACCCCAACCCCAACCCCAAC	22680
QY	21541	GACCGGCAACCTTCTGCAAGCACTTCCAGGCACTCGCGGAG	21600	Db	22621	CACCACTACACCCACCAACCAACCCCAACCCCAACCCCAAC	22680
Db	21541	GACCGGCAACCTTCTGCAAGCACTTCCAGGCACTCGCGGAG	21600	QY	22681	TACCCCTTCAACACCACTTCTGCTGGAATACCAAGCGGCA	22740
QY	21601	GTCATCCAGAGCGCCCGGAGCGGAGCGGAGCGGAGCGGAG	21660	Db	22681	TACCCCTTCAACACCACTTCTGCTGGAATACCAAGCGGCA	22740
Db	21601	GTCATCCAGAGCGCCCGGAGCGGAGCGGAGCGGAGCGGAG	21660	QY	22741	CAAGGCGTCTCGCGCTCGGCTCGAGACCGCGGAGTCTGGAG	22800
QY	21661	TTTATCTGCTCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	21720	Db	22741	CAAGGCGTCTCGCGCTCGGCTCGAGACCGCGGAGTCTGGAG	22800
Db	21661	TTTATCTGCTCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG	21720	QY	22801	AACGAGGAAGACCTTCCAGAGCTTCCGCGAAACCTTCGAC	22860
QY	21721	CACCCGCTTCTCGCGCGGCACTCAACGACATCTGACCCCA	21780	Db	22801	AACGAGGAAGACCTTCCAGAGCTTCCGCGAAACCTTCGAC	22860
Db	21721	CACCCGCTTCTCGCGCGGCACTCAACGACATCTGACCCCA	21780	QY	22861	ACGCTGTGCGGCACTCTCGGCTTGGGACCGGCAACCAAG	22920
QY	21781	CACCCGCTTCTCGCGCGGCACTCAACGACATCTGACCCCA	21840	Db	22861	ACGCTGTGCGGCACTCTCGGCTTGGGACCGGCAACCAAG	22920
Db	21781	CACCCGCTTCTCGCGCGGCACTCAACGACATCTGACCCCA	21840	QY	22921	ACCTGGAACCTTACAGGAAACCTTGAACCCCTTCCACCA	22980
QY	21841	GCACTGTCTCAGAGCGGAGCGGAGCGGAGCGGAGCGGAG	21900	Db	22921	ACCTGGAACCTTACAGGAAACCTTGAACCCCTTCCACCA	22980
Db	21841	GCACTGTCTCAGAGCGGAGCGGAGCGGAGCGGAGCGGAG	21900	QY	22981	CAAACTTGGCTCATCGGCATCCCGGAAACCCAGACCCCA	23040
QY	21901	CACCGCTTCTCAGAGCGGAGCGGAGCGGAGCGGAGCGGAG	21960	Db	22981	CAAACTTGGCTCATCGGCATCCCGGAAACCCAGACCCCA	23040
Db	21901	CACCGCTTCTCAGAGCGGAGCGGAGCGGAGCGGAGCGGAG	21960	QY	23041	CTGACCACTTCAACAGCGGATCAACCGGATCCGCTTCACT	23100
QY	21961	GGGGAATCAACCGCGGCGGCACTCGCGGCGGATCTTCA	22020	Db	23041	CTGACCACTTCAACAGCGGATCAACCGGATCCGCTTCACT	23100
Db	21961	GGGGAATCAACCGCGGCGGCACTCGCGGCGGATCTTCA	22020	QY	23101	ACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	23160
QY	22021	ATCACCAAGCGGCGGCACTTCAACCACTTCAACCACTTCA	22080	Db	23101	ACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	23160
Db	22021	ATCACCAAGCGGCGGCACTTCAACCACTTCAACCACTTCA	22080	QY	23161	ACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	23220
QY	22081	ACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	22140	Db	23161	ACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	23220
Db	22081	ACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	22140	QY	23221	CACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	23280
QY	22141	GCATCAACACCCCACTTCAACCACTTCAACCACTTCAAC	22200	Db	23221	CACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	23280
Db	22141	GCATCAACACCCCACTTCAACCACTTCAACCACTTCAAC	22200	QY	23281	CAAAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	23340
QY	22201	ACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	22260	Db	23281	CAAAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	23340
Db	22201	ACCAACCCCAACACCTTCAACCACTTCAACCACTTCAAC	22260	QY	23341	AACGACCCCTTCAACCACTTCAACCACTTCAACCACTTCA	23400
QY	22261	CACCTCCCGGCAACCACTTCAACCACTTCAACCACTTCA	22320	Db	23341	AACGACCCCTTCAACCACTTCAACCACTTCAACCACTTCA	23400
Db	22261	CACCTCCCGGCAACCACTTCAACCACTTCAACCACTTCA	22320	QY	23401	CTGAAACACCCCAACCACTTCAACCACTTCAACCACTTCA	23460
QY	22321	TACGACCAACCCCACTTCAACCACTTCAACCACTTCAAC	22380	Db	23401	CTGAAACACCCCAACCACTTCAACCACTTCAACCACTTCA	23460
Db	22321	TACGACCAACCCCACTTCAACCACTTCAACCACTTCAAC	22380	QY	23461	ACCTTCCACCACTTCAACCACTTCAACCACTTCAACCACT	23520
QY	22381	CCCCACTTGGACCAACCACTTCAACCACTTCAACCACTT	22440	Db	23461	ACCTTCCACCACTTCAACCACTTCAACCACTTCAACCACT	23520
Db	22381	CCCCACTTGGACCAACCACTTCAACCACTTCAACCACTT	22440	QY	23521	CGCAACCAACCCCAACCACTTCAACCACTTCAACCACTTCA	23580
QY	22441	CTCCACCAACCGGCGTCAACCACTTCAACCACTTCAACCA	22500	Db	23521	CGCAACCAACCCCAACCACTTCAACCACTTCAACCACTTCA	23580
Db	22441	CTCCACCAACCGGCGTCAACCACTTCAACCACTTCAACCA	22500	QY	23581	CCACCAACCCCAACCACTTCAACCACTTCAACCACTTCAAC	23640
QY	22501	CTCACCAACCACTTCAACCACTTCAACCACTTCAACCACT	22560	Db	23581	CCACCAACCCCAACCACTTCAACCACTTCAACCACTTCAAC	23640
Db	22501	CTCACCAACCACTTCAACCACTTCAACCACTTCAACCACT	22560				





D	b	25801	CTGGGATCCCTCAAAATCGAATCATCGGGCAGCGACAGCGCCCGCGGGCGGTGGCGGAGTCC	25860
Q	y	25861	ATCAAGATGATGATGGCCCTCGCGAAACGGGCTGTGTCACAGACACCTTCCACGTGGACGAG	25920
D	b	25861	ATCAAGATGATGATGGCCCTCGCGAAACGGGCTGTGTCACAGACACCTTCCACGTGGACGAG	25920
Q	y	25921	CCACCCGCCAGTGTGATCTGGTTCACAGGGCGAGTACAATCTCTGACACAACCCGGTGGCC	25980
D	b	25921	CCACCCGCCAGTGTGATCTGGTTCACAGGGCGAGTACAATCTCTGACACAACCCGGTGGCC	25980
Q	y	25981	TGGCCCGCGGACCCGGCCGCGGCGACCGACCGCGCGGTGTTCATCTTGGCGGTGAGC	26040
D	b	25981	TGGCCCGCGGACCCGGCCGCGGCGACCGACCGCGCGGTGTTCATCTTGGCGGTGAGC	26040
Q	y	26041	GGCACCAACGCCACATCATCTCTGAAAGACACCACTCCCGAGGACGAGTACCGAC	26100
D	b	26041	GGCACCAACGCCACATCATCTCTGAAAGACACCACTCCCGAGGACGAGTACCGAC	26100
Q	y	26101	GACGAAACCGGCTGCGAAGCGACCGACCGCGCGGTGTTCATCTTCCCGTGGCGGTG	26160
D	b	26101	GACGAAACCGGCTGCGAAGCGACCGACCGCGCGGTGTTCATCTTCCCGTGGCGGTG	26160
Q	y	26161	TCGGCGAGGTCTGAGGCGGGTTCGGGCGGCGAGCGACAGCGGTTCGCCAGTACGTGGCA	26220
D	b	26161	TCGGCGAGGTCTGAGGCGGGTTCGGGCGGCGAGCGACAGCGGTTCGCCAGTACGTGGCA	26220
Q	y	26221	GCCCGCCGGACATGTCACTCTCGCGACATTTGGTGGGTCTGGCCCGCGCGCGGTGTA	26280
D	b	26221	GCCCGCCGGACATGTCACTCTCGCGACATTTGGTGGGTCTGGCCCGCGCGCGGTGTA	26280
Q	y	26281	CTGGAAACACCGCGCGGTCTCTGGCGCGGACCGCGAGGAACTGGCGCAGGCACTGACA	26340
D	b	26281	CTGGAAACACCGCGCGGTCTCTGGCGCGGACCGCGAGGAACTGGCGCAGGCACTGACA	26340
Q	y	26341	GCCCTGGCGCGCGGAAACCCACCCCACTACACACAGCGACACACCGCGGCGGTGAC	26400
D	b	26341	GCCCTGGCGCGCGGAAACCCACCCCACTACACACAGCGACACACCGCGGCGGTGAC	26400
Q	y	26401	CGCGCGCGGTCTGCTTCTTCCCGGACAGGGCGCGAGTGGCGCGGATGGCGCCTG	26460
D	b	26401	CGCGCGCGGTCTGCTTCTTCCCGGACAGGGCGCGAGTGGCGCGGATGGCGCCTG	26460
Q	y	26461	ACCTGTCTACCTCTTCAACCGGTCTTCGCGGAAACATCGACGATCGGAGAAAGCCCTC	26520
D	b	26461	ACCTGTCTACCTCTTCAACCGGTCTTCGCGGAAACATCGACGATCGGAGAAAGCCCTC	26520
Q	y	26521	ACCCCTTGGGTGCGCTGCTGACCGAATCTCTGCAACCGGACCGCGACCGCGCA	26580
D	b	26521	ACCCCTTGGGTGCGCTGCTGACCGAATCTCTGCAACCGGACCGCGACCGCGCA	26580
Q	y	26581	TGGCAACAGCGAGTGGTTCAGCGGTCTTTCAGCATATGTTCTCTCTCGCGGC	26640
D	b	26581	TGGCAACAGCGAGTGGTTCAGCGGTCTTTCAGCATATGTTCTCTCTCGCGGC	26640
Q	y	26641	CTGTGGCGCTCTTACGCGCATCGAACCGACCGCGCTCTCGCGGCCTCTCTCTCGCGGC	26700
D	b	26641	CTGTGGCGCTCTTACGCGCATCGAACCGACCGCGCTCTCGCGGCCTCTCTCTCGCGGC	26700
Q	y	26701	GCCCGCGCGCATCTCGCGGCACTCAGCGCTGAAAGACCGCGCGCAAAACCGTTGCACTG	26760
D	b	26701	GCCCGCGCGCATCTCGCGGCACTCAGCGCTGAAAGACCGCGCGCAAAACCGTTGCACTG	26760
Q	y	26761	CGACGCGCGACCTGGCGCGGTACAGGCGCGGGCGCCATGCGCTCACTGCCCCCTGCC	26820
D	b	26761	CGACGCGCGACCTGGCGCGGTACAGGCGCGGGCGCCATGCGCTCACTGCCCCCTGCC	26820
Q	y	26821	GCCAGGACGTGACGAGCTCATTTTCGAAACCGGTGGGAGGCGAGTTGTGGGTGGCAGCC	26880
D	b	26821	GCCAGGACGTGACGAGCTCATTTTCGAAACCGGTGGGAGGCGAGTTGTGGGTGGCAGCC	26880
Q	y	26881	CTCAAACCGGCGCGCATCTCAACAACCGTCTCGCGGACACCAAGCGCGGTGATGAGTGTG	26940
D	b	26881	CTCAAACCGGCGCGCATCTCAACAACCGTCTCGCGGACACCAAGCGCGGTGATGAGTGTG	26940



Db 30181 CGCAGCTGGGGTTGACTCGCTCA CGCGGTCGAGCTGCGCAACCGTCTCTACGCGCGCG 30240  
Qy 30241 ACGGGCTCGCGTCGCGCCACGCTTGGCTTCGATTTCCACACCCCGCAGCGCTGCGC 30300  
Db 30241 ACGGGCTCGCGTCGCGCCACGCTTGGCTTCGATTTCCACACCCCGCAGCGCTGCGC 30300  
Qy 30301 GAGCACTTGGCGAGCGTCTGCTTCCGACAGGAGGCCACCGGGCGAGCAAGCCGCGCAT 30360  
Db 30301 GAGCACTTGGCGAGCGTCTGCTTCCGACAGGAGGCCACCGGGCGAGCAAGCCGCGCAT 30360  
Qy 30361 CAGCTCTCCGGCGGAGCGAGAGACGTACGACGCTTCTGACGCTTCGATTCGATTCGCGC 30420  
Db 30361 CAGCTCTCCGGCGGAGCGAGAGACGTACGACGCTTCTGACGCTTCGATTCGATTCGCGC 30420  
Qy 30421 ACGCTGCGGAGCGCGGCTCTCGGCCCCCTGCTCAGCTCGCGGACACGCGCGCGCGC 30480  
Db 30421 ACGCTGCGGAGCGCGGCTCTCGGCCCCCTGCTCAGCTCGCGGACACGCGCGCGCGC 30480  
Qy 30481 GCCTCGGCGCGCGCAGGTCGCGAGGACGCGCGCCCTCCGCGCAGGACACACCGCGCT 30540  
Db 30481 GCCTCGGCGCGCGCAGGTCGCGAGGACGCGCGCCCTCCGCGCAGGACACACCGCGCT 30540  
Qy 30541 CCGCTCTCGATCGACGAGATGACATCGACGACCTGATGATCTGGCGACGCGGATGCGC 30600  
Db 30541 CCGCTCTCGATCGACGAGATGACATCGACGACCTGATGATCTGGCGACGCGGATGCGC 30600  
Qy 30601 ACCGACCGCGCGCTGAGCCCGCAGCGAGGACTCGTCTCATCAGAAACCGGACA 30660  
Db 30601 ACCGACCGCGCGCTGAGCCCGCAGCGAGGACTCGTCTCATCAGAAACCGGACA 30660  
Qy 30661 CACCACACACAGAGGTGAGACAGCGTGA 30690  
Db 30661 CACCACACACAGAGGTGAGACAGCGTGA 30690

RESULT 2

AAA92301  
ID AAA92301 standard; DNA; 30690 BP.  
XX  
AC AAA92301;  
XX  
DT 10-JAN-2001 (first entry)  
DE S. avermitilis avermectin aglycon synthase DNA aveAI SEQ ID NO:1.  
KW Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis;  
KW multifunctional enzyme; polyketide; avermectin; veterinary drug;  
KW agrochemical; ds.  
XX  
OS Streptomyces avermitilis.  
XX  
FH Key Location/Qualifiers  
CDS 1..11919  
FT /\*tag= a  
FT /note= "avermectin aglycon synthase protein"  
CDS 11971..30690  
FT /\*tag= b  
FT /note= "avermectin aglycon synthase protein"  
XX  
PN WO200050605-A1.  
XX  
PD 31-AUG-2000.  
XX  
PF 23-FEB-2000; 2000WO-JP01041.  
XX  
PR 24-FEB-1999; 95UP-0046961.  
XX  
PA (KITA ) KITASATO INST.  
XX  
PI Omura S, Ikeda H;  
XX  
DR WPI; 2000-565458/52.  
P-PSDB; AAB23749, AAB23750.

XX  
PT  
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PT  
XX:  
PS  
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SQ  
Query Match 99.9%; Score 30672.4; DB 21; Length 30690;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 30679; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
Qy 1 GTGCAGAGGATGGACGCGCGGGAAGAACCCCGCCCTCGCGCAGGAGGTCTCGGAGTG 60  
Db 1 GTGCAGAGGATGGACGCGCGGGAAGAACCCCGCCCTCGCGCAGGAGGTCTCGGAGTG 60  
Qy 61 GCCACGAGGCGGACGCGCGCTCTGCTTTTCCCGGCGAGGCGCCCAATGGCG 120  
Db 61 GCCACGAGGCGGACGCGCGCTCTGCTTTTCCCGGCGAGGCGCCCAATGGCG 120  
Qy 121 GGCATGGAGGGAACCTTCGACGCTTCGACGCTTCGCGGAGAGGTCCGCGCTGC 180  
Db 121 GGCATGGAGGGAACCTTCGACGCTTCGACGCTTCGCGGAGAGGTCCGCGCTGC 180  
Qy 181 GAAGCGCGTTTCGCGCCCTACGTCGCTGCTGGTGGAGCAGGTGTTGCGGAGTCTGCGCG 240  
Db 181 GAAGCGCGTTTCGCGCCCTACGTCGCTGCTGGTGGAGCAGGTGTTGCGGAGTCTGCGCG 240  
Qy 241 GACGCTCCGCGGTGGACCGGCTGCGCTGTCAGCGCCCTGTTGCGCGTCAATGATC 300  
Db 241 GACGCTCCGCGGTGGACCGGCTGCGCTGTCAGCGCCCTGTTGCGCGTCAATGATC 300  
Qy 301 TCCCTGCGCGCCCTCTGCGCTCGCAAGGCTCGAGCGGTGCGCGTCTGGGACACAGC 360  
Db 301 TCCCTGCGCGCCCTCTGCGCTCGCAAGGCTCGAGCGGTGCGCGTCTGGGACACAGC 360  
Qy 361 CTGGCGGAGATCGCGGACGCCACGCTCTCGGAGGCTGTCCCTGCGCGACGCCGACGC 420  
Db 361 CTGGCGGAGATCGCGGACGCCACGCTCTCGGAGGCTGTCCCTGCGCGACGCCGACGC 420  
Qy 421 GTGTGAGCGCTTTGGAGCCAGGACAGACACCCCTTGC CGGAGACCGGCGCTCTCTCC 480  
Db 421 GTGTGAGCGCTTTGGAGCCAGGACAGACACCCCTTGC CGGAGACCGGCGCTCTCTCC 480  
Qy 481 GTCCCGCGCACCGCGGATGAGTCTCTGCCCGAATCGCTCGCTGACCGAGGACACCCG 540  
Db 481 GTCCCGCGCACCGCGGATGAGTCTCTGCCCGAATCGCTCGCTGACCGAGGACACCCG 540  
Qy 541 GCGCGGCTCGCGCTCGCAGCGCTCAACGAGCCCGGAGCAGTCGTTTCGCTGCGCGC 600  
Db 541 GCGCGGCTCGCGCTCGCAGCGCTCAACGAGCCCGGAGCAGTCGTTTCGCTGCGCGC 600  
Qy 601 GAGCGCTCGCGGACCTGCTGGCGGACCTCAACCGCGCGAGGTGCGCACGCGCATGATC 660  
Db 601 GAGCGCTCGCGGACCTGCTGGCGGACCTCAACCGCGCGAGGTGCGCACGCGCATGATC 660  
Qy 661 CCGGTGAGCGTTCGCGCGGCTCTCCCGCTGATGATGATGATGATGATGATGATGATGATG 720  
Db 661 CCGGTGAGCGTTCGCGCGGCTCTCCCGCTGATGATGATGATGATGATGATGATGATGATG 720

Avermectin aglycone synthase DNA and proteins encoded by all or part of it for the production of avermectin and its derivatives for drug and agrochemical use

Claim 2; Page 66-134; 314pp; Japanese.

The present sequence represents DNA which encodes avermectin aglycon synthase proteins. Also described are: (1) polypeptides encoded by all or part of the DNA; (2) expression vectors containing the DNA; (3) host cells transformed by the vectors; (4) preparation of the polypeptides by culture of the transformants; (5) preparation of avermectin aglycon or its derivatives by culture of transformed avermectin-producing microorganisms; and (6) oligonucleotides of 5-60 bases in length containing sense or antisense sequences from the avermectin aglycon synthase DNA. The enzymes are useful for the production of modified forms of avermectin and of the intermediates in its biosynthesis, for use as drugs, veterinary drugs and agrochemicals.

Sequence 30690 BP; 5356 A; 12454 C; 8617 G; 4263 T; 0 other;

QY 721 GGCCTGCTGCCATCACCCACGCGCCCTCCCGGATCCCTTCCACTCTCTCGGTGACCGGC 780  
DB 721 GGCCTGCTGCCATCACCCACGCGCCCTCCCGGATCCCTTCCACTCTCTCGGTGACCGGC 780  
QY 781 GCGCGCTCGACACCGCGAGCTAGACGGGGGTACTGTAACGCAACATGTCGAGCAG 840  
DB 781 GCGCGCTCGACACCGCGAGCTAGACGGGGGTACTGTAACGCAACATGTCGAGCAG 840  
QY 841 GTCCGGTTCGAGCCGCGCCCGCGCTTCTGACAGAGGGGCCCAAGAGCTTCGTCGAG 900  
DB 841 GTCCGGTTCGAGCCGCGCCCGCGCTTCTGACAGAGGGGCCCAAGAGCTTCGTCGAG 900  
QY 901 ATGAGCCGACACCGGTGCTGACATGGGCTTCAGAGAGCTCGCCCGGACCTCGGCGAC 960  
DB 901 ATGAGCCGACACCGGTGCTGACATGGGCTTCAGAGAGCTCGCCCGGACCTCGGCGAC 960  
QY 961 ACCACGGCACCGCGACACCTGATCATGGGACGCTCGCGCGCGGCGGACAGGACCCCTG 1020  
DB 961 ACCACGGCACCGCGACACCTGATCATGGGACGCTCGCGCGCGGCGGACAGGACCCCTG 1020  
QY 1021 GACCACTTCTGACGTCTCTGCCCAACTACGGGGGCACTGGTGAACAGCTCGGCGACCA 1080  
DB 1021 GACCACTTCTGACGTCTCTGCCCAACTACGGGGGCACTGGTGAACAGCTCGGCGACCA 1080  
QY 1081 GTCTCTCGGACAGCTGACCGGTGTCCCGACGACAGAGAGTGGTCTCTGAGAC 1140  
DB 1081 GTCTCTCGGACAGCTGACCGGTGTCCCGACGACAGAGAGTGGTCTCTGAGAC 1140  
QY 1141 CTGGTGGCGCCACACCATGCGGTGCTGAACAGACGACGGAAACGAGCGCACCGGTG 1200  
DB 1141 CTGGTGGCGCCACACCATGCGGTGCTGAACAGACGACGGAAACGAGCGCACCGGTG 1200  
QY 1201 GATGCGGCGCCATCGGCGAGTTTCGCCACCTCGGCTTCGATCTCGGTATGGGTGCGAA 1260  
DB 1201 GATGCGGCGCCATCGGCGAGTTTCGCCACCTCGGCTTCGATCTCGGTATGGGTGCGAA 1260  
QY 1261 CTGGCAACCGCTGACGAGGCGACGGGCTTCGGTTCGGGTGACCGTCTATCTTCGAC 1320  
DB 1261 CTGGCAACCGCTGACGAGGCGACGGGCTTCGGTTCGGGTGACCGTCTATCTTCGAC 1320  
QY 1321 CACACACCGCGCGCGGTGCGCGGCTTCGGACCGCGCGGCTCGGCAACCTCGAC 1380  
DB 1321 CACACACCGCGCGCGGTGCGCGGCTTCGGACCGCGCGGCTCGGCAACCTCGAC 1380  
QY 1381 GAGGACACCGCGCGGTACCGGACTCACCGAGCGCCACGAGGACAGCGCGCGGAC 1440  
DB 1381 GAGGACACCGCGCGGTACCGGACTCACCGAGCGCCACGAGGACAGCGCGCGGAC 1440  
QY 1441 GACCGGATCGGCATCATCGGCATGGCATGCCGTTTCCCGGGCGGAGTCCGGTCCCGAAG 1500  
DB 1441 GACCGGATCGGCATCATCGGCATGGCATGCCGTTTCCCGGGCGGAGTCCGGTCCCGAAG 1500  
QY 1501 GACCTGTGGAGCTGGCGCTCGGGCGGAGAGCGCATCGGGCGGTTCCCGACCGACCGC 1560  
DB 1501 GACCTGTGGAGCTGGCGCTCGGGCGGAGAGCGCATCGGGCGGTTCCCGACCGACCGC 1560  
QY 1561 GGATGGCCCAACGAGGTCACGCCACGAGACCCCAACGAGCGCGGACGTTCTATCG 1620  
DB 1561 GGATGGCCCAACGAGGTCACGCCACGAGACCCCAACGAGCGCGGACGTTCTATCG 1620  
QY 1621 CAGGAGGCGGTCTCTTCAACGCGGCGCACTTCGACCGCGGTCTTCGGAATCAAT 1680  
DB 1621 CAGGAGGCGGTCTCTTCAACGCGGCGCACTTCGACCGCGGTCTTCGGAATCAAT 1680  
QY 1681 CCACGTGAGGCACTGGCGATGATCCGACGAGCGCTGCTGCTGGAGAGCGTCTGGGAG 1740  
DB 1681 CCACGTGAGGCACTGGCGATGATCCGACGAGCGCTGCTGCTGGAGAGCGTCTGGGAG 1740  
QY 1741 GCGTTTCGAGCGGCGGAATCGATCGCTGTGCTACGCGGTTCGCTACGCGGTCTTC 1800  
DB 1741 GCGTTTCGAGCGGCGGAATCGATCGCTGTGCTACGCGGTTCGCTACGCGGTCTTC 1800  
QY 1801 GCGGGCGCCCTCTCTTCCGATACGCGCCCGGATAGGACACCGCGTCTCGAGGGCGCC 1860

DB 1801 GCGGGCGCCCTCTCTTCCGATACGCGCCCGGATAGGACACCGCGTCTCGAGGGCGCC 1860  
QY 1861 GCGACGTGGAGGGCACATCTCACCGGTACACGGGACAGCTCTCTCGGGCGGTATC 1920  
DB 1861 GCGACGTGGAGGGCACATCTCACCGGTACACGGGACAGCTCTCTCGGGCGGTATC 1920  
QY 1921 GCCTACAGCTTCGGGCTGGAAGGCGGCGATCACCGTGGACACGGGCTGCTCGGCATCG 1980  
DB 1921 GCCTACAGCTTCGGGCTGGAAGGCGGCGATCACCGTGGACACGGGCTGCTCGGCATCG 1980  
QY 1981 CTGCTGACGTGTCATCTGGCGTGCAGTCTGGCTCGGCTCGGCTGAGTGCACGCTCGGGCTG 2040  
DB 1981 CTGCTGACGTGTCATCTGGCGTGCAGTCTGGCTCGGCTCGGCTGAGTGCACGCTCGGGCTG 2040  
QY 2041 GCGGCGCGCTCTCGGTCTGTCACCTCGGCATGTTTCATCGAGTCTCTCCGGCAGCGC 2100  
DB 2041 GCGGCGCGCTCTCGGTCTGTCACCTCGGCATGTTTCATCGAGTCTCTCCGGCAGCGC 2100  
QY 2101 GGGCTGTCTGGTGGACGAGTCAAGCGTACTCGGCTGACGCGGACCGGCTGG 2160  
DB 2101 GGGCTGTCTGGTGGACGAGTCAAGCGTACTCGGCTGACGCGGACCGGCTGG 2160  
QY 2161 GCGAGGGCGCTCGGATCTGTTGGTGGAGCGGTTCGCGATGCGGCTCGGGCTGGGGCAT 2220  
DB 2161 GCGAGGGCGCTCGGATCTGTTGGTGGAGCGGTTCGCGATGCGGCTCGGGCTGGGGCAT 2220  
QY 2221 CGGGTGTGGCGGTGGTACGCGGAGTCCGCTCAACAGGACGCTGCGATCGAATGGGCTG 2280  
DB 2221 CGGGTGTGGCGGTGGTACGCGGAGTCCGCTCAACAGGACGCTGCGATCGAATGGGCTG 2280  
QY 2281 ACGGCGCGAACCGTTCGGCTCAGAGCGGTGATCGGCGAGGCGTTGCGCAACCGGG 2340  
DB 2281 ACGGCGCGAACCGTTCGGCTCAGAGCGGTGATCGGCGAGGCGTTGCGCAACCGGG 2340  
QY 2341 TTGTCGTGGCGGATGTTGGATGTTGGTGGAGGGGACCGGACCGGACACGCTGGGTGAT 2400  
DB 2341 TTGTCGTGGCGGATGTTGGATGTTGGTGGAGGGGACCGGACCGGACACGCTGGGTGAT 2400  
QY 2401 CCGATCGAGGACAGGCGTTGCTCGCACGTTACGGGACCGGCGGCTGACAGCGCGGTG 2460  
DB 2401 CCGATCGAGGACAGGCGTTGCTCGCACGTTACGGGACCGGCGGCTGACAGCGCGGTG 2460  
QY 2461 TGGCTGGGGTCTCTGAAGTCCAACATCGGGCACACCATGGCTGCGCGGCTGGGTGG 2520  
DB 2461 TGGCTGGGGTCTCTGAAGTCCAACATCGGGCACACCATGGCTGCGCGGCTGGGTGG 2520  
QY 2521 GTCATCAAGATGTTGATGGCGTTGGGAGGGGGTGTTCGCGGACGCTTGCATGTGGAT 2580  
DB 2521 GTCATCAAGATGTTGATGGCGTTGGGAGGGGGTGTTCGCGGACGCTTGCATGTGGAT 2580  
QY 2581 AAGCGCTCGCGCAGGTGAGTCTCGCGGGGGGCTCGGCTGCTCACGAGGCGGTG 2640  
DB 2581 AAGCGCTCGCGCAGGTGAGTCTCGCGGGGGGCTCGGCTGCTCACGAGGCGGTG 2640  
QY 2641 CCGTGGCGGGGACGCGGACAGGCGGTTCGCGGGGCGGAGTGTCTGTTGGGATC 2700  
DB 2641 CCGTGGCGGGGACGCGGACAGGCGGTTCGCGGGGCGGAGTGTCTGTTGGGATC 2700  
QY 2701 GCGGCAACGATGCGCATGTAATTTGGAGAGGCGCGCGGCGGGGGCTGTGTGGC 2760  
DB 2701 GCGGCAACGATGCGCATGTAATTTGGAGAGGCGCGCGGCGGGGGCTGTGTGGC 2760  
QY 2761 GGGGTGGGGTGGAGGGGCTCGGGTCTTCCATTTTGGTGGCTGAGTTCGGTGGCC 2820  
DB 2761 GGGGTGGGGTGGAGGGGCTCGGGTCTTCCATTTTGGTGGCTGAGTTCGGTGGCC 2820  
QY 2821 GCTCAGTGGGTGTCTGCGCGCGGTGCTGAGTGGGTGCGGGTGCCTGCGGTGCGG 2880  
DB 2821 GCTCAGTGGGTGTCTGCGCGCGGTGCTGAGTGGGTGCGGGTGCCTGCGGTGCGG 2880  
QY 2881 GTTCTGTGCGGTGTGCGGTGAGTCTGAGGCTGGGTTCGCGGCGGACGCGGAGGCGGTG 2940



D	b	2881	GTTCTGTGCCGGTGTCCGCTAGAGTCTGAGCGTCGGGTTCGGCGCAGCGAGCGCGCTTG	2940
Q	y	2941	CGTCAGTAGCTGGCAGTCCGGCCCGGACGTTTTTCGCTTCGCCATGTGGGTGC GG GTCTCGGCC	3000
D	b	2941	CGTCAGTAGCTGGCAGTCCGGCCCGGACGTTTTTCGCTTCGCCATGTGGGTGC GG GTCTCGGCC	3000
Q	y	3001	TGTGGCGGGCTGTGCTGTGAACATGTGCGGTCTCTCTGGCCGCGAACCTGTGAGGAGCTG	3060
D	b	3001	TGTGGCGGGCTGTGCTGTGAACATGTGCGGTCTCTCTGGCCGCGAACCTGTGAGGAGCTG	3060
Q	y	3061	GTGCAGGGTTGGGGCGCTGGCGCGGGTGAGCCGATCGGCGGGTGACCA CGSGT CAT	3120
D	b	3061	GTGCAGGGTTGGGGCGCTGGCGCGGGTGAGCCGATCGGCGGGTGACCA CGSGT CAT	3120
Q	y	3121	CGCCCGGGTGTGACCGGGGCGGTGTGCTCTTTCGTGTTC CCGCACAGG GTGGG CAG TGG	3180
D	b	3121	CGCCCGGGTGTGACCGGGGCGGTGTGCTCTTTCGTGTTC CCGCACAGG GTGGG CAG TGG	3180
Q	y	3181	CGCGGGATGGGTGTGCTGTGCTCGCTCTCTCCGCTGTTC CCGCGCGAATGC A GCGG	3240
D	b	3181	CGCGGGATGGGTGTGCTGTGCTCGCTCTCTCCGCTGTTC CCGCGCGAATGC A GCGG	3240
Q	y	3241	TGCGAGGAGCTCTGGCGCGCTGGTGGCATGTGCTTCAGCTGTGCTGGGACATCTCTGGCGGGAC	3300
D	b	3241	TGCGAGGAGCTCTGGCGCGCTGGTGGCATGTGCTTCAGCTGTGCTGGGACATCTCTGGCGGGAC	3300
Q	y	3301	CGCGGGATGGGTGTGGAGCGGGCGCATGTGCTTCAGCTGTGCTGGTTCAGCGT CATG	3360
D	b	3301	CGCGGGATGGGTGTGGAGCGGGCGCATGTGCTTCAGCTGTGCTGGTTCAGCGT CATG	3360
Q	y	3361	GTGTCTTTGGTGTCTGTGSCGTTCTTA CGGTATCGAA CCGACGCGTCTTTGGCCAT	3420
D	b	3361	GTGTCTTTGGTGTCTGTGSCGTTCTTA CGGTATCGAA CCGACGCGTCTTTGGCCAT	3420
Q	y	3421	TCCAGGCGGAGATCGCGCGCGCCATGTGTGTGGCGCTGAGCTGAAAGAGCAGCGCG	3480
D	b	3421	TCCAGGCGGAGATCGCGCGCGCCATGTGTGTGGCGCTGAGCTGAAAGAGCAGCGCGCG	3480
Q	y	3481	AAGACTGTTGGCTGCGCAGCGGGCGCTGCGCTGTGCGGGCGCGGGCGCGCATGGCC	3540
D	b	3481	AAGACTGTTGGCTGCGCAGCGGGCGCTGCGCTGTGCGGGCGCGGGCGCGCATGGCC	3540
Q	y	3541	TCAGTGCCTGCTGCCCCAGGAGTGAGCAGCTCATTTGGTTCAGCGGTGGCGGGCGCG	3600
D	b	3541	TCAGTGCCTGCTGCCCCAGGAGTGAGCAGCTCATTTGGTTCAGCGGTGGCGGGCGCG	3600
Q	y	3601	TTGTGGGTGGCGCGGTCAA CGGCCCGCTCAACCGCCGTCTCTGGGGGATGCCAGAGCG	3660
D	b	3601	TTGTGGGTGGCGCGGTCAA CGGCCCGCTCAACCGCCGTCTCTGGGGGATGCCAGAGCG	3660
Q	y	3661	GTGACAGAGTGTGGGTGACTGTGCGCGGACCGGGGTGCGGGCGCGCGGATCCCGGTCT	3720
D	b	3661	GTGACAGAGTGTGGGTGACTGTGCGCGGACCGGGGTGCGGGCGCGCGGATCCCGGTCT	3720
Q	y	3721	GACTATGCTCGCACTGCCCCCATGTGCAGCCCCCTGCGGGAGGAGTTGCTGAGAGTCTCTG	3780
D	b	3721	GACTATGCTCGCACTGCCCCCATGTGCAGCCCCCTGCGGGAGGAGTTGCTGAGAGTCTCTG	3780
Q	y	3781	GGGAGCATACAGCCC CGAGCTCGGCGTGTGCTTCTTCACAGGTGAGAGGACA CTG G	3840
D	b	3781	GGGAGCATACAGCCC CGAGCTCGGCGTGTGCTTCTTCACAGGTGAGAGGACA CTG G	3840
Q	y	3841	CTGGACACCACAACCTCTGGAGCGCGCTACTGTTACCGCAACTGCACCGAGCGGTCCGT	3900
D	b	3841	CTGGACACCACAACCTCTGGAGCGCGCGCTACTGTTACCGCAACTGCACCGAGCGGTCCGT	3900
Q	y	3901	TTACAGCGATGCGTTCAGGCGCTGGCGGATGACGGACACCGCGCTCTTCTGTCGAGAGTCAGC	3960
D	b	3901	TTACAGCGATGCGTTCAGGCGCTGGCGGATGACGGACACCGCGCTCTTCTGTCGAGAGTCAGC	3960
Q	y	3961	CCCCACCCACCTCTGTC CGCGCATCGAAGACACCA CCGAAGACACCGCCGAGAGCTG	4020
D	b	3961	CCCCACCCACCTCTGTC CGCGCATCGAAGACACCA CCGAAGACACCGCCGAGAGCTG	4020

QY	4021	ACCGGATCGGCAGCTTCGCGCGGGCGGACAA	CGACACCGCGCGCTTCTCACCGCGCTC	4080
DB	4021	ACCGCGATCGCGAGCTTCGCGCGGGCGAACA	CGACACCGCGCGCTTCTCACCGCGCTC	4080
QY	4081	GCCACACCCATACCAACGGCATCGGCACAC	CCACACCTGGCACCACTACACCCAC	4140
DB	4081	GCCACACCCATACCAACGGGATCGGCACAC	CCACACCTGGCACCACTACACCCAC	4140
QY	4141	CACACACCCACACCCCAACCCCAAC	CCCAACCTGACACCTTCCAACTC	4200
DB	4141	CACACACCCACACCCCAACCCCAAC	CCCAACCTGACACCTTCCAACTC	4200
QY	4201	CAGCACTACTGGCTCGAGAGCTCACACCG	GGTTCGGGTTCGGGTTCGGGTTCGGGTTC	4260
DB	4201	CAGCACTACTGGCTCGAGAGCTCACACCG	GGTTCGGGTTCGGGTTCGGGTTCGGGTTC	4260
QY	4261	GGTTCGGGTTCGGGTTCGGGTTCGGGTTC	GGGTTCGGGTTCGGGTTCGGGTTCGGGTTC	4320
DB	4261	GGTTCGGGTTCGGGTTCGGGTTCGGGTTC	GGGTTCGGGTTCGGGTTCGGGTTCGGGTTC	4320
QY	4321	CGGTTCTGGGACGGGTGGCGCGCAGGACT	CTGGAAACGGTTCGGACACACTGGCGGTG	4380
DB	4321	CGGTTCTGGGACGGGTGGCGCGCAGGACT	CTGGAAACGGTTCGGACACACTGGCGGTG	4380
QY	4381	CCCCCTTCGCGCGCTTGACACGGTGGTGC	CGCGACTCTCTCGCTTCGGCACCGCCACCA	4440
DB	4381	CCCCCTTCGCGCGCTTGACACGGTGGTGC	CGCGACTCTCTCGCTTCGGCACCGCCACCA	4440
QY	4441	CAGCAACAAGCCGCGCATCAACACTTGGAC	CTTACAGGAAACCTGGAAACCCCTCACCCCTC	4500
DB	4441	CAGCAACAAGCCGCGCATCAACACTTGGAC	CTTACAGGAAACCTGGAAACCCCTCACCCCTC	4500
QY	4501	CCGACACCCACCAACCCCAACCAACCTGG	CTCATCGGCATCCCGGAAACCCGACGCGAC	4560
DB	4501	CCGACACCCACCAACCCCAACCAACCTGG	CTCATCGGCATCCCGGAAACCCGACGCGAC	4560
QY	4561	CACCCCACTACCAACATCTCTCACCAACCT	CCACACCGGACCTCACCCCGCATCCCC	4620
DB	4561	CACCCCACTACCAACATCTCTCACCAACCT	CCACACCGGACCTCACCCCGCATCCCC	4620
QY	4621	CTCACCTTAACACACCGACACCCCGCAAC	CTCGACACGCTTCACACGCTTCACACAC	4680
DB	4621	CTCACCTTAACACACCGACACCCCGCAAC	CTCGACACGCTTCACACGCTTCACACAC	4680
QY	4681	CGACAAAGCCCAAAACCAACACACCGGAG	CCATCACCGGCTGTCTCTCCCTTCCTCGCC	4740
DB	4681	CGACAAAGCCCAAAACCAACACACCGGAG	CCATCACCGGCTGTCTCTCCCTTCCTCGCC	4740
QY	4741	CTGGAAGAAACACCCCAACCCCAACCAAC	CCCAACGCTTCCTTCACACCTC	4800
DB	4741	CTGGAAGAAACACCCCAACCCCAACCAAC	CCCAACGCTTCCTTCACACCTC	4800
QY	4801	ACCTCAACCCAAACCCCAACCCCAACCCCA	ACCCCTCTGGTACGCGCACCC	4860
DB	4801	ACCTCAACCCAAACCCCAACCCCAACCCCA	ACCCCTCTGGTACGCGCACCC	4860
QY	4861	AAGCCCAACCAACCCCAACCCCAACCCCA	ACCCCTCACACCCCAACCCCAACCTTG	4920
DB	4861	AAGCCCAACCAACCCCAACCCCAACCCCA	ACCCCTCACACCCCAACCCCAACCTTG	4920
QY	4921	GGACTCGCCCGACGACCTCTCTGAAACAC	CCCCCAGCCCAACCTTCGACCTC	4980
DB	4921	GGACTCGCCCGACGACCTCTCTGAAACAC	CCCCCAGCCCAACCTTCGACCTC	4980
QY	4981	CCCAACACCCCAACCCCAACCCCAACCCCA	ACCTTCAGCACTTCAACCCCAACCCCA	5040
DB	4981	CCCAACACCCCAACCCCAACCCCAACCCCA	ACCTTCAGCACTTCAACCCCAACCCCA	5040
QY	5041	CACAAACCCCAACTGGCATTCGCAACCGG	CAACCGGCAACCTTCACCCCAACCCCA	5100
DB	5041	CACAAACCCCAACTGGCATTCGCAACCGG	CAACCGGCAACCTTCACCCCAACCCCA	5100



Db 7261 CCGCTGTGGCTGGCTGGCTCAAGTCCAATGTGGTCAACACAGGCTGCCGCGGGCTC 7320  
Qy 7321 GCGGGGTGATCAAGATGTGATGCGCTGCGGATGCTGCTGCCGCGGAGCTTGAT 7380  
Db 7321 GCGGGGTGATCAAGATGTGATGCGCTGCGGATGCTGCTGCCGCGGAGCTTGAT 7380  
Qy 7381 GTGGATGAGCGCTGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7440  
Db 7381 GTGGATGAGCGCTGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7440  
Qy 7441 ACGGTGTGCTGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7500  
Db 7441 ACGGTGTGCTGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7500  
Qy 7501 GTGAGGACCAACGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7560  
Db 7501 GTGAGGACCAACGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7560  
Qy 7561 GGACCAACCGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7620  
Db 7561 GGACCAACCGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7620  
Qy 7621 GGGGTGTGCTGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7680  
Db 7621 GGGGTGTGCTGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7680  
Qy 7681 GCGCTGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7740  
Db 7681 GCGCTGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7740  
Qy 7741 CTGCGCGCATGTGACTGGTCCGCGGGTGCAGTGTGCTGACGGAG 7800  
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Qy 7861 AGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7920  
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Qy 8221 GCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8280  
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Qy 8341 ATACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8400  
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Qy 8401 ACCTCCCTGCTCATCAGCGGCAACCCCAACCGTCCAAACACATCACACCGCTCTGCCAA 8460  
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Qy 8581 ACCCCCTCATCAGCGGCAACCCCAACCGTCCAAACCGTCTCATCTACCAACCGGCG 8640  
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QY 10561 CGGTGGTTGATGTATCGGGTCCGGAGGTGTTGCGGTGTGTGCGGTGGGTGGTGG 10620  
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QY 10621 GTGACGGGTGGAGCGGGTGTGCTGGTGCGGGTGGCGCGGATCTGGCTGGTGTGTGT 10680  
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QY 10621 GTGACGGGTGGAGCGGGTGTGCTGGTGCGGGTGGCGCGGATCTGGCTGGTGTGTGT 10680  
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QY 10681 GGGGTGCGGGATCTGCTGTTTGGTGAGCGGGTGTGCTGGATGTCTCCGGTGGCGAGGT 10740  
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QY 10681 GGGGTGCGGGATCTGCTGTTTGGTGAGCGGGTGTGCTGGATGTCTCCGGTGGCGAGGT 10740  
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QY 10741 CTGGGGCGGAGCTGGCCCGCTTGGGGCGGAGGTGGGATGTTGCTGTGTGATGTGGG 10800  
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QY 10741 CTGGGGCGGAGCTGGCCCGCTTGGGGCGGAGGTGGGATGTTGCTGTGTGATGTGGG 10800  
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QY 11401 CTGACGCGCGCTGCGCGCGGACACACGAAACAGCACACACCTCTCTCGCCCTG 11460  
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QY 11641 ACCCTCA CCGCACCACTCCACACAACTCAGGCCACAAACCGGACAA CCGTGTGCGCCC 11700  
DB |||||





QY 13861 CTGAGCCCCACCTCGACACACCCCTCTCTCCCTCTCTCTCAACCGAGACCCCAACACCCAG 13920  
DB 13861 CTGAGCCCCACCTCGACACACCCCTCTCTCCCTCTCTCTCAACCGAGACCCCAACACCCAG 13920  
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DB 13921 GACACACACCTCGAAGAGGCGGCGCACTGCTCCAGCAGACCGCTACGCCAGGCC 13980  
QY 13981 GCCCTTTCCGCTTCAGGTGCGCTTCAACCGCTCTCTCAACCGAGGCTTACACATCAC 14040  
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DB 14401 CTCGACGAGCAACCCAAACCTCTACCTAACACCAACCGCGCTCAACACCTTCAACCAA 14460  
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DB 14461 AACACCCACCGGACCACTCTACCCCGCATTAACACCCCTCTCTCTCAACCAAACCGCGCAC 14520  
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DB 14521 GTGAGCTAGCGCAACCAACCGCTTCACTCCCGCGCATTAACACCCCTCTCTCTCAACCAA 14580  
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DB 15001 GTTCCGAACAAGGCCCTTCAAGAGCTGGTGTGATTTCTCTCGCGCAATTCAGCTTGT 15060  
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QY 15361 AACCGGACCGGACCAACCGAGCACAGCTTACCCCGGCGGCGGATTCCTTTACGAC 15420  
DB 15361 AACCGGACCGGACCAACCGAGCACAGCTTACCCCGGCGGCGGATTCCTTTACGAC 15420  
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QY 15661 GGCAGTATCGCTCGGCTGCTGCTTACGCTTCTCGGCTGGAAGGTTCCGCGCTTCA 15720  
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QY 15961 TCGAGCGGCTGAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 16020  
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QY 16021 CAGACGCTGCGAGCAACGCGCTGAGCGCGCCCAACGCGGCGCTGCCAGAGGCTGCTCATC 16080





Db	20401	ATCCGTACGGCCCGGAGCGGTACCGAGGATTCGTCTTCAACCGGGGAGCCACCAAGCATC	20450
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Db	20461	GCCTCGGCGCGAATCTCTACATCTCTCGGTTGGAGGCGCTGCGGTACACCTTCGACACA	20520
Qy	20521	GGGTGTTCTCTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGA	20580
Db	20521	GGGTGTTCTCTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGA	20580
Qy	20581	TGACCATGCGCTTGGCGCGGCGGCGCACGGTATGACACACCCCGATCATCTTCCACGAA	20640
Db	20581	TGACCATGCGCTTGGCGCGGCGGCGCACGGTATGACACACCCCGATCATCTTCCACGAA	20640
Qy	20641	TTTGGCCGCGCAACGGGACTCGCCCGGACGGCGGTTGCAAGCGGTTCTCGGGCGGCT	20700
Db	20641	TTTGGCCGCGCAACGGGACTCGCCCGGACGGCGGTTGCAAGCGGTTCTCGGGCGGCT	20700
Qy	20701	GACGGTACCGGCTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGG	20760
Db	20701	GACGGTACCGGCTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGG	20760
Qy	20761	CGCGCAACGGTCAACGGTCTCTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGG	20820
Db	20761	CGCGCAACGGTCAACGGTCTCTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGG	20820
Qy	20821	GGAGCAACGGTCTGACCGCGCGCCCAACGGCGGCTTCCAGCAGCGGTATCGCGCAGGCG	20880
Db	20821	GGAGCAACGGTCTGACCGCGCGCCCAACGGCGGCTTCCAGCAGCGGTATCGCGCAGGCG	20880
Qy	20881	CTCGCCCAACCGGACTGACCGCGCGCCCAACGGCGGCTTCCAGCAGCGGTATCGCGCAGGCG	20940
Db	20881	CTCGCCCAACCGGACTGACCGCGCGCCCAACGGCGGCTTCCAGCAGCGGTATCGCGCAGGCG	20940
Qy	20941	ACCACTTTGGGGGAGCCGATCGAGGCGCCAGGCGCATCTCGGACCTTACGACAGGCGT	21000
Db	20941	ACCACTTTGGGGGAGCCGATCGAGGCGCCAGGCGCATCTCGGACCTTACGACAGGCGT	21000
Qy	21001	CCCGGCAACGGCGCGTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG	21060
Db	21001	CCCGGCAACGGCGCGTGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG	21060
Qy	21061	GGGGGGGGGGTGGCGGAGTGATGAAGATGGTGGGCTTCCGCGGCGGCGGCGGCGGCGGCGG	21120
Db	21061	GGGGGGGGGGTGGCGGAGTGATGAAGATGGTGGGCTTCCGCGGCGGCGGCGGCGGCGGCGG	21120
Qy	21121	CGGACTCTCCACGGGATGAGCGCTGCGCGCATGTGGACTGGCTGGCTGGCTGGCTGGCTGGCTGG	21180
Db	21121	CGGACTCTCCACGGGATGAGCGCTGCGCGCATGTGGACTGGCTGGCTGGCTGGCTGGCTGGCTGG	21180
Qy	21181	CTGCTGACGGAGACGTCCTTGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21240
Db	21181	CTGCTGACGGAGACGTCCTTGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	21240
Qy	21241	TCATCATTCGGGCTGAGCGGCGCAACCGCCACGTCATCTCGAAGAAAGCAACCGCGCGAC	21300
Db	21241	TCATCATTCGGGCTGAGCGGCGCAACCGCCACGTCATCTCGAAGAAAGCAACCGCGCGAC	21300
Qy	21301	GACGTTTCGGGGGGGACCAACCGCGCGAGAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG	21360
Db	21301	GACGTTTCGGGGGGGACCAACCGCGCGAGAGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG	21360
Qy	21361	GGGAGTCTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG	21420
Db	21361	GGGAGTCTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGG	21420
Qy	21421	CAGGCGCCAGGCGCTGACCGCCACCTCACCGACCAACCGCGGCTCGACCTCGCGGACGTC	21480
Db	21421	CAGGCGCCAGGCGCTGACCGCCACCTCACCGACCAACCGCGGCTCGACCTCGCGGACGTC	21480
Qy	21481	GGATACACCTCGCGCGACCGCGCGGCTTGCACCGCGCGCACCTCATTCGCGCGC	21540
Db	21481	GGATACACCTCGCGCGACCGCGCGGCTTGCACCGCGCGCACCTCATTCGCGCGC	21540

Qy	21541	GACCGGACACCTTCTCTCAAGCACTCCAGGCACCTCGCGGAGGCGAAGCAACCCACCCCGCC	21600
Db	21541	GACCGGACACCTTCTCTCAAGCACTCCAGGCACCTCGCGGAGGCGAAGCAACCCACCCCGCC	21600
Qy	21601	GTCTATCCACAGCAGCGCCCGGAGGCGGACCGGAGACCGGGAGGCGCGAGGAAGACCGCA	21660
Db	21601	GTCTATCCACAGCAGCGCCCGGAGGCGGACCGGAGACCGGGAGGCGCGAGGAAGACCGCA	21660
Qy	21661	TTCTATCTCTCGGACAGGCGCACCAACCGCGCGGCGATGGCCCGGCTTCTACACACCC	21720
Db	21661	TTCTATCTCTCGGACAGGCGCACCAACCGCGCGGCGATGGCCCGGCTTCTACACACCC	21720
Qy	21721	CACCGCGCTTTCGCGCGCGCATCAACGACATCTGACCCACCTCGACCCCGACCTCGAC	21780
Db	21721	CACCGCGCTTTCGCGCGCGCATCAACGACATCTGACCCACCTCGACCCCGACCTCGAC	21780
Qy	21781	CACCGCGCTTTCGCGCGCGCATCAACGACATCTGACCCACCTCGACCCCGACCTCGAC	21840
Db	21781	CACCGCGCTTTCGCGCGCGCATCAACGACATCTGACCCACCTCGACCCCGACCTCGAC	21840
Qy	21841	GCATGCTTCCAGCAGACCGCGTACCGCGCGCGCTTTCGCGCTTTCGAGTTCGCGCTC	21900
Db	21841	GCATGCTTCCAGCAGACCGCGTACCGCGCGCGCTTTCGCGCTTTCGAGTTCGCGCTC	21900
Qy	21901	CACCGCGCTTTCGCGCGCGCATCAACGACATCTGACCCCGACCTTTCGCGCTTTCGAGTTCGCGCTC	21960
Db	21901	CACCGCGCTTTCGCGCGCGCATCAACGACATCTGACCCCGACCTTTCGCGCTTTCGAGTTCGCGCTC	21960
Qy	21961	GGGAAATACCGCGCGCGCATCTCGCGCGCATCTCACCTCACCGCGCGCACCAACCTC	22020
Db	21961	GGGAAATACCGCGCGCGCATCTCGCGCGCATCTCACCTCACCGCGCGCACCAACCTC	22020
Qy	22021	ATCACCGAAGCGGCGACCTTATGGAACGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22080
Db	22021	ATCACCGAAGCGGCGACCTTATGGAACGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22080
Qy	22081	ACCAACCGGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22140
Db	22081	ACCAACCGGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22140
Qy	22141	GCCATCAACCGCGCGCGCATCTCGTATAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22200
Db	22141	GCCATCAACCGCGCGCGCATCTCGTATAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22200
Qy	22201	ACCAACCGGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22260
Db	22201	ACCAACCGGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22260
Qy	22261	CACCTCCCGCGCGCGCATCTCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22320
Db	22261	CACCTCCCGCGCGCGCATCTCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22320
Qy	22321	TACCAACCGCGCGCGCATCTCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22380
Db	22321	TACCAACCGCGCGCGCATCTCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22380
Qy	22381	CCCACTTCTGCGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22440
Db	22381	CCCACTTCTGCGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22440
Qy	22441	CTCCACCAACCGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22500
Db	22441	CTCCACCAACCGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22500
Qy	22501	CTCAACCGCGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22560
Db	22501	CTCAACCGCGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22560
Qy	22561	CACCAACCGCGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22620
Db	22561	CACCAACCGCGCGCGCGCATCAACGACCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22620

QY	22621	CAACCTACACCCACCAACAAACAAACCCACACCCACACCCACCTCGACCTCCCCACC	22680	Db	23701	CGAACGGGCCCCACACCCCCACACACACCTCACACCCAACTCCAAACAAAAGGC	23760
Db	22621	CACCACTACACCCACCAACAAACAAACCCACACCCACACACCTCGACCTCCCCACC	22680	QY	23761	ATCCACCTCACCACCTCACCACCTCGACACCCAGCAACCCAGACCAACTCCAAACATCTCTC	23820
QY	22681	TACCCCTTCCAAACACCACTACTGGCTCGAACTACCCAGCGCCCAACACGACCCCGGT	22740	Db	23761	ATCCACCTCACCACCTCACCACCTCGACACCCAGCAACCCAGACCAACTCCAAACATCTCTC	23820
Db	22681	TACCCCTTCCAAACACCACTACTGGCTCGAACTACCCAGCGCCCAACACGACCCCGGT	22740	QY	23821	AAACACATCCCCCAACACACCCCTCACACCTCATCCACCGCAGGCGTCAATCTC	23880
QY	22741	CAAAAGCGTTCTCGCGCTCGGCTCCAGACACCGCGAGTTCGGAGTTCTGGAGCGGGTG	22800	Db	23821	AAACACATCCCCCAACACACCCCTCACACCTCATCCACCGCAGGCGTCAATCTC	23880
Db	22741	CAAAAGCGTTCTCGCGCTCGGCTCCAGACACCGCGAGTTCGGAGTTCTGGAGCGGGTG	22800	QY	23881	TTGCGCCCGGTGTCGGAAACCGATCCGAAATCCTTCTCTTCGTTACGCGACGAAGGCA	23940
QY	22801	AACGAGGAAGACTCCAGAGCTCGCGAAACCTTCGACATCGACGCTCTGCTCGGAC	22860	Db	23881	TTGCGCCCGGTGTCGGAAACCGATCCGAAATCCTTCTCTTCGTTACGCGACGAAGGCA	23940
Db	22801	AACGAGGAAGACTCCAGAGCTCGCGAAACCTTCGACATCGACGCTCTGCTCGGAC	22860	QY	23941	ACGGCGCGGGGATTCGATGAGTTGCTGAGCAATGAAACGCTTGAACACTTTCAT	24000
QY	22861	ACGGTGTGCGCGCACTCTCGCTCGGCAACCGCCAGCCACCAACAGCAACCAAGCCGATCAAC	22920	Db	23941	ACGGCGCGGGGATTCGATGAGTTGCTGAGCAATGAAACGCTTGAACACTTTCAT	24000
Db	22861	ACGGTGTGCGCGCACTCTCGCTCGGCAACCGCCAGCCACCAACAGCAACCAAGCCGATCAAC	22920	QY	24001	CTCTTCTCGTCCGGCGCGCGCTTGGGGCAGCGGGAATCAGTGCGCATACTCGCGGCGC	24060
QY	22921	ACCTGACCTACAGGAACCTTGGAAACCCCTCACCTCCCAACCAACCAACCAACCCAC	22980	Db	24001	CTCTTCTCGTCCGGCGCGCGCTTGGGGCAGCGGGAATCAGTGCGCATACTCGCGGCGC	24060
Db	22921	ACCTGACCTACAGGAACCTTGGAAACCCCTCACCTCCCAACCAACCAACCAACCCAC	22980	QY	24061	AACGATACCTGGAACGCGCTCGGACGATCGTCAAGACATGAGACTTCCCGGGGCGATCG	24120
QY	22981	CAAACTGGCTCATCGCCATCCCGAAACCCAGACCCACGACCCCAACATCAACCAATC	23040	Db	24061	AACGATACCTGGAACGCGCTCGGACGATCGTCAAGACATGAGACTTCCCGGGGCGATCG	24120
Db	22981	CAAACTGGCTCATCGCCATCCCGAAACCCAGACCCACGACCCCAACATCAACCAATC	23040	QY	24121	ATCGCTCGGGGCGCGCTTGGGGCAGCGGGAATGTCGGCGGTGATCGGCTCATGCTTAC	24180
QY	23041	CTCACCACTCCACACACGCGATCACCCGATCCCTTCACTGTGAACCAACCCAC	23100	Db	24121	ATCGCTCGGGGCGCGCTTGGGGCAGCGGGAATGTCGGCGGTGATCGGCTCATGCTTAC	24180
Db	23041	CTCACCACTCCACACACGCGATCACCCGATCCCTTCACTGTGAACCAACCCAC	23100	QY	24181	CTGGAAGAGCGCGATTCGCGATGAGCAGCAGCAGTGGCGCTCGCGCATTCATCTG	24240
QY	23101	ACCAACCCCAACACCTCCACACACCTCCACCAACCGCAACCAAGCCCAAAACCAAC	23160	Db	24181	CTGGAAGAGCGCGATTCGCGATGAGCAGCAGCAGTGGCGCTCGCGCATTCATCTG	24240
Db	23101	ACCAACCCCAACACCTCCACACACCTCCACCAACCGCAACCAAGCCCAAAACCAAC	23160	QY	24241	GCGCGGGCGAGCGCGCGGAAATTCGAACTGATCGGGGAATCGA CTGGAGGCGCTTC	24300
QY	23161	ACACGGAGCCATACCGGCTGCTCTCTCTCGCTCGAGCAACACCCCAACCC	23220	Db	24241	GCGCGGGCGAGCGCGCGGAAATTCGAACTGATCGGGGAATCGA CTGGAGGCGCTTC	24300
Db	23161	ACACGGAGCCATACCGGCTGCTCTCTCTCGCTCGAGCAACACCCCAACCC	23220	QY	24301	GTCCCGGCTTCAACCGCTCGACCGCACAGCCGCTCATCGAGGACATTCGGAGGTTCCG	24360
QY	23221	CACCAACCCCAACACCGGACCTCTCACTCACTTCCCTCCCAACCCCAACCC	23280	Db	24301	GTCCCGGCTTCAACCGCTCGACCGCACAGCCGCTCATCGAGGACATTCGGAGGTTCCG	24360
Db	23221	CACCAACCCCAACACCGGACCTCTCACTCACTTCCCTCCCAACCCCAACCC	23280	QY	24361	CAAGCGGCTCAGGAGCTGGAAGCAGCTGCTCGAAGGCAAGCAACCAACAGCTCAGCG	24420
QY	23281	CAAAACCCCAACACCCCTCTGTGTAGCGCACCAACCAAGCCCAACCAACCC	23340	Db	24361	CAAGCGGCTCAGGAGCTGGAAGCAGCTGCTCGAAGGCAAGCAACCAACAGCTCAGCG	24420
Db	23281	CAAAACCCCAACACCCCTCTGTGTAGCGCACCAACCAAGCCCAACCAACCC	23340	QY	24421	ATTGCGAGCTCTCTCGTGAGCGATTGGCCGACTGAGCTCTCAAAGCAGAACCAAGTG	24480
QY	23341	AACGACCCCTCACACACCCCAACCAAGCCCAACCTTGGGAGCTCGCCGCGACCCCTC	23400	Db	24421	ATTGCGAGCTCTCTCGTGAGCGATTGGCCGACTGAGCTCTCAAAGCAGAACCAAGTG	24480
Db	23341	AACGACCCCTCACACACCCCAACCAAGCCCAACCTTGGGAGCTCGCCGCGACCCCTC	23400	QY	24481	CTGCTCGGCTGATTCGGACAGGATCTGCAACCTTCTCGGCTTCTGTAATCCGGAAGGC	24540
QY	23401	CTGGAACACCCCAACCGCGGAAATCATGAGCTTCCCAACCAACCCCAACCC	23460	Db	24481	CTGCTCGGCTGATTCGGACAGGATCTGCAACCTTCTCGGCTTCTGTAATCCGGAAGGC	24540
Db	23401	CTGGAACACCCCAACCGCGGAAATCATGAGCTTCCCAACCAACCCCAACCC	23460	QY	24541	ATCGAGGACCAACAGACCTTCGCGACCTTCGACTTCGACTCGCTGAGCTCAGTTTC	24600
QY	23461	ACCTTCCACCACTCACCAACCCCTCACCAACCCCAACCAACCAACCAACCTCGGCATC	23520	Db	24541	ATCGAGGACCAACAGACCTTCGCGACCTTCGACTTCGACTCGCTGAGCTCAGTTTC	24600
Db	23461	ACCTTCCACCACTCACCAACCCCTCACCAACCCCAACCAACCAACCAACCTCGGCATC	23520	QY	24601	AGCAAGAACTCGCGCAAGAAACCGGA CTGCACTCCCGCTCCCTGCTTCTTCACTAT	24660
QY	23521	CGGACACCGGACCAACCGCGCTCACCCCAACCAACCTTCAACCCCAACCAAC	23580	Db	24601	AGCAAGAACTCGCGCAAGAAACCGGA CTGCACTCCCGCTCCCTGCTTCTTCACTAT	24660
Db	23521	CGGACACCGGACCAACCGCGCTCACCCCAACCAACCTTCAACCCCAACCAAC	23580	QY	24661	CCCACCCCGAGGATGCTGCCCATCTGGGCAACACTCGTCACTAGACGCA	24720
QY	23581	CCACCCACCCCAACCCCAACCCCTCATCACCGGGGAACCGGGCGCTTCGCC	23640	Db	24661	CCCACCCCGAGGATGCTGCCCATCTGGGCAACACTCGTCACTAGACGCA	24720
Db	23581	CCACCCACCCCAACCCCAACCCCTCATCACCGGGGAACCGGGCGCTTCGCC	23640	QY	24721	GAGGACGGGACCTGCTGAAATGCTCTCGGCAAGTGGGCCCATCGGGTACCGTTCGAGGAC	24780
QY	23641	ACCCACCTCACCACTCACCAACCCCAACCCCTCATCACCGGGGAACCGGGCGCTTCGCC	23700	Db	24721	GAGGACGGGACCTGCTGAAATGCTCTCGGCAAGTGGGCCCATCGGGTACCGTTCGAGGAC	24780
Db	23641	ACCCACCTCACCACTCACCAACCCCAACCCCTCATCACCGGGGAACCGGGCGCTTCGCC	23700	QY	24781	GAAACCGATCGGCATCATCGGTATGCTGCTTCCCGGGCGGCTACGTTCTCGCGAC	24840
QY	23701	CGAACGGGCCCCACACCCCAACCGCAACACCTCACCAACCCCAACCTCCAAACAAAAGGC	23760				



[illegible]

QY	25921	CCAC	CCCCCAGGTGCACTGGTCCACAGCGCGAGTACAACTCCTGACACAACACCGGTGCCC	25980
DB	25921	CCAC	CCCCCAGGTGCACTGGTCCACAGCGCGAGTACAACTCCTGACACAACACCGGTGCCC	25980
QY	25981	TGG	CCGCGAGACCCGCGCGGCGCACCGCCAGCGCGGTGTCATCATTTCCGGCGTCAAGC	26040
DB	25981	TGG	CCGCGCGACCCGCGCGGCGCACCGCCAGCGCGGTGTCATCATTTCCGGCGTCAAGC	26040
QY	26041	GGCAC	CAAGCCCCACATCATCTTCGAAGAACCAACCATCTCCCGAGACAGGATACCGAC	26100
DB	26041	GGCAC	CAAGCCCCACATCATCTTCGAAGAACCAACCATCTCCCGAGACAGGATACCGAC	26100
QY	26101	GAG	CAACCGCTGCCAAACGACACAGCCCTGCCCATCCCTCCCTTCCCGTGCCTGGTG	26160
DB	26101	GAG	CAACCGCTGCCAAACGACACAGCCCTGCCCATCCCTCCCTTCCCGTGCCTGGTG	26160
QY	26161	TCGG	CAGGCTTCGAGCCCGGTTTGGCGGCGCAGGACAGGCGTTCGCGCAGTACGTGGCA	26220
DB	26161	TCGG	CAGGCTTCGAGCCCGGTTTGGCGGCGCAGGACAGGCGTTCGCGCAGTACGTGGCA	26220
QY	26221	GCG	CGCCGACATGTTCACCTGCCGACATTTGGTGGGGTCTGGCCCGCGGCGCGGCGCTA	26280
DB	26221	GCG	CGCCCGCGACATGTTCACCTGCCGACATTTGGTGGGGTCTGGCCCGCGGCGCGGCGCTA	26280
QY	26281	CTG	GAACACCGCCGCTCATCTCTGGCGCGGACCGCGAGGAACCTGGCGCAGGCACTGACA	26340
DB	26281	CTG	GAACACCGCCGCTCATCTCTGGCGCGGACCGCGAGGAACCTGGCGCAGGCACTGACA	26340
QY	26341	GCCT	TGCGAGCCGGAACCCCAACCCCAACATCAACACAGGCCAACCCCGGGCGGTGAC	26400
DB	26341	GCCT	TGCGAGCCGGAACCCCAACCCCAACATCAACACAGGCCAACCCCGGGCGGTGAC	26400
QY	26401	CGCG	CGGGTCTCTTCCTTCCCGACAGGGCGGCGCAGTGGCGCGGATGGGCGCTG	26460
DB	26401	CGCG	CGGGCGGGTCTCTTCCTTCCCGACAGGGCGGCGCAGTGGCGCGGATGGGCGCTG	26460
QY	26461	ACCT	GTCTACCTCTCTCACCCCGTGTTCGCGCGAACCATCGACGCGATGCGAGAAAGCCCTC	26520
DB	26461	ACCT	GTCTACCTCTCTCACCCCGTGTTCGCGCGAACCATCGACGCGATGCGAGAAAGCCCTC	26520
QY	26521	ACCC	CTGGGTGGCTTGGTCCCTGACCGACATCTTGACCGCGACCCCGACGACCCCGCA	26580
DB	26521	ACCC	CTGGGTGGCTTGGTCCCTGACCGACATCTTGACCGCGACCCCGACGACCCCGCA	26580
QY	26581	TGG	CAACAGCGCCAGCTGGTGCAGACCGCGTCTCTTCAGCATCATGGTCTCCCTCGCGCGC	26640
DB	26581	TGG	CAACAGCGCCAGCTGGTGCAGACCGCGTCTCTTCAGCATCATGGTCTCCCTCGCGCGC	26640
QY	26641	CTGT	GGCGCTCTACGGCATTCGAACCCGACCGCGTCTTCGGGCACTCTCCAGGGAGAAATC	26700
DB	26641	CTGT	GGCGCTCTCTACGGGCATTCGAACCCGACCGCGTCTTCGGGCACTCTCCAGGGAGAAATC	26700
QY	26701	GCG	CGCCACATCTCGCGCGCATCAGCCTGAAAGACCGCGCCAAACCGTTCGACTG	26760
DB	26701	GCG	CGCCCGCCACATCTCGCGCGCATCAGCCTGAAAGACCGCGCCAAACCGTTCGACTG	26760
QY	26761	CGC	AGCCGCACTGGCCCGCGTACGAGCGCGGGCGCATGGCCCTCACTGCCCCCTGCC	26820
DB	26761	CGC	AGCCCGCGCATCTGGCCCGCGTACGAGCGCGGGCGCATGGCCCTCACTGCCCCCTGCC	26820
QY	26821	GCC	AGGACGTGACAGCTCATTTCCGAACCGTGGGAGGGCAGTTGTGGGTGGCAGCC	26880
DB	26821	GCC	AGGACGTGACAGCTCATTTCCGAACCGTGGGAGGGCAGTTGTGGGTGGCAGCC	26880
QY	26881	CTCA	AGGGCCCCCACTCCACACCGTCTCCGCGCACACCAAGCGCGGTGGATCAGGTGCTG	26940
DB	26881	CTCA	AGGGCCCCCACTCCACACCGTCTCCGCGCACACCAAGCGCGGTGGATCAGGTGCTG	26940
QY	26941	GCG	CATGCAACGACACCGGCTTACGGGCGAAACGATCCCCCGTTCGACTGACCCCTCCAC	27000
DB	26941	GCG	CATGCAACGACACCGGCTTACGGGCGAAACGATCCCCCGTTCGACTGACCCCTCCAC	27000



Db 29161 CCCGCGTGGCGTACCGTACGCGGTCAACGAGCGGTACCGGAGCGGGTCCCTTCTT 29220  
Qy 29221 CCGGCGGACCGTGTGATACCGCGCGAAACCGGTGTCTTGGGCGGGTCTGTGGCCCGG 29280  
Db 29221 CCGGCGGACCGTGTGATACCGCGCGAAACCGGTGTCTTGGGCGGGTCTGTGGCCCGG 29280  
Qy 29281 CATCTGTGTGGAGCGCACCGGCTACCGGATCTGTGTGGCGGGTCTGGGCGGACCGGAC 29340  
Db 29281 CATCTGTGTGGAGCGCACCGGCTACCGGATCTGTGTGGCGGGTCTGGGCGGACCGGAC 29340  
Qy 29341 GCCGAGGTTGCCCGGAGTTGCCGCGGAGTCTGGTGGGCTCGGCGCGACCGGTGAGGTC 29400  
Db 29341 GCCGAGGTTGCCCGGAGTTGCCGCGGAGTCTGGTGGGCTCGGCGCGACCGGTGAGGTC 29400  
Qy 29401 GTCCGCTGGACCGCGGACCGGACGAGCTGGCGGACCTGCTACACGGATCCCGAC 29460  
Db 29401 GTCCGCTGGACCGCGGACCGGACGAGCTGGCGGACCTGCTACACGGATCCCGAC 29460  
Qy 29461 GATCGGCGCTGACCGGTTCTGTGACAGTGGCGGATCCTTGACGAGCGGTGATCAG 29520  
Db 29461 GATCGGCGCTGACCGGTTCTGTGACAGTGGCGGATCCTTGACGAGCGGTGATCAG 29520  
Qy 29521 TCGCTGTTCGCGGAGCGGCTCGGCGCGTCTCGGCGCAAGCGCGTGGCTGCTT 29580  
Db 29521 TCGCTGTTCGCGGAGCGGCTCGGCGCGTCTCGGCGCAAGCGCGTGGCTGCTT 29580  
Qy 29581 CTGCGAGAGTACCGCGCGGCGGACGAGCTGTGGCTTTCTGATCTTCTTCTCGGCTCG 29640  
Db 29581 CTGCGAGAGTACCGCGCGGCGGACGAGCTGTGGCTTTCTGATCTTCTTCTCGGCTCG 29640  
Qy 29641 GCGGTGGTTCGCTCGCGCGGCGGCAACTACGCGCGCGCAACGCGGTCTCTCGACTTC 29700  
Db 29641 GCGGTGGTTCGCTCGCGCGGCGGCAACTACGCGCGCGCAACGCGGTCTCTCGACTTC 29700  
Qy 29701 CTTGCTCATTCGCGCGCGCGGCTCGGCGGCTCTCTCTCGCTGGGCGCTGTGG 29760  
Db 29701 CTTGCTCATTCGCGCGCGCGGCTCGGCGGCTCTCTCTCGCTGGGCGCTGTGG 29760  
Qy 29761 GAAGAGGACAGGATGACGGGCGGACCTGAGCTTCGAGCATCGGCGGATGACGCG 29820  
Db 29761 GAAGAGGACAGGATGACGGGCGGACCTGAGCTTCGAGCATCGGCGGATGACGCG 29820  
Qy 29821 GCGGGAATCGGCGCGCTGCCGACTGCGGAGGCTCTGGGCGCTTTCGACGCGGCTTGCC 29880  
Db 29821 GCGGGAATCGGCGCGCTGCCGACTGCGGAGGCTCTGGGCGCTTTCGACGCGGCTTGCC 29880  
Qy 29881 GACGCGAGCGCTTCTGATCGGCTCGGCTCGACCTCACGCGCGTACGCTGCTGCG 29940  
Db 29881 GACGCGAGCGCTTCTGATCGGCTCGGCTCGACCTCACGCGCGTACGCTGCTGCG 29940  
Qy 29941 GCGTCCGACCGGTGCGCGCGCTGCTGCAAGTCTGCTTACGCTGGCTCGGCTCG 30000  
Db 29941 GCGTCCGACCGGTGCGCGCGCTGCTGCAAGTCTGCTTACGCTGGCTCGGCTCG 30000  
Qy 30001 GCGCGCGCGCGCGCGCGCATCGGCGCGGCGGAGCGGCGGCGCTGGCGTGAG 30060  
Db 30001 GCGCGCGCGCGCGCGCGCATCGGCGCGGCGGAGCGGCGGCGGCGCTGGCGTGAG 30060  
Qy 30061 CCGTCTGGCGCGGAGGTCGCGGTGAGCGGAGGCGGCTGCTGCGCTGGTGGCGTGG 30120  
Db 30061 CCGTCTGGCGCGGAGGTCGCGGTGAGCGGAGGCGGCTGCTGCGCTGGTGGCGTGG 30120  
Qy 30121 CATCTCGCGCGGTGCTGGCCATAGCGGTGCGGAGGATCGACGATCGGCGGCTTC 30180  
Db 30121 CATCTCGCGCGGTGCTGGCCATAGCGGTGCGGAGGATCGACGATCGGCGGCTTC 30180  
Qy 30181 CCGGAGCTGGGTTGACTGCTGCTGCGGCGGCTGAGCTGCGGCAACCGTCTCACGCGCG 30240  
Db 30181 CCGGAGCTGGGTTGACTGCTGCTGCGGCGGCTGAGCTGCGGCAACCGTCTCACGCGCG 30240  
Qy 30241 ACGGCGCTGCGGCTGCGGCGGACGCTGCGCTTTCGATTTCCGACCCCGGACGCTGGCC 30300  
Db 30241 ACGGCGCTGCGGCTGCGGCGGACGCTGCGCTTTCGATTTCCGACCCCGGACGCTGGCC 30300

Qy 30301 GAGCACTTGGCGGAGCTCTCTTCCGACACGAGGCGCACGGCGAGCAAGCCGCGAT 30360  
Db 30301 GAGCACTTGGCGGAGCTCTCTTCCGACACGAGGCGCACGGCGAGCAAGCCGCGAT 30360  
Qy 30361 CAGCTCTCCGCGCGGAGGAGCTACGCGAGCTCTTGAAGTCTCATTTCCGATCGGC 30420  
Db 30361 CAGCTCTCCGCGCGGAGGAGCTACGCGAGCTCTTGAAGTCTCATTTCCGATCGGC 30420  
Qy 30421 AGGCTGCGGAGCGGCGGCTCTCGGCGGCTCTGCTCAGCTTCGCGGACACGGGCGCGGC 30480  
Db 30421 AGGCTGCGGAGCGGCGGCTCTCGGCGGCTCTGCTCAGCTTCGCGGACACGGGCGCGGC 30480  
Qy 30481 GCCTCGGCGCGCGGAGGTCGCGGAGCGCGCGCTCTCGGCGGACACACCGGCT 30540  
Db 30481 GCCTCGGCGCGCGGAGGTCGCGGAGCGCGCGCTCTCGGCGGACACACCGGCT 30540  
Qy 30541 CCCGTCTCGATCGAGAGATGACATCGACACCTGATGGATCTGGCGCACCGGCGATGCG 30600  
Db 30541 CCCGTCTCGATCGAGAGATGACATCGACACCTGATGGATCTGGCGCACCGGCGATGCG 30600  
Qy 30601 ACCGACCCGCGGCTGAGCCCGCGAGCGCGGAGGAGCTGCTCATCAGCAACCGGACA 30660  
Db 30601 ACCGACCCGCGGCTGAGCCCGCGAGCGCGGAGGAGCTGCTCATCAGCAACCGGACA 30660  
Qy 30661 CACCACACACAGAGGTGAGACAGCGTGA 30690  
Db 30661 CACCACACACAGAGGTGAGACAGCGTGA 30690

## RESULT 3

AAH79279

ID AAH79279 standard; DNA; 11916 BP.

XX AC AAH79279;

XX DT 04-DEC-2001 (first entry)

XX DE Streptomyces avermectilis coding sequence derivative SEQ ID NO: 3.

XX KW Avermectin aglycone synthase; AAS; avermectin derivative;

XX OS Synthetic.

XX FT Key

XX CDS 1..11916

XX FT /\*tag= a

XX FT /product= "AAG65268"

XX FT /partial

XX PN WO200162939-A1.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-JP01381.

XX PR 24-FEB-2000; 2000JP-0047405.

XX PA (KYOWA) KYOWA HAKKO KOGYO KK.

XX PA (KITA) KITASATO INST.

XX PI Endo H, Yamaguchi H, Kanda Y, Hashimoto S, Omura S, Ikeda H;

XX DR WPI; 2001-582053/65.

XX DR P-PSDB; AAG65268.

XX PT New modified avermectin aglycone synthase derived from Streptomyces

XX PT avermectilis used in production of 22,23-dihydroavermectin B1a used in

XX PS drugs and pesticides -

XX PS Claim 10; Page 149-167; 257pp; Japanese.

CC The present invention relates to the production of modified derivatives  
CC of avermectin aglycone synthase (AAS) derived from Streptomyces  
CC avermilitis. The activity of an acyl carrier protein (ACP),  
CC beta-ketoacyl carrier protein synthase (KS), acyltransferase (AT),  
CC beta-ketoacyl carrier protein reductase (KR), dehydratase (DH), enoyl  
CC reductase (ER) and/or thioesterase (TE) domain may be reduced or  
CC suppressed. The process can be used in the production of drugs, veterinary  
CC drugs and pesticides. The present sequence is modified version of a  
CC fragment of the *S. avermilitis* genome.

xx  
SQ Sequence 11916 BP; 1831 A; 4428 C; 3820 G; 1837 T; 0 other;

Query Match 38.8%; Score 11914.4; DB 22; Length 11916;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 11915; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GTGCAGAGTGGACGGCGGGAGAAACCCCGCCCTGGCGACAGGAGGTCTCCGAGTG	60
DB	1	GTGCAGAGTGGACGGCGGGAGAAACCCCGCCCTGGCGACAGGAGGTCTCCGAGTG	60
QY	61	GCCGACGAGGCGACGGCGGCTGCTTTTCCGGGACAGGCGCCGCAATGGCGG	120
DB	61	GCCGACGAGGCGACGGCGGCTGCTTTTCCGGGACAGGCGCCGCAATGGCGG	120
QY	121	GGCATGGAGGGAATCTTCGACGCTTCGAGCTTCGCGGAGAGGTCCGCGCTGC	180
DB	121	GGCATGGAGGGAATCTTCGACGCTTCGAGCTTCGCGGAGAGGTCCGCGCTGC	180
QY	181	GAAGCCGCTTCGCGCCCTACGTCGACCTGCTGGTGGAGGAGGTCTCCGCGG	240
DB	181	GAAGCCGCTTCGCGCCCTACGTCGACCTGCTGGTGGAGGAGGTCTCCGCGG	240
QY	241	GACGCTCCCGGCTGGACGGGTGACGCTCGTCAGCCGACCCCTGTCGCGCTCATGATC	300
DB	241	GACGCTCCCGGCTGGACGGGTGACGCTCGTCAGCCGACCCCTGTCGCGCTCATGATC	300
QY	301	TCCCTGGCGCCCTCTCGCGCTCGAAGGGTTCGAGCCGTGCGCGGTCTGGGACACAGC	360
DB	301	TCCCTGGCGCCCTCTCGCGCTCGAAGGGTTCGAGCCGTGCGCGGTCTGGGACACAGC	360
QY	361	CTGGGCGAGATCGGGGAGCCACGCTCTCGGAGGCTGTCCTGGCGGACGCGCGCAGC	420
DB	361	CTGGGCGAGATCGGGGAGCCACGCTCTCGGAGGCTGTCCTGGCGGACGCGCGCAGC	420
QY	421	GTGTGTAGCTTTGGAGCCAGGCAAGACACCTTTCGCGGACCGCGCGCTCGTCTCC	480
DB	421	GTGTGTAGCTTTGGAGCCAGGCAAGACACCTTTCGCGGACCGCGCGCTCGTCTCC	480
QY	481	GTGCGCGGACCGCGGATGAGCTCTGCGCCGAAATCGCTCCGTGGACCGAACAACCG	540
DB	481	GTGCGCGGACCGCGGATGAGCTCTGCGCCGAAATCGCTCCGTGGACCGAACAACCG	540
QY	541	GCGGCGCTCGCGGTCGAGCCGTCAGACCCCGGAGCAGTGGTTCGGTCCGCGCCG	600
DB	541	GCGGCGCTCGCGGTCGAGCCGTCAGACCCCGGAGCAGTGGTTCGGTCCGCGCCG	600
QY	601	GAGGCGCTCGCGGACCTGGTGCCGACCTCACCGCGCGGAGGTGCGCAACGCAATGATC	660
DB	601	GAGGCGCTCGCGGACCTGGTGCCGACCTCACCGCGCGGAGGTGCGCAACGCAATGATC	660
QY	661	CCGTTGGAAGCTTCCCGCCACTCCCGCTGTATGTAAGCCATCGAGGAACGGGTGATCAGC	720
DB	661	CCGTTGGAAGCTTCCCGCCACTCCCGCTGTATGTAAGCCATCGAGGAACGGGTGATCAGC	720
QY	721	GGCTGTGTCCTACACCCACGCGCTCCCGCATCCCTTCCACTCTCGTGCACCGGC	780
DB	721	GGCTGTGTCCTACACCCACGCGCTCCCGCATCCCTTCCACTCTCGTGCACCGGC	780
QY	781	GCGCGCTTCGACACCCCGGAGTACAGCGGGGTACTGTACCGCAACATGTCCAGACACG	840
DB	781	GCGCGCTTCGACACCCCGGAGTACAGCGGGGTACTGTACCGCAACATGTCCAGACACG	840
QY	841	GTCCGGTTTCGAGCCCGCCCGGCTGCTTCTGACGACGGGCGCCCAAGACGTTCTGTCGAG	900

DB	841	GTCCGGTTTCGAGCCCGCCCGGCTGCTTCTGACGACGGGCGCCCAAGACGTTCTGTCGAG	900
QY	901	ATGAGCCCGACCCCGGTGTCTGACCATGGGCTTCAGGAGCTTCGCCCGGACTTGGCGCAC	960
DB	901	ATGAGCCCGACCCCGGTGTCTGACCATGGGCTTCAGGAGCTTCGCCCGGACTTGGCGCAC	960
QY	961	ACCACCGGACCCCGGACACCGTGTATCATGGGACGCTGCGCGCGGACAGGCAACCTG	1020
DB	961	ACCACCGGACCCCGGACACCGTGTATCATGGGACGCTGCGCGCGGACAGGCAACCTG	1020
QY	1021	GACCACTTCTGACGCTCTCTGCCCAACTACGGGGGCAATGCTGAGACGTCGGCGACAC	1080
DB	1021	GACCACTTCTTGTGACGCTCTCTGCCCAACTACGGGGGCAATGCTGAGACGTCGGCGACAC	1080
QY	1081	GTCTCTCTGGGACGCTGTGACCGGCTGTGCCCCACGACGACGAGCAGTCTCTCTGAC	1140
DB	1081	GTCTCTCTGGGACGCTGTGACCGGCTGTGCCCCACGACGACGAGCAGTCTCTCTGAC	1140
QY	1141	CTGTGCGCGCCACACCATGGCGGTGTGAACACGACGAAACGAGCGCACCGCGTCG	1200
DB	1141	CTGTGCGCGCCACACCATGGCGGTGTGAACACGACGAAACGAGCGCACCGCGTCG	1200
QY	1201	GATCGCGCCCATCGGCGAGTTTCCGCCACTCTCGGCTTCGACTCGGTCTATGGGTGTGAA	1260
DB	1201	GATCGCGCCCATCGGCGAGTTTCCGCCACTCTCGGCTTCGACTCGGTCTATGGGTGTGAA	1260
QY	1261	CTGCGCAACCGCTCAGCAAGGCCACGCGGCTGCGGCTTCCCGGTGACGCTCATCTTCGAC	1320
DB	1261	CTGCGCAACCGCTCAGCAAGGCCACGCGGCTGCGGCTTCCCGGTGACGCTCATCTTCGAC	1320
QY	1321	CACACCGCGCGCGGCTGCGCGCGCTTTCGACCGCGGCTTCGCGGCTTCGCGGCTTCGAC	1380
DB	1321	CACACCGCGCGCGGCTGCGCGCGCTTTCGACCGCGGCTTCGCGGCTTCGCGGCTTCGAC	1380
QY	1381	GAGGACACCGCGCCGTAACGGAATCTACCCAGCGGCAACGAGGAGCAAGGAGCGGAC	1440
DB	1381	GAGGACACCGCGCCGTAACGGAATCTACCCAGCGGCAACGAGGAGCAAGGAGCGGAC	1440
QY	1441	GACCGGATCGCCATCATCGGATGCGGCTTCCGGGCGGAGTCCGCTCCCGGAG	1500
DB	1441	GACCGGATCGCCATCATCGGATGCGGCTTCCGGGCGGAGTCCGCTCCCGGAG	1500
QY	1501	GACCTGTGGAGCTGCGCGCTTCGCGGCGGAGACGCACTTCGCGGCTTCGCCACCGACGC	1560
DB	1501	GACCTGTGGAGCTGCGCGCTTCGCGGCGGAGACGCACTTCGCGGCTTCGCCACCGACGC	1560
QY	1561	GGATGGCCACCGGAAAGCGTACGCGCCAGGACCCCAACGAGCCCGGCACTTCTATCCG	1620
DB	1561	GGATGGCCACCGGAAAGCGTACGCGCCAGGACCCCAACGAGCCCGGCACTTCTATCCG	1620
QY	1621	CAGGAGCGGGTCTTTCAGACGCGCGGCTTCGACCGCGGCTTCGCGGCTTCGGAATCAGT	1680
DB	1621	CAGGAGCGGGTCTTTCAGACGCGCGGCTTCGACCGCGGCTTCGCGGCTTCGGAATCAGT	1680
QY	1681	CCAGTGGGACATCGCGATGGATCCGACGAGCGGCTGCTGCTGGAGACGCTCTGGGAG	1740
DB	1681	CCAGTGGGACATCGCGATGGATCCGACGAGCGGCTGCTGCTGGAGACGCTCTGGGAG	1740
QY	1741	GCGTTTCGAGCGGGCGGAAATCGATCCGCTGTGCGTAACGCGGCTTCGCTACGGGCTCTTC	1800
DB	1741	GCGTTTCGAGCGGGCGGAAATCGATCCGCTGTGCGTAACGCGGCTTCGCTACGGGCTCTTC	1800
QY	1801	GCGGCGCGCTCTCTTTCGATACGCGCGCGGATGGACACCGGCTCGTGGAGGGCGCC	1860
DB	1801	GCGGCGCGCTCTCTTTCGATACGCGCGCGGATGGACACCGGCTCGTGGAGGGCGCC	1860
QY	1861	GCGGCGTGGAGGCGCACATCTCCTCACCGGTACACGCGGACGCTCTGTGGGCGGTATC	1920
DB	1861	GCGGCGTGGAGGCGCACATCTCCTCACCGGTACACGCGGACGCTCTGTGGGCGGTATC	1920
QY	1921	GCCTACAGCTTCGGGCTGGAGGCGCGGCGATCACCGTGGACACGGGGTGTCTGGGCACTG	1980

Db 1921 GCCTACAGCTTCGGGCTGGAAGGGCGGCGATCAACGTTGGAACACGGGGGGCTCGGCATCG 1980  
Qy 1981 CTCTGTAAGCTCATCTGSCGTGCCAGTCCGCTCGGCTGGGTGAGTGCACGCTCCGCTG 2040  
Db 1981 CTCTGTAAGCTCATCTGSCGTGCCAGTCCGCTCGGCTGGGTGAGTGCACGCTCCGCTG 2040  
Qy 2041 GCCGGCGGCTCTCGGTGATGCTCCACCTCTGGCATGTTTCATCAGTTCCTCCGGCAGGCG 2100  
Db 2041 GCCGGCGGCTCTCGGTGATGCTCCACCTCTGGCATGTTTCATCAGTTCCTCCGGCAGGCG 2100  
Qy 2101 GGGCTGTCTGGTGGACGGCAGGTGCAAGGCGTACTCGGTGCAAGCGCACCGGCTGG 2160  
Db 2101 GGGCTGTCTGGTGGACGGCAGGTGCAAGGCGTACTCGGTGCAAGCGCACCGGCTGG 2160  
Qy 2161 GGGAGGGCGTGGGATGCTGTTGGTGGAGCGGTTGTCCGATGCGGTGGGTCGGGTCAT 2220  
Db 2161 GGGAGGGCGTGGGATGCTGTTGGTGGAGCGGTTGTCCGATGCGGTGGGTCGGGTCAT 2220  
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Qy 11041 GGGCAGGGCAATACGCGCGGCCAATGCGCTCTGGAAGAGGCGGCGG 11100  
Db 11041 GGGCAGGGCAATACGCGCGGCCAATGCGCTCTGGAAGAGGCGGCGG 11100  
Qy 11101 GGGCGGGTCTGCGGGGGTGTGCGTGGCGTGGGGGCTGTGGAGAGGCGGCGGATG 11160  
Db 11101 GGGCGGGTCTGCGGGGGTGTGCGTGGCGTGGGGGCTGTGGAGAGGCGGCGGATG 11160  
Qy 11161 ACCGGGCACTTGGCGGCGGACCAACCGCGGCAATCATCCGTTCGGGTCTGATCCCATG 11220  
Db 11161 ACCGGGCACTTGGCGGCGGACCAACCGCGGCAATCATCCGTTCGGGTCTGATCCCATG 11220  
Qy 11221 TGAACCCGCGAGCACTGCGCTCTTTCGATGCGGCTTGGTCTGGAACGCGGCTCTG 11280  
Db 11221 TGAACCCGCGAGCACTGCGCTCTTTCGATGCGGCTTGGTCTGGAACGCGGCTCTG 11280  
Qy 11281 CTGCGCGGAGCTGGTCCGCGCGGCGGCTGCGCGGCTGCTGCGAGGCTCTGCGCC 11340  
Db 11281 CTGCGCGGAGCTGGTCCGCGCGGCGGCTGCGCGGCTGCTGCGAGGCTCTGCGCC 11340  
Qy 11341 GCGACCCGCGCGGCGGACCAACCGCGGCACTTACCGGTGGTGGGCAACAGCGCGCCAG 11400  
Db 11341 GCGACCCGCGCGGCGGACCAACCGCGGCACTTACCGGTGGTGGGCAACAGCGCGCCAG 11400  
Qy 11401 TGGGCGCGGCTGGCGGCGGAGACACAGAAACAGCAACACCTCTCTGCGGCTG 11460  
Db 11401 TGGGCGCGGCTGGCGGCGGAGACACAGAAACAGCAACACCTCTCTGCGGCTG 11460  
Qy 11461 GTCCGCTCCACATGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11520  
Db 11461 GTCCGCTCCACATGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11520  
Qy 11521 GCGCGGTTCCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 11580  
Db 11521 GCGCGGTTCCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 11580  
Qy 11581 TCCGCGACACCGGAGTCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 11640  
Db 11581 TCCGCGACACCGGAGTCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 11640  
Qy 11641 ACCCTCACCCACCTCCACACCACTCCAGGCAACCGGCAACCGGCTGCGGCTGCGG 11700  
Db 11641 ACCCTCACCCACCTCCACACCACTCCAGGCAACCGGCAACCGGCTGCGGCTGCGG 11700  
Qy 11701 GTGTTGGGGAGCTGCAAACTCGAATCCGCGCTCTCGGCTTCCGAAACCGGAGC 11760  
Db 11701 GTGTTGGGGAGCTGCAAACTCGAATCCGCGCTCTCGGCTTCCGAAACCGGAGC 11760  
Qy 11761 GCGAGGAAAGTCACTGCGGCTGAGTCACTCATGTTGAGTGAACGACCCCG 11820  
Db 11761 GCGAGGAAAGTCACTGCGGCTGAGTCACTCATGTTGAGTGAACGACCCCG 11820

Qy 11821 CATCGACAGCCGAAAGCGCTGATGACGACGAGAAGTTTCATCGGCAACAGAGGCTGAG 11880  
Db 11821 CATCGACAGCCGAAAGCGCTGATGACGACGAGAAGTTTCATCGGCAACAGAGGCTGAG 11880  
Qy 11881 ATTTTCAAATTCATTTGACAAACGACCTCGGCTGTCC 11916  
Db 11881 ATTTTCAAATTCATTTGACAAACGACCTCGGCTGTCC 11916

## RESULT 4

AAZ58381  
ID AAZ58381 standard; DNA; 12381 BP.  
XX AAZ58381;  
AC AAZ58381;  
XX 23-MAY-2000 (first entry)  
DT Streptomyces avermitilis avermectin polyketide synthase modules 1+2.  
DE Polyketide synthase; avermectin; insecticide; ss.  
KW Streptomyces avermitilis.  
XX OS  
XX WO200001827-A2.  
XX 13-JAN-2000.  
XX 06-JUL-1999; 99WO-GB02158.  
XX 06-JUL-1998; 98GB-0014622.  
XX (BIOT-) BIOTICA TECHNOLOGY LTD.  
PA (PFIZ ) PFIZER INC.  
XX Kellenberger JL, Leadlay PF, Staunton J, Stutzman-Engwall KJ;  
PI McArthur HAI;  
XX WPI; 2000-182117/16.

DR WPI; 2000-182117/16.  
XX Mutated Type I polyketide synthase containing a polylinker site in an  
PT extension module for replacement of a reductive loop sequence, for  
PT producing polyketides, e.g. B1 avermectin -  
XX Disclosure; Fig 7a-f; 75pp; English.

CC The present sequence is that of DNA encoding the first 2 modules  
CC of the avermectin polyketide synthase (PKS) of Streptomyces  
CC avermitilis. The invention relates to nucleic acids encoding a  
CC Type I PKS such as avermectin in which a polylinker with multiple  
CC restriction sites replaces or 1 more PKS genes encoding enzymes  
CC associated with reduction. Novel PKS are provided in which in  
CC which the reductive loop in a selected module of the Type I PKS is  
CC replaced with the equivalent segment from the same or different  
CC PKS gene cluster or by a mutated or synthetic segment. Vectors and  
CC host cells, and methods for producing novel polyketides by  
CC culturing host cells are claimed. The polyketides obtained are  
CC useful as antibiotics and insecticides. Fermentation products  
CC containing C22-C23 dihydroavermectin, ivermectin and B1  
CC avermectins are claimed.

SQ Sequence 12381 BP; 1884 A; 4561 C; 4005 G; 1931 T; 0 other;

Query Match 37.6%; Score 11548; DB 21; Length 12381;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 11554; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GTGCAGAGGATGGACGCGGGGAAGAACCCCGCTCGGCGAGGAGTCTCGGAGTG 60  
Db 818 GTGCAGAGGATGGACGCGGGGAAGAACCCCGCTCGGCGAGGAGTCTCGGAGTG 877  
Qy 61 GCCGACGAGCGGACGCGGCGTCTGTTTCCCGGCGAGGCGCCCAATGGCG 120

878 GCGGACGAGCGGACGGCGGCTGCTCTTCGTTTTTCCCGGGGACGGGCGCGCAATGGCGG 937  
121 GGCATGGGAAGGAACCTTCTCGACGCTTCGACGCTTCCGGGAGAGCGTCCGGCGCTGC 180  
938 GGCATGGGAAGGAACCTTCTCGACGCTTCGACGCTTCCGGGAGAGCGTCCGGCGCTGC 997  
181 GAAGCGCGCTTCGGCGCTTACGTCGACTGCTGGTGGAGCAGGTGTGGGGACTCGCGG 240  
998 GAAGCGCGCTTCGGCGCTTACGTCGACTGCTGGTGGAGCAGGTGTGGGGACTCGCGG 1057  
241 GACGCTCCCGGGCTGGACCGGGTGGAGCGTCTCCAGCGGACCGCTGTTCGCGCTCATGATC 300  
1058 GACGCTCCCGGGCTGGACCGGGTGGAGCGTCTCCAGCGGACCGCTGTTCGCGCTCATGATC 1117  
301 TCCCTGGCGCCCTTCGGCGCTTCGAAAGGGGTGGAGCGGCTGGCGGTGTGGGGACACAGC 360  
1118 TCCCTGGCGCCCTTCGGCGCTTCGAAAGGGGTGGAGCGGCTGGCGGTGTGGGGACACAGC 1177  
361 CTGGGGGAGATCGCGGACGCCACAGTCTCGGGAGGCTGTCTCTGGCGGACCGCGCACGC 420  
1178 CTGGGGGAGATCGCGGACGCCACAGTCTCGGGAGGCTGTCTCTGGCGGACCGCGCACGC 1237  
421 GTGGTGACGCTTTGGAGCCAGGACACAGACACCTTGGCGGGACCGCGCGCTCGTCTCC 480  
1238 GTGGTGACGCTTTGGAGCCAGGACACAGACACCTTGGCGGGACCGCGCGCTCGTCTCC 1297  
481 GTCGCGCCACGCGGATGAGTCTCTGCCCGCAATCGCTCCGTTGGACCGAGCAACCGG 540  
1298 GTCGCGCCACGCGGATGAGTCTCTGCCCGCAATCGCTCCGTTGGACCGAGCAACCGG 1357  
541 GCGCGCTCGCGTTCGACGCTTAACGGACCCCGGAGCACAGTCTGTTTCGGTGGCGCG 600  
1358 GCGCGCTCGCGTTCGACGCTTAACGGACCCCGGAGCACAGTCTGTTTCGGTGGCGCG 1417  
601 GAGGCGCTCGGACCTGTGGCGGACCTCACGCGCGCGAGTGGCGACCGCGCATGATC 660  
1418 GAGGCGCTCGGACCTGTGGCGGACCTCACGCGCGCGAGTGGCGACCGCGCATGATC 1477  
661 CGGTGGAGCTTCCGCGCCACTCCCGCTGATGTAGCCATCGAGGAACGGGTCTGTACG 720  
1478 CGGTGGAGCTTCCGCGCCACTCCCGCTGATGTAGCCATCGAGGAACGGGTCTGTACG 1537  
721 GGCCTGCTGCCATACCCACGCGCTTCGCGATCCCTTTCATCTCTCGTGGACCGGC 780  
1538 GGCCTGCTGCCATACCCACGCGCTTCGCGATCCCTTTCATCTCTCGTGGACCGGC 1597  
781 GCGCGCTCGACACCGCGAGTACGCGGGGTACTGTACCGCAACATGTTCGACGACG 840  
1598 GCGCGCTTCGACACCGCGAGTACGCGGGGTACTGTACCGCAACATGTTCGACGACG 1657  
841 GTCCGGTTCGAGCGCGCGGCTGTCTTCGACGAGGGGCCAAGACGTTCTGTTCGAG 900  
1658 GTCCGGTTCGAGCGCGCGGCTGTCTTCGACGAGGGGCCAAGACGTTCTGTTCGAG 1717  
901 ATGAGCCCGCACCGGTGTGACCATGGGCTTCAGAGAGCTCGCCCCCGACCTGGGCGAC 960  
1718 ATGAGCCCGCACCGGTGTGACCATGGGCTTCAGAGAGCTCGCCCCCGACCTGGGCGAC 1777  
961 ACCACCGGACCGCGACACCGTATCATGGGACGCTGGCGCGGGCCAGGGACCCCTG 1020  
1778 ACCACCGGACCGCGACACCGTATCATGGGACGCTGGCGCGGGCCAGGGACCCCTG 1837  
1021 GACCACTTCTGACGCTCTCTCGCCCAACTACGGGGGATGTGAGACGTCGCGGACCAAC 1080  
1838 GACCACTTCTGACGCTCTCTCGCCCAACTACGGGGGATGTGAGACGTCGCGGACCAAC 1897  
1081 GTCTCTTCGGGACGCTGACCGGCTGTCCCCACGACGACGAGTCTGCTCTCTGGAC 1140  
1898 GTCTCTTCGGGACGCTGACCGGCTGTCCCCACGACGACGAGTCTGCTCTCTGGAC 1957  
1141 CTGGTGGCGGCCACACCATGGGGGTCTGTAACGACGACGGAACGAGGCGACCGGCTG 1200  
1958 CTGGTGGCGGCCACACCATGGGGGTCTGTAACGACGACGGAACGAGGCGACCGGCTG 2017  
1201 GATGCGGCGCCCATCGGCGAGTTTCCGCCACCTCGGCTTCGACTCCGTCATCGGTCGAA 1260  
2018 GATGCGGCGCCCATCGGCGAGTTTCCGCCACCTCGGCTTCGACTCCGTCATCGGTCGAA 2077  
1261 CTGCGCAACCGCTCAGCAAGGCCACGAGGCTTCGCGGTCGCGTCACTCTTCGAC 1320  
2078 CTGCGCAACCGCTCAGCAAGGCCACGAGGCTTCGCGGTCGCGTCACTCTTCGAC 2137  
1321 CACACACGCGGCGCGCTCGCGCGCTTCGAGACCGGCGCTTCGCGCACCTCGAC 1380  
2138 CACACACGCGGCGCGCTCGCGCGCTTCGAGACCGGCGCTTCGCGCACCTCGAC 2197  
1381 GAGGACACCGGCGCGCTACCGGACTCACCCAGCGGCCACGAGGACACGCGCGGAC 1440  
2198 GAGGACACCGGCGCGCTACCGGACTCACCCAGCGGCCACGAGGACACGCGCGGAC 2257  
1441 GACCGATCGGCATCATCGGCATGCGCTTCGCGGGGAGTCCGCTCCCGAAG 1500  
2258 GACCGATCGGCATCATCGGCATGCGCTTCGCGGGGAGTCCGCTCCCGAAG 2317  
1501 GACCTGTGGAGCTGGCGCGCTTCGCGGGAGAGCGCATCGGCGCTTCGCCACCGACGC 1560  
2318 GACCTGTGGAGCTGGCGCGCTTCGCGGGAGAGCGCATCGGCGCTTCGCCACCGACGC 2377  
1561 GGATGGCCACCGGAAACAGCGTCACGCCAGGACCCACGACCGCGGACGTTCTATCGG 1620  
2378 GGATGGCCACCGGAAACAGCGTCACGCCAGGACCCACGACCGCGGACGTTCTATCGG 2437  
1621 CAGGAGGCGGGTTCCTTTCAGACGCGGCGCATCTTCGAGCGCGCTTCTTCGGAATCAGT 1680  
2438 CAGGAGGCGGGTTCCTTTCAGACGCGGCGCATCTTCGAGCGCGCTTCTTCGGAATCAGT 2497  
1681 CCACGTGAGGCACTGGCGATGATCCGAGACGCGGCTGCTGCTGGAGACGTCCTGGGAG 1740  
2498 CCACGTGAGGCACTGGCGATGATCCGAGACGCGGCTGCTGCTGGAGACGTCCTGGGAG 2557  
1741 GCGTTCGAGCGGGGGAATCGATCCGCTGTGCTACCGGCTCCGTCACGGGCGTCTTC 1800  
2558 GCGTTCGAGCGGGGGAATCGATCCGCTGTGCTACCGGCTCCGTCACGGGCGTCTTC 2617  
1801 GCGGCGCGCTCTCTTCGACTACGCGCGGCTATGGACACCGCTCTCGGAGGCGGC 1860  
2618 GCGGCGCGCTCTCTTCGACTACGCGCGGCTATGGACACCGCTCTCGGAGGCGGC 2677  
1861 GCGGAGGTGAGGGCCACATCTCACCGGTACGAGGCGGCTCTTCGCGGCGGTATC 1920  
2678 GCGGAGGTGAGGGCCACATCTCACCGGTACGAGGCGGCTCTTCGCGGCGGTATC 2737  
1921 GCCTACAGCTTCGGGCTGGAAGGGCGGCGATCACCGTGGACACGGGCTGCTCGGCATCG 1980  
2738 GCCTACAGCTTCGGGCTGGAAGGGCGGCGATCACCGTGGACACGGGCTGCTCGGCATCG 2797  
1981 CTGTGACGCTGCACTCTGGCGTGCAGTCTGCGGTGCGGTGAGTGAAGTCTCGCGCTG 2040  
2798 CTGTGACGCTGCACTCTGGCGTGCAGTCTGCGGTGCGGTGAGTGAAGTCTCGCGCTG 2857  
2041 GCGGCGGCGCTCTGCTCATCTCCACCTCGGCACTTCATCGAGTCTTCGCGGACGCG 2100  
2858 GCGGCGGCGCTCTGCTCATCTCCACCTCGGCACTTCATCGAGTCTTCGCGGACGCG 2917  
2101 GGGCTGTCTGGAGCGGAGTGCAGGCTGCTCGGCTGACGCGGACGCGGACCGGCTGG 2160  
2918 GGGCTGTCTGGAGCGGAGTGCAGGCTGCTCGGCTGACGCGGACGCGGACCGGCTGG 2977  
2161 GCGGAGGCGCTCGGATCTGTGTGAGCGGTTGTGAGTGCAGTGCAGTGCAGTGCAGTGC 2220  
2978 GCGGAGGCGCTCGGATCTGTGTGAGCGGTTGTGAGTGCAGTGCAGTGCAGTGCAGTGC 3037  
2221 CGGGTGCTGGCGGTGAGTACGCGGACGCTGCGGTTCACGAGGCGGTCGCTCGAATGGGCTG 2280  
3038 CGGGTGCTGGCGGTGAGTACGCGGACGCTGCGGTTCACGAGGCGGTCGCTCGAATGGGCTG 3097



QY 2281 ACCGGCCGAAACGGTCCGCTCAGAGCGGGTGATCCGGCAGCGGTGGCGAAACCGGG 2340  
DB ACAGCGCCGAAACGGTCCGCTCAGAGCGGGTGATCCGGCAGCGGTGGCGAAACCGGG 3157  
QY 2341 TTGTCGGTGGCGGATGTGATGTGTGGAGGGGACGGGACCGGGGACGACGCTGGGTGAT 2400  
DB TTGTCGGTGGCGGATGTGATGTGTGGAGGGGACGGGACCGGGGACGACGCTGGGTGAT 3217  
QY 2401 CCGATCAGGACAGCGGTGCTCCGACAGTACGGGACGGGCGGGTGGTACAGGCGGCTG 2460  
DB CCGATCAGGACAGCGGTGCTCCGACAGTACGGGACGGGCGGGTGGTACAGGCGGCTG 3277  
QY 2461 TGGCTGGGGTCTCTGAAGTCCAACTACGGGACACCATGCTGCGCGGGTGTGGGTGGG 2520  
DB TGGCTGGGGTCTCTGAAGTCCAACTACGGGACACCATGCTGCGCGGGTGTGGGTGGG 3337  
QY 2521 GTTCATCAAGATGGTGTGATGTGGGAGGGGGTGTGTCGCCGACAGTGTGATGTGGAT 2580  
DB GTTCATCAAGATGGTGTGATGTGGGAGGGGGTGTGTCGCCGACAGTGTGATGTGGAT 3397  
QY 2581 AAGCCGTCCGCGAGGTGACCTGCTCCGCGGGGGGTGCGGCTGTGACGAGGGGGT 2640  
DB AAGCCGTCCGCGAGGTGACCTGCTCCGCGGGGGGTGCGGCTGTGACGAGGGGGT 3457  
QY 2641 CCGTGGCCCGGGGACCGCGCAGGGGGTGTGCGCGGGGGGGTGGTGGTGGTGGTGGT 2700  
DB CCGTGGCCCGGGGACCGCGCAGGGGGTGTGCGCGGGGGGGTGGTGGTGGTGGTGGT 3517  
QY 2701 GCGCGACCAATGCGCATGTGATTTTGGAGGAGGCGCGCGCGGGGGGGTGTGTGGC 2760  
DB GCGCGACCAATGCGCATGTGATTTTGGAGGAGGCGCGCGCGGGGGGGTGTGTGGC 3577  
QY 2761 GGGGGTGGGGTCTCGAGGGTCTCGGGTCTTGGCATTTTGGTGGTGGTGGTGGC 2820  
DB GGGGGTGGGGTCTCGAGGGTCTCGGGTCTTGGCATTTTGGTGGTGGTGGTGGC 3637  
QY 2821 GCTCAGTGGCTGTGTCTCGCGCGGTGGTGTGAGTGGTGGTGGTGGTGGTGGTGGC 2880  
DB GCTCAGTGGCTGTGTCTCGCGCGGTGGTGTGAGTGGTGGTGGTGGTGGTGGTGGC 3697  
QY 2881 GTTCTGTGCGGTGTGAGTGTGAGGTGTGGTGTGGGCGGAGCGGAGCGGTG 2940  
DB GTTCTGTGCGGTGTGAGTGTGAGGTGTGGTGTGGGCGGAGCGGAGCGGTG 3757  
QY 2941 CGTGAGTACGTGCGGAGTCCGCGCGGAGCTTTCGCTTGGCATGTGGGTGGGTGGC 3000  
DB CGTGAGTACGTGCGGAGTCCGCGCGGAGCTTTCGCTTGGCATGTGGGTGGGTGGC 3817  
QY 3001 TGTGGGCGGGCTGTGTGAGCATCGTGGTGTGCTGGCGCGGACCGTGGAGGCTG 3060  
DB TGTGGGCGGGCTGTGTGAGCATCGTGGTGTGCTGGCGCGGACCGTGGAGGCTG 3877  
QY 3061 GTGCAAGGTGGGGCGCTGCGCGGGTGTGAGCGGATCGCGGGTGTGACACGGGTGAT 3120  
DB GTGCAAGGTGGGGCGCTGCGCGGGTGTGAGCGGATCGCGGGTGTGACACGGGTGAT 3937  
QY 3121 GCGCGGGTGTGACCGGGCGGTGTGCTTTCGTTTCCCGGACAGGGTGGGAGTGG 3180  
DB GCGCGGGTGTGACCGGGCGGTGTGCTTTCGTTTCCCGGACAGGGTGGGAGTGG 3997  
QY 3181 GCGCGGATGGGTGTGCTGTGCTGCTCCTCCTCGGGTGTGCGCGGGCGGATGAGGCG 3240  
DB GCGCGGATGGGTGTGCTGTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 4057  
QY 3241 TCGAGAGGCTCTGCGCGGTGGGTGTGAGTGGTGTGAGTGGTGTGAGTGGTGTGAGTGG 3300  
DB TCGAGAGGCTCTGCGCGGTGGGTGTGAGTGGTGTGAGTGGTGTGAGTGGTGTGAGTGG 4117  
QY 3301 GCGGGGATGCGGTGTGGGAGCGGCGGATGTGGTGTGAGTGGTGTGAGTGGTGTGAGTGG 3360  
DB GCGGGGATGCGGTGTGGGAGCGGCGGATGTGGTGTGAGTGGTGTGAGTGGTGTGAGTGG 4177  
QY 3361 GTGCTTTTGGTCTGTGGGCTTCTACGGTATCGAAACCGGACCGGCTCCTTGGCCAT 3420

DB GTGCTTTTGGTCTGTGGGCTTCTACGGTATCGAAACCGGACCGGCTCCTTGGCCAT 4237  
QY 3421 TCCAGGGCGAGATCGCGCGCGCATGTGTGTGGGGGCTGTGAGCTGAAGACCGCGCG 3480  
DB TCCAGGGCGAGATCGCGCGCGCATGTGTGTGGGGGCTGTGAGCTGAAGACCGCGCG 4297  
QY 3481 AAGACTGTGCTGCGCAGCGCGGCTGTGCGGGGCTGTGCGGGGCGGCGGATGGCC 3540  
DB AAGACTGTGCTGCGCAGCGCGGCTGTGCGGGGCTGTGCGGGGCGGCGGATGGCC 4357  
QY 3541 TCAGTGGCGCTGCTGCGCAGGAGTGTGAGCAGCTCATTTGTGTGAGCGGTGGCGGGCGG 3600  
DB TCAGTGGCGCTGCTGCGCAGGAGTGTGAGCAGCTCATTTGTGTGAGCGGTGGCGGGCGG 4417  
QY 3601 TTGTGGGTGGCGGGGTCAACGGGCGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCGG 3660  
DB TTGTGGGTGGCGGGGTCAACGGGCGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCGG 4477  
QY 3661 GTGGACGAGGTGTGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCGG 3720  
DB GTGGACGAGGTGTGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCGG 4537  
QY 3721 GACTATGCTCGCAGTGTGCGGCGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 3780  
DB GACTATGCTCGCAGTGTGCGGCGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4597  
QY 3781 GGGGACATCAGCGCGCGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 3840  
DB GGGGACATCAGCGCGCGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4657  
QY 3841 CTGGACACCAACCTGTGAGCGCGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 3900  
DB CTGGACACCAACCTGTGAGCGCGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4717  
QY 3901 TTGAGCGATGCGGTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 3960  
DB TTGAGCGATGCGGTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4777  
QY 3961 CCCACACCCCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4020  
DB CCCACACCCCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4837  
QY 4021 ACCGCGATCGGAGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4080  
DB ACCGCGATCGGAGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4897  
QY 4081 GCCCACACCCCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4140  
DB GCCCACACCCCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4957  
QY 4141 CACACACCCCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4200  
DB CACACACCCCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 5017  
QY 4201 CAGCACTACTGGCTGTGAGAGTGTGAGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4260  
DB CAGCACTACTGGCTGTGAGAGTGTGAGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 5077  
QY 4261 GGTTCGGGTGCGGTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 4320  
DB GGTTCGGGTGCGGTGTGCGGGGCTGTGCGGGGCTGTGCGGGGCTGTGCGGGGATGCGGAGCTGTG 5137  
QY 4321 CGGTTCGGGACCGGGTGGCGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTG 4380  
DB CGGTTCGGGACCGGGTGGCGGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTG 5197  
QY 4381 CCCCGCTCGCGCGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTG 4440  
DB CCCCGCTCGCGCGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTG 5257  
QY 4441 CACACCAAGCCCGATCAACCTGTGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTGAGAGCTGTG 4500

[illegible]

QY 6661 GGCCAGTCAACCGATGGTTTTCGACTGACCGAAACCGCGGAGCGGTCTATCTCCGGTGT 6720  
DB 7478 GGCCAGTCAACCGATGGTTTTCGACTGACCGAAACCGCGGAGCGGTCTATCTCCGGTGT 7537  
QY 6721 ATCTCGTACACGTTTGGTTTGGAGGTCTCTGCGGTGTCGTTGGGACACGGCTTGTCTCTCG 6780  
DB 7538 ATCTCGTACACGTTTGGTTTGGAGGTCTCTGCGGTGTCGTTGGGACACGGCTTGTCTCTCG 7597  
QY 6781 TCGTTGGTGGCTTTCGATCTGCGCTGTCAGGCGTTCGCTGCGGCTGAGTGTCTGATGGCG 6840  
DB 7598 TCGTTGGTGGCTTTCGATCTGCGCTGTCAGGCGTTCGCTGCGGCTGAGTGTCTGATGGCG 7657  
QY 6841 CTTTGGCGGGGTGTGACCGTGTATGTCGTCTCCGGGTGCTTCTGCTGGAGTTTTCGCGGAG 6900  
DB 7658 CTTTGGCGGGGTGTGACCGTGTATGTCGTCTCCGGGTGCTTCTGCTGGAGTTTTCGCGGAG 7717  
QY 6901 CGGGGTCTGGCGCGGACCGGCAATTCGAAGGCTTCTCGCGCGCGCGGACCGGACCGGC 6960  
DB 7718 CGGGGTCTGGCGCGGACCGGCAATTCGAAGGCTTCTCGCGCGCGCGGACCGGACCGGC 7777  
QY 6961 TGGGGTGAAGGTGTGGGATGCTGTGTGGAGCGGCTCTCGAGCGCCATCGCAACGGT 7020  
DB 7778 TGGGGTGAAGGTGTGGGATGCTGTGTGGAGCGGCTCTCGAGCGCCATCGCAACGGT 7837  
QY 7021 CACCGTGTCTGGCGGTGTGGGATGCTGTGTGGAGCGGCTCTCGAGCGCCATCGCAACGGT 7080  
DB 7838 CACCGTGTCTGGCGGTGTGGGATGCTGTGTGGAGCGGCTCTCGAGCGCCATCGCAACGGT 7897  
QY 7081 CTGACCGCGGCCCAACGGGCGGTCTCGAGAGCGTGTCTATCCGCGGCGCTTCGCCAACGCC 7140  
DB 7898 CTGACCGCGGCCCAACGGGCGGTCTCGAGAGCGTGTCTATCCGCGGCGCTTCGCCAACGCC 7957  
QY 7141 GCGTGTGTGGCGGTGTGTCACCGGCTGTGGAGCGGCTCTCGAGCGCCATCGCAACGGT 7200  
DB 7958 GCGTGTGTGGCGGTGTGTCACCGGCTGTGGAGCGGCTCTCGAGCGCCATCGCAACGGT 8017  
QY 7201 GACCCGATCGAGCGGCCAGGCCCTCTCGGACCTACGAGACAGGACCGTGTGGCGGAGGG 7260  
DB 8018 GACCCGATCGAGCGGCCAGGCCCTCTCGGACCTACGAGACAGGACCGTGTGGCGGAGGG 8077  
QY 7261 CGCGTGTGGCTGGGTCTGGGTCAAGTCTCAATGTGCGTCAACACAGGCTGTGGCGGCGTC 7320  
DB 8078 CGCGTGTGGCTGGGTCTGGGTCAAGTCTCAATGTGCGTCAACACAGGCTGTGGCGGCGTC 8137  
QY 7321 GCGGGGTGTACAGATGTGTGCTGCGGTGCGGATGCTGCTGCGCGGAGCGTGTGCAT 7380  
DB 8138 GCGGGGTGTACAGATGTGTGCTGCGGTGCGGATGCTGCTGCGCGGAGCGTGTGCAT 8197  
QY 7381 GTGGATGAGCCCTCGCCGCGATGTGACTGCTGCGGGGTGCGGTGCGAGCTGTGACGGAG 7440  
DB 8198 GTGGATGAGCCCTCGCCGCGATGTGACTGCTGCGGGGTGCGGTGCGAGCTGTGACGGAG 8257  
QY 7441 ACGGTGCGCTGCGCGCGGAGGGGCGGTCTACCGCGGCGGAGGAGTGTCTATCTCGGC 7500  
DB 8258 ACGGTGCGCTGCGCGCGGAGGGGCGGTCTACCGCGGCGGAGGAGTGTCTATCTCGGC 8317  
QY 7501 GTACGGGACCAACGCCCAAGTCTCTGAGAGAGCACCGCGCGAGCGTTCGCGG 7560  
DB 8318 GTACGGGACCAACGCCCAAGTCTCTGAGAGAGCACCGCGCGAGCGTTCGCGG 8377  
QY 7561 GGACCAACCGCGCGGAGGGTGTGACCGGCGGACGACGATGAGGCTGTGCGGCGAGTCT 7620  
DB 8378 GGACCAACCGCGCGGAGGGTGTGACCGGCGGACGACGATGAGGCTGTGCGGCGAGTCT 8437  
QY 7621 GGGGTGTGGCGGTGTGCTGTGCGGCAAGTGTGCGAGCGGCGCTTCGCGGCGGAGCCAG 7680  
DB 8438 GGGGTGTGGCGGTGTGCTGTGCGGCAAGTGTGCGAGCGGCGCTTCGCGGCGGAGCCAG 8497  
QY 7681 GCGCTGTGAGCGCCACTCACCGACCAACCGCGGCTTCGAGCTGTGCGGATGATGATAC 7740  
DB 8498 GCGCTGTGAGCGCCACTCACCGACCAACCGCGGCTTCGAGCTGTGCGGATGATGATAC 8557  
QY 7741 CTCGCCCAACCGCGCGGCGGTGTTCGACCAACCGCGGCGGACCGCTCTATCGCGCGGACCGCGAG 7800

DB 8558 CTGCGCCAGCGCGCGCGGTGTTCGACCAACCGCGGCGGACCGCTCTATCTGCGCGGAGCGCGAC 8617  
QY 7801 ACGTTCCTGCAAGCACTTCAGGCACTGCGCGGAGGAGCGGCGGCGGCGGCTATCTCAC 7860  
DB 8618 ACGTTCCTGCAAGCACTTCAGGCACTGCGCGGAGGAGCGGCGGCGGCGGCTATCTCAC 8677  
QY 7861 AGCAGCGCGCGGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 7920  
DB 8678 AGCAGCGCGCGGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8737  
QY 7921 TCCGAGCAGGCGGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 7980  
DB 8738 TCCGAGCAGGCGGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8797  
QY 7981 TCCGCGCGGCGGAGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8040  
DB 8798 TCCGCGCGGCGGAGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8857  
QY 8041 CTCCCGCTCTCACCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8100  
DB 8958 CTCCCGCTCTCACCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8917  
QY 8101 ACCGCTAGCGCGGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8160  
DB 8918 ACCGCTAGCGCGGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8977  
QY 8161 GACGGTGTACACATCAACCGGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8220  
DB 8978 GACGGTGTACACATCAACCGGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 9037  
QY 8221 GCGGCGGCGGAGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8280  
DB 9038 GCGGCGGCGGAGCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 9097  
QY 8281 ACCCTCATGCAACCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 8340  
DB 9098 ACCCTCATGCAACCGGAGCGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAGCGGAGGAG 9157  
QY 8341 ATACCGACACACTTCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8400  
DB 9158 ATACCGACACACTTCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9217  
QY 8401 ACCTCTCTGTCATCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8460  
DB 9218 ACCTCTCTGTCATCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9277  
QY 8461 CAACAAGGCGATCAAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8520  
DB 9278 CAACAAGGCGATCAAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9337  
QY 8521 AACCCGATCTCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8580  
DB 9338 AACCCGATCTCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9397  
QY 8581 ACCCGCTCTACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8640  
DB 9398 ACCCGCTCTACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9457  
QY 8641 CAACAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8700  
DB 9458 CAACAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9517  
QY 8701 GTACACACCTTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8760  
DB 9518 GTACACACCTTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9577  
QY 8761 CTCCCGAACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8820  
DB 9578 CTCCCGAACCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9637  
QY 8821 CACCTCTCTACACCTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 8880

Db	9638	CACCTCCTCACCACCTCCCAAAACCACCAACCACTGGGACCCCACTACACCCAC	9697
Qy	8881	CACGACAAACACCCACACCAACCACTCCGACCTCCCAACCTACCCCTTCCAACAC	8940
Db	9698	CACCAACCAACCCACACCAACCACTCCGACCTCCCAACCTACCCCTTCCAACAC	9757
Qy	8941	CACCACTACTGGCTCGAAAGCAACAGCCCGGTGCGGCAACGTTGACAGCCGGAATC	9000
Db	9758	CACCACTACTGGCTCGAAAGCAACAGCCCGGTGCGGCAACGTTGACAGCCGGAATC	9817
Qy	9001	GACCCACCAACACCCCTACTCCGCGCCACATTTGGAACTCGGACCTGACCGTGAGCG	9060
Db	9818	GACCCACCAACACCCCTACTCCGCGCCACATTTGGAACTCGGACCTGACCGTGAGCG	9877
Qy	9061	CTTCTTTCAGAGCGCTTGTCTTTGAGGTGCGCATCGGTGCTGCTGACCATCGCGTCGGC	9120
Db	9878	CTTCTTTCAGAGCGCTTGTCTTTGAGGTGCGCATCGGTGCTGCTGACCATCGCGTCGGC	9937
Qy	9121	GGCAGGTGCTGCTGTCGGGCGCACCTTCTCTGAACTCGCCCTTTCATGCGGCGCAATAC	9180
Db	9938	GGCAGGTGCTGCTGTCGGGCGCACCTTCTCTGAACTCGCCCTTTCATGCGGCGCAATAC	9997
Qy	9181	GTGGGCTGCGACCGAGTGATGAGCTGACGCTGCAATGCGCCGCTGCTGCTGCTGAT	9240
Db	9998	GTGGGCTGCGACCGAGTGATGAGCTGACGCTGCAATGCGCCGCTGCTGCTGCTGAT	10057
Qy	9241	GGGGGTGTGAGTGTGACAGTTCGGGTTCGGGTGCGGATGGGAGGGCGGCTTTGGTG	9300
Db	10058	GGGGGTGTGAGTGTGACAGTTCGGGTTCGGGTGCGGATGGGAGGGCGGCTTTGGTG	10117
Qy	9301	AGTGTGTATGCGCGGGTGGAAGTGTCTGTGTGCGGGGTGCTGCGTGGGGGTGG	9360
Db	10118	AGTGTGTATGCGCGGGTGGAAGTGTCTGTGTGCGGGGTGCTGCGTGGGGGTGG	10177
Qy	9361	AGTGTGTATGCGCGGGGTGCTGTTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	9420
Db	10178	AGTGTGTATGCGCGGGGTGCTGTTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG	10237
Qy	9421	CTGGCGGGGTGTGGCGCGGGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG	9480
Db	10238	CTGGCGGGGTGTGGCGCGGGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG	10297
Qy	9481	CGTTTGGCTGGGGCTGTTGTTTGGGGCGGGTGGTGGGGCTGGTGGGGCTGGTGG	9540
Db	10298	CGTTTGGCTGGGGCTGTTGTTTGGGGCGGGTGGTGGGGCTGGTGGGGCTGGTGG	10357
Qy	9541	CGTGATGGGGGATTTGCTGCTGAGGTGTCTGCTGCGGAGAGCGCTGGGTGATGCG	9600
Db	10358	CGTGATGGGGGATTTGCTGCTGAGGTGTCTGCTGCGGAGAGCGCTGGGTGATGCG	10417
Qy	9601	GCTGTTTGGGCTGCATCCGGCGTTGCTGGATGGTGGTCCAGCCGTTGTGGGTGG	9660
Db	10418	GCTGTTTGGGCTGCATCCGGCGTTGCTGGATGGTGGTCCAGCCGTTGTGGGTGG	10477
Qy	9661	CTTCCGGGTGGACCGGGTTTCGGGAGGGGCGGGTTTCGGGAGGGGTTCGGGTGCG	9720
Db	10478	CTTCCGGGTGGACCGGGTTTCGGGAGGGGCGGGTTTCGGGAGGGGTTCGGGTGCG	10537
Qy	9721	GCTGTGTGGGGTGTGCTGCTTCAACCGGGCGGGTGTGACCGGTGTGCGGGTGGT	9780
Db	10538	GCTGTGTGGGGTGTGCTGCTTCAACCGGGCGGGTGTGACCGGTGTGCGGGTGGT	10597
Qy	9781	TCGGCTGTGCGGCGGGCGGGCGGTGAGGGCGGTGCTGGTGGTGGGATGAGGCG	9840
Db	10598	TCGGCTGTGCGGCGGGCGGGCGGTGAGGGCGGTGCTGGTGGTGGGATGAGGCG	10657
Qy	9841	GCTGTGCGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	9900
Db	10658	GCTGTGCGGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	10717
Qy	9901	CGTGTCTGCTCGGTTCGGCGGGCGGGCGGGGTTCGTGTATGCGGTGAGTGGGCTGAG	9960
Db	10718	CGTGTCTGCTCGGTTCGGCGGGCGGGCGGGGTTCGTGTATGCGGTGAGTGGGCTGAG	10777
Qy	9961	GTGGGTCTGTGTCGGCTGTGTGGGCGAGGCTGTGGGCTGGGACGAGAGCTGGGTGAGAGC	10020
Db	10778	GTGGGTCTGTGTCGGCTGTGTGGGCGAGGCTGTGGGCTGGGACGAGAGCTGGGTGAGAGC	10837
Qy	10021	GCTGTGGGCTGTGTCGGGCGGGGTGTGTGGTTCGGGTCGCCGATGCGGTCGCCGTGGC	10080
Db	10838	GCTGTGGGCTGTGTCGGGCGGGGTGTGTGGTTCGGGTCGCCGATGCGGTCGCCGTGGC	10897
Qy	10081	GCTGTGGGCTGTGTCGGGCGGGGTGTGTGGTTCGGGTCGCCGATGCGGTCGCCGTGGC	10140
Db	10898	GCTGTGGGCTGTGTCGGGCGGGGTGTGTGGTTCGGGTCGCCGATGCGGTCGCCGTGGC	10957
Qy	10141	GTGACGGGTGTGCTGGGCTGTGAGCGGTTTCGGGCTTCGCGCTGCTGGTGGTGGTGGT	10200
Db	10958	GTGACGGGTGTGCTGGGCTGTGAGCGGTTTCGGGCTTCGCGCTGCTGGTGGTGGTGGT	11017
Qy	10201	GCTGGGTGTGTCGGGCGGGCGGAGGACCGGCGGGGTGGATGCTGGGTGCGTGGGTGGC	10260
Db	11018	GCTGGGTGTGTCGGGCGGGCGGAGGACCGGCGGGGTGGATGCTGGGTGCGTGGGTGGC	11077
Qy	10261	GCGCTGGGTGCTTCGGGCGAGCTGAGCATCCGAGACCGGTTTGTCTCTCGACCTCGAC	10320
Db	11078	GCGCTGGGTGCTTCGGGCGAGCTGAGCATCCGAGACCGGTTTGTCTCTCGACCTCGAC	11137
Qy	10321	ACCGACACCGGACACCGACCTCGACACCGGTCGTGGTGGGCGGTGGATGGTGGG	10380
Db	11138	ACCGACACCGGACACCGACCTCGACACCGGTCGTGGTGGGCGGTGGATGGTGGG	11197
Qy	10381	CGTGTGGGCGGGTGTGTGGCTGAGCCGCGCATGTTGGGCGGTGCTGGGTGGGAGCGGTTG	10440
Db	11198	CGTGTGGGCGGGTGTGTGGCTGAGCCGCGCATGTTGGGCGGTGCTGGGTGGGAGCGGTTG	11257
Qy	10441	CTGGCGGACACCGCTGACACGCTTGGATCATCCGGTGGTGGTGGGCGGTGGGCTGGG	10500
Db	11258	CTGGCGGACACCGCTGACACGCTTGGATCATCCGGTGGTGGTGGGCGGTGGGCTGGG	11317
Qy	10501	GACACACGAGCCCGGCTCGGACGCTGCTGCCACGCGCTCCGCTGGGCTGGCTGGCTGG	10560
Db	11318	GACACACGAGCCCGGCTCGGACGCTGCTGCCACGCGCTCCGCTGGGCTGGCTGGCTGG	11377
Qy	10561	CGGTGGGTGGATGATTCGGGTGGGAGGCTGTCGGCTGGGTGGTGGGTGGGTGGGTGG	10620
Db	11378	CGGTGGGTGGATGATTCGGGTGGGAGGCTGTCGGCTGGGTGGTGGGTGGGTGGGTGG	11437
Qy	10621	GTGACGGGTGGAGCGGGTGTGCTGGGTGGGCGGGTGGGCGGCACTGGCTGGGTGGT	10680
Db	11438	GTGACGGGTGGAGCGGGTGTGCTGGGTGGGCGGGTGGGCGGCACTGGCTGGGTGGT	11497
Qy	10681	GGGGTGGCGGATCTGCTGTGGTGGGCGGGTGGTGGGATGCTCCGGGTGGCGAGGGT	10740
Db	11498	GGGGTGGCGGATCTGCTGTGGTGGGCGGGTGGTGGGATGCTCCGGGTGGCGAGGGT	11557
Qy	10741	CTGCGGGCGGAGCTGGCGGCTTGGGGCGGAGGTCGGAATGTTGGTGGTGGATGTTGGG	10800
Db	11558	CTGCGGGCGGAGCTGGCGGCTTGGGGCGGAGGTCGGAATGTTGGTGGTGGATGTTGGG	11617
Qy	10801	GAGCGGGCGGAGCTGGCGGCTGCTGGGAGGGTGTTCCTGGGCGGGTGGCTGGAGCGGT	10860
Db	11618	GAGCGGGCGGAGCTGGCGGCTGCTGGGAGGGTGTTCCTGGGCGGGTGGCTGGAGCGGT	11677
Qy	10861	GTGCTGATCGGGTGGTGTGCTGGATCGACGATCGGCTGCTCTCAACCGGCGGAGGG	10920
Db	11678	GTGCTGATCGGGTGGTGTGCTGGATCGACGATCGGCTGCTCTCAACCGGCGGAGGG	11737
Qy	10921	CTGGGACCGGTGTTTCGGGCGCAAGGTGGATGCGGCTCTTTTGTGGATGAGTGGAGCGG	10980
Db	11738	CTGGGACCGGTGTTTCGGGCGCAAGGTGGATGCGGCTCTTTTGTGGATGAGTGGAGCGG	11797
Qy	10981	GATATGAGAGCTGTGGGCGGTTCGTGCTGCTGGGCGGGGATGCTTGGGGTGGGCTG	11040
Db	11798	GATATGAGAGCTGTGGGCGGTTCGTGCTGCTGGGCGGGGATGCTTGGGGTGGGCTG	11857

QY 11041 GGGAGGCACTACCGCGGCAATGCGCTCTGGAGCGCTGCGTACCGGCGCG 11100  
 DB 11858 GGGAGGCACTACCGCGGCAATGCGCTCTGGAGCGCTGCGTACCGGCGCG 11917  
 QY 11101 GGGCGGGTCTGCGGGGCTGCTGCTGGGCTGTGGAGAGCCAGCGGGATG 11160  
 DB 11918 GGGCGGGTCTGCGGGGCTGCTGCTGGGCTGTGGAGAGCCAGCGGGATG 11977  
 QY 11161 ACCGGCACCTGGCGGCAACGACACCGCGGCATCATCGTTCGGTCTGATCCCATG 11220  
 DB 11978 ACCGGCACCTGGCGGCAACGACACCGCGGCATCATCGTTCGGTCTGATCCCATG 12037  
 QY 11221 TCGACCCCGAGCACTGGCCCTCTTCGATGCGGCGCTGCTGACCGCGCGTCTG 11280  
 DB 12038 TCGACCCCGAGCACTGGCCCTCTTCGATGCGGCGCTGCTGACCGCGCGTCTG 12097  
 QY 11281 CTGCGCGGCACTGGCTCCGCGCCCGCCCTGCGGCGCTGCTGAGGACCTCTCGGCC 11340  
 DB 12098 CTGCGCGGCACTGGCTCCGCGCCCGCCCTGCGGCGCTGCTGAGGACCTCTCGGCC 12157  
 QY 11341 GCCACCGCGCGGCAACCGCACCGCACCTACCGGTGTGGGACCAACGCGGCCAG 11400  
 DB 12158 GCCACCGCGCGGCAACCGCACCGCACCTACCGGTGTGGGACCAACGCGGCCAG 12217  
 QY 11401 CTGACCGCGGCTGGCGGCGGAGACACAGAACACAGCACACACCTCTCGCCCTG 11460  
 DB 12218 CTGACCGCGGCTGGCGGCGGAGACACAGAACACAGCACACACCTCTCGCCCTG 12277  
 QY 11461 GTCCGCTCCACATGCCACCGTCTGGGCGCACACACCCCGGACACCATCCCGCGAC 11520  
 DB 12278 GTCCGCTCCACATGCCACCGTCTGGGCGCACACACCCCGGACACCATCCCGCGAC 12337  
 QY 11521 CCGCGGTTCGCGACCTGGCTTCGACTCCCTCAGCGCGCTCGA 11564  
 DB 12338 CCGCGGTTCGCGACCTGGCTTCGACTCCCTCAGCGCGCTCGA 12381

## RESULT 5

AAA92302

ID AAA92302 standard; DNA; 31422 BP.

AC AAA92302;

10-JAN-2001 (first entry)

S. avermitilis avermectin aglycon synthase DNA aveAII SEQ ID NO:2.

KW Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis;  
 KW multifunctional enzyme; polyketide; avermectin; veterinary drug;  
 KW agrochemical; ds.

OS Streptomyces avermitilis.

FH Key Location/Qualifiers

CDS 1..14646

FT /\*tag= a

FT /note= "avermectin aglycon synthase protein"

FT 14824..31422

FT /\*tag= b

FT /note= "avermectin aglycon synthase protein"

XX WO200050605-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-JP01041.

XX 24-FEB-1999; 99JP-0046961.

XX (KITA) KITASATO INST.

XX Omura S, Ikeda H;

XX

PI

DR WPI; 2000-565458/52.  
 DR P-PSDB; AAB23751, AAB23752.  
 XX Avermectin aglycone synthase DNA and proteins encoded by all or part of  
 PT it for the production of avermectin and its derivatives for drug and  
 PT agrochemical use  
 XX Claim 2; Page 134-203; 314pp; Japanese.  
 PS  
 XX The present sequence represents DNA which encodes avermectin aglycon  
 CC synthase proteins. Also described are: (1) polypeptides encoded by all  
 CC or part of the DNA; (2) expression vectors containing the DNA; (3) host  
 CC cells transformed by the vectors; (4) preparation of the polypeptides  
 CC by culture of the transformants; (5) preparation of avermectin aglycon  
 CC or its derivatives by culture of transformed avermectin-producing  
 CC microorganisms; and (6) oligonucleotides of 5-60 bases in length  
 CC containing sense or antisense sequences from the avermectin aglycon  
 CC synthase DNA. The enzymes are useful for the production of modified  
 CC forms of avermectin and of the intermediates in its biosynthesis, for  
 CC use as drugs, veterinary drugs and agrochemicals.  
 XX Sequence 31422 BP; 4136 A; 10238 C; 11677 G; 5371 T; 0 other;  
 SQ

Query Match 21.0%; Score 6437.2; DB 21; Length 31422;  
 Best Local Similarity 69.9%; Pred. No. 0;  
 Matches 9934; Conservative 0; Mismatches 2928; Indels 1350; Gaps 39;  
 QY 1423 GGCACGGCAGCGGGAGCAGCCGATCGCCATCATCGGCATGGCATCGCTTTCCCGGGC 1482  
 DB 14917 GCCATGGAGGGTCCAGCGAGCCGATTCGATTTGGGGATGGCGTGTCTTTCCGGGT 14976  
 QY 1483 GGATTCGGTCCCGAGGACCTGTGGAGCTGGCGCTGGGGGAGAGCGCATCGG 1542  
 DB 14977 GGGGTGTTCGCGGAGAGTTGTGGAGCTGGTTCGGTGGGGTGGGATGCGATTGGT 15036  
 QY 1543 CCGTTCCCGACCGCGGATGGCCACGACGATCGCCAGCGATCGCCAGCCCGACCGAG 1602  
 DB 15037 GAATTCGCGCGGTGGGGTGGGATCTGGAGGGTGTGTTGATTCGACCTGACCGG 15096  
 QY 1603 CCGGCGAGTTCTATCCGACGGAGGGGTTCCTTACAGACGGCGGCGCATTCGACGCC 1662  
 DB 15097 TCGGGGACGTCTGACGCGCGGTATGGCGGGTTCCTGTATGAGGGGGGAGTTCGATCG 15156  
 QY 1663 GGCTTCTTCGGAATCAGTCCACGAGGACCTGGCGATGGATCGGCACGCGGTGCTG 1722  
 DB 15157 GACTTCTTCGGGATCAGTCCGCGGTGAGCGTGGCGATGGATCGGCACGCGGTGTGTG 15216  
 QY 1723 CTGGAGACGTCTTCGGAGCGCTTCGAGCGGCGGGAATCGATCGGCTCTCGGTACCGGG 1782  
 DB 15217 CTGGAGACGTCTTCGGAGCGCTTCGAGCGGCGGATTCGATCCGCTCGATCGGTGGC 15276  
 QY 1783 TCCGTAAGCGGCTTCGCGGGCGCCCTCTCTTCGACTACGCGCCCGGTATGACACC 1842  
 DB 15277 TCCGTAAGCGGCTTCGCGGGGTGATGTACACGACTACGATCCGCTCGGTACC 15336  
 QY 1843 GCGTCTCGAGGGGCGCGGACGTGGAGGGCGACATCTCTACGCGGTACACCGGGGAGC 1902  
 DB 15337 -----ATCCCCGAGGGATTCGAGGGCTACATCGGCAACGGTAGCGGGGCGCC 15384  
 QY 1903 GTCCTGTGGGCGGTATCGCCTACAGCTTCGGGCTGGAAGGCGCGCGGATCACCGTGGAC 1962  
 DB 15385 GTCGCGTGGGCGCGCTCGCTACACGCTCGGTCTCGAGGGCGCTGCGCTCTCGGTGGAC 15444  
 QY 1963 ACGGGGTCTCGGCATCGCTCGTACGCTGATCTGGCGTCCAGTCTCGGTGCGGT 2022  
 DB 15445 ACGGCATGTTCTGCTGCTGGTGGCGGTGATCTGGCGTCCAGTCTCGGTGCGGT 15504  
 QY 2023 GAGTGCAGCTCGCGTGGCGGGCGGTCTCGGTGATGTCACCTCGGATGTTATC 2082  
 DB 15505 GAGTGCAGCTCGCGTGGCGGGCGGTGACGGTGTGATGACACCGGACCTCTTCTC 15564  
 QY 2083 GAGTTCCTCCGCGACGCGGGCTCTCGGTGACGCGGAGGTGCAAGGGGTACTCTCGGTGCA 2142



Db	15565	GAGTTCTCAGCCAGCGGGA	CTGTGGTGGACGCGCGCTGCAAGTCTCTTCGCGGTGA	15624
Qy	2143	GCCGACGACCGGCTGGGGCGAGGCGCTCGGGA	TGCTTGGTGGAGCGGTGTTCGGAT	2202
Db	15625	GCCGACGACCGGCA	TGGCGAGGCGGTTCGGGATGCTGTTGGTGGAGCGGTGTTCGGAT	15684
Qy	2203	GGGTGCGGCTGGGGCATCGGGTGTGCGGTGTGCGGTGGTACGCGGCAGTGCGGTCAACGAGAC	2262	
Db	15685	GGGTGCGGCTGGGGCATCGGGTGTGCGGTGTGCGGTGCTGCGCGGCA	TGCGGTCAATCAGGAC	15744
Qy	2263	GGTGGCTCGAATGGCTGACGCGCGGACGCGTCCGGCTCAGGAGCGGGTGTATCCGGCAG	2322	
Db	15745	GGTGGCTCGAATGGGTTCAGCGCGCGCAATGGTCCGGCTCAGGAGCGGGTGTATCCGGCAG	15804	
Qy	2323	GGTGGGCAACCGGGGTTCCTGGCGGATGTGGATGTGGTGGAGGGGACGCGGACG	2382	
Db	15805	GGTGGGCAACCGGGGTTCCTGGCGGATGTGGATGTGGTGGAGGGGATGGGACG	15864	
Qy	2383	GGCAGACGCTGGGTGATCCGATTCBAGGCA	CAGGCGTTCGCGCACATCGGGCAGCGG	2442
Db	15865	GGCAGACGCTGGGTGATCCGATTCBAGGCGCAGGCGTTCGCGCACATCGGGCAGCGG	15924	
Qy	2443	GCCGCTGACAGCCGCTGGCTGGCTGGGCTCTGAAGTCCAAATCGGGCAGACCATGGT	2502	
Db	15925	GCCGCTGACAGCCGCTGGCTGGCTGGGATCGGTGAAATCGAAATCGGGCAGACCATGGT	15984	
Qy	2503	GCCGCGGTGTGGGTGGGTATCAAGATGGTGTGGCGTTCGCGGAGGGGTGTTCGCG	2562	
Db	15985	GCCGCGGTGTGGGTGGGTATCAAGATGGTGTGGCGTTCGCGGAGGGGTGTTCGCG	16044	
Qy	2563	CGGAGTGTGATGTGGATTAAGCCGTGCGCGCAGGTGGATGCTGCTCGCGGGCGGTTCGCG	2622	
Db	16045	CGGAGTGTGATGTGGATTAAGCCGTGCGCGCAGGTGGATGCTGCTCGCGGGCGGTTCGCG	16104	
Qy	2623	CTGCTGACGAGCGGCTGGCTGGCGGGGACGCGGACGCGGCTGGCGGGCGGGA	2682	
Db	16105	CTGCTGACGAGCGGCTGGCTGGCGGGGACGCGGACGCGGCTGGCGGGCGGGA	16164	
Qy	2683	GTGCTGCTCGTTCGGGATCGGCGGACGAATGCGCATGTGATTTGGAGAGCGCGGCG	2742	
Db	16165	GTGCTGCTCGTTCGGGATCGGCGGACGAATGCGCATGTGATTTGGAGAGCGCGCGGCG	16224	
Qy	2743	CGCGGGGCTGTGTTCCCGGGGTGGGTGTTGGAGGGTGTCCGGGTTCGCCATTTGCG	2802	
Db	16225	CGCGGGGCTGTGTTCCCGGGGTGGGTGTTGGAGGGTGTCCGGGTTCGCCATTTGCG	16284	
Qy	2803	GTGGCTGAGTCCGTGGCGCTCCAGTGGCTGTCTGCGCCGGTGGCTGAGTCCGTGCGG	2862	
Db	16285	GTGGCTGAGTCCGTGGCGCTCCAGTGGCTGTCTGCGCCGGTGGCTGAGTCCGTGCGG	16344	
Qy	2863	GTGCGGCTGCGGCTGCGGCTTCCTGTGCGGGTGTGGCTGAGGCTGAGGCTGGGTTGCGG	2922	
Db	16345	GTGCGGCTGCGGCTGCGGCTTCCTGTGCGGGTGTGGCTGAGGCTGAGGCTGGGTTGCGG	16404	
Qy	2923	CGCAGGCGGAGCGGTTCGCTCAGTACGTGGCAGTCCGCGCGGACGTTTCGCTTCGCGAT	2982	
Db	16405	CGCAGGCGGAGCGGTTCGCTCAGTACGTGGCAGTCCGCGCGGACGTTTCGCTTCGCGAT	16464	
Qy	2983	GTGGGTGCGGCTGCGCTGTGGCGGGCTGTGCTGGAGCATGCTGCGGTCTCTGCGC	3042	
Db	16465	GTGGGTGCGGCTGCGCTGTGGCGGGCTGTGCTGGAGCATGCTGCGGTCTCTGCGC	16524	
Qy	3043	CGGGACCGTGGAGCTGTGCAAGGTTGGGGGCGCTGGCGCGGGTGGAGCGGATCGG	3102	
Db	16525	CGGGACCGTGGAGCTGTGCAAGGTTGGGGGCGCTGGCGCGGGTGGAGCGGATCGG	16584	
Qy	3103	CGGGTGACCA	CGCGGGTGTGACCGGGGCGGTGCTCTTCGTTGTTTCC	3162
Db	16585	CGGGTGACCA	CGCGGGTGTGACCGGGGCGGTGCTCTTCGTTGTTTCC	16644
Qy	3163	GGACAGGGTGGGAGTGGCGCGGGATGGGTGTGCTGCTGCGCTCTCTCGGTGTTTC	3222	
Db	16645	GGACAGGGTGGGAGTGGCGCGGGATGGGTGTGCTGCTGCGCTCTCTCGGTGTTTC	16704	
Qy	3223	CCCCGGGGATGCAAGGCTGCGAGAGGCTCTGCGCGCGTGGGTGGAGTGGTCTGTGTG	3282	
Db	16705	CCCCGGGGATGCAAGGCTGCGAGAGGCTCTGCGCGCGTGGGTGGAGTGGTCTGTGTG	16764	
Qy	3283	GACATCTGCGCGGGACCGGGGATGCGGTGTGGAGCGGGCGGATGTTGGTCCAGCT	3342	
Db	16765	GACATCTGCGCGGGACCGGGGATGCGGTGTGGAGCGGGCGGATGTTGGTCCAGCT	16824	
Qy	3343	GTGCTGTTACGCTCATGCTGCTGTTGGCTGCTGTTGGCGTTCCTACGCTATCGAACCC	3402	
Db	16825	GTGCTGTTACGCTCATGCTGCTGTTGGCTGCTGTTGGCGTTCCTACGCTATCGAACCC	16884	
Qy	3403	GACGCGGTCTTGGCCATTCCAGGGCAGATCGCGCGCGCCATGTTGTGTGGGCGGTG	3462	
Db	16885	GACGCGGTCTTGGCCATTCCAGGGCAGATCGCGCGCGCCATGTTGTGTGGGCGGTG	16944	
Qy	3463	AGCCTGAAGACCGGCGGAACTGTTGCGCTGCGAGCGGGCGCTGGCGCTGTGCGG	3522	
Db	16945	AGCCTGAAGACCGGCGGAACTGTTGCGCTGCGAGCGGGCGCTGGCGCTGTGCGG	17004	
Qy	3523	GCGCGGGCGCATGGCTCAGTGCCTGCTGCCAGAGGTGGAGCAGCTCATTTGT	3582	
Db	17005	GCGCGGGCGCATGGCTCAGTGCCTGCTGCCAGAGGTGGAGCAGCTCATTTGT	17064	
Qy	3583	GAGCGGTGGCGGGCGGTGTTGTTGGTGGCGCGGTCAACGGGCCCCCGCTCCACCGCGCTC	3642	
Db	17065	GAGCGGTGGCGGGCGGTGTTGTTGGTGGCGCGGTCAACGGGCCCCCGCTCCACCGCGCTC	17124	
Qy	3643	TCGGGGATGCGGAGCGGCTGAGAGTGTGCGGTATCTGTGCGGGCAGCGGGGTGCGG	3702	
Db	17125	TCGGGGATGCGGAGCGGCTGAGAGTGTGCGGTATCTGTGCGGGCAGCGGGGTGCGG	17184	
Qy	3703	GCCCGGGATGCCGCTCGACTATGCTGCGACATGCCCCCATGTGACGCCCTCGCGGAG	3762	
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Query Match 10.2%; Score 3142; DB 20; Length 80161;
Best Local Similarity 49.2%; Pred. No. 0;
Matches 15063; Conservative 0; Mismatches 12830; Indels 2753; Gaps 147;

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RESULT 14
AAZ21501
ID AAZ21501 standard; DNA; 80161 BP.
AC AAZ21501;
XX
XX 01-DEC-1999 (first entry)
DE DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes.
KW Spinosyn biosynthetic enzyme; open reading frame; ORF; insecticidal
KW microlides; arachnid; nematode; insect; polyketide; polyketide synthase;
KW PKS; extender module; initiator module; acyl transferase domain; AT;
KW acyl carrier protein; ACP; beta-ketosynthase domain; KS; KR;
KW dehydratase domain; DH; enoyl reductase domain; ER; beta-ketoreductase;
KW insecticide; ss.
XX
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Qy 25380 GGGTGTGACGCTGATGCTCTCCGGGTACGTTTGTGGAGTTCTCAGCTCAGCGGGTCT 25439  
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Qy 25440 GCGCGGAGCGGCGGCTGCAAGGCTTATTGCGCGCTGCTGACGCTACCGCTGGGCGCA 25499  
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Db 33254 GTGCTGGCGGGCAGGGCGTTATGCGCGCGGATGCTTGTGATGGTGTGGCGCAGC 33313  
Qy 19370 ACCGCCACACCCACCACTCCCGCCACACAGATCGCTGGGGCACCTGGGCAAGAAACG 19429  
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Qy 19430 GACTGGCGACTGGTCAAGTCAAGCAACATCTCGCGCGCGCGGGATGTTGGCCATCGCGC 19489  
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Db 35222 AACCAACACCTCGA-----ACCAGCGAGATCGACCAAT 35257  
Qy 21344 CGGAGGAGGCTGTGCGCGGAGTCTGGGGTGTGGCGGTGGCTGTGTCGCGCAAGTGC 21403  
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Qy	17174	CCCTCCACCGCCTCCTCACCAGAGCGGTACCAATCACCACCCCACTACTACGCGGAGACT	17233
Db	31145	GACT---CTGGAGATTGTTGGGTTCGTGGGGTGTTCGGGCCGCTGTGTGTCTGGGCCACT	31201
Qy	17234	CCCTCGCGCAAAATCACCGCGCGCCCACTCGCCGGCATCCTCACCTCATCCGACGCCACCA	17293
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Qy	17411	CCATCGCCGCCATCAACACCCCACTCCTCCTCGTCATCAGCGGCAACCCCAACACCGTCC	17470
Db	31382	GGATCGCGGGGTCAACGCTCCGGGTGGTGTCTCTCCGGTGTATCGGAGTGTGCTCG	31441
Qy	17471	AACATATACACCCCTCTGCGCAACAAAGGATCAAAACCAAAACCTCCCAACCAAAA	17530
Db	31442	ATGACATTCGGGTCCGCTGGACGGGCAAGGATCCGTCACAGTGTGTTCGGGTTTCGC	31501
Qy	17531	ACGCTTCCACTCCCCCAACCAACCCCATCCTCAACCACTCCACAGACACACCAAA	17590
Db	31502	ATCGCTTTCATTGCGCATCGATGGATTCGATGCTGGCGAGTTACCGAAATCGCCGGGA	31561
Qy	17591	CCCTCACTTACCAACCAACCCCAACCCCTCATCACGCCCAACAC-----CC	17638
Db	31562	CGGTGCACTACCGGTCTCAGGGCTGCCGATCGTGTGAGCTGTGAGCGGTGAGCTCGATG	31621
Qy	17639	CACCCGACCAACTCTCAACCCCACTACTGTGACCAACAAAGCCCGCAACACCGTCTGACT	17698
Db	31622	AGGTTCGCATGCGGGTACGCGGAGTATTGGGTGCGCAGGTGGAGAAACCCGTCGCCCT	31681
Qy	17699	ACGCCACCAACCCCAAAACCTCCACCAACAGGGGTACACCTTACATCGAATCTCGGAC	17758
Db	31682	TCGCCGACGGTGTGTGTCGGCTCGCGGTTCAGCGGTGAGCACCGTCTCGAGGTCTCGT	31741
Qy	17759	CCGACAACACCTTCACACCTCACCCACCAACCTCCCCAAACCCCAACCAACCCAC	17818
Db	31742	CGATGGGGTGTGTTCGGGCTGGTCAGAGATGCGCGCCGGATCCGATCAGGGCGGAC	31801
Qy	17819	TCACCTTCACCAACCCCAACCAACCCCAACCAACCTCTCAACCACTCTGCAAAA	17878
Db	31802	GGGTGGCGGGTTCGCTCATGCGAGCAATTCGCGACGAGCGCACACGGTGACAACGG	31861
Qy	17879	CCACCAACCTTGCAACCCCAACCACTACCAACCAACCAACCAACCAACCAACCAAC	17938
Db	31862	CATTGGCGCAGATCCATGTGCTGTGTGCTGAGGTGACTTGGCGGTCTGTTTTTCGCGGTA	31921
Qy	17939	CC-----CACCTCGACTCCCCCACTTACCCCTTCCAAACACGAGCACTACTGGCTCG	17989
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Qy	17990	AAAGCAACAGCGGGTGGCGATCCGGTTCGGTTCGGTTCGGGGCGGGCAGGGACTG	18049
Db	31982	ACTCACCAT-----CCGAACCGGT-----CGGGCAATCCGCGCATC	32017
Qy	18050	CGGGCGGACGGCAGAGTGGATCGGGTTCGGGACCGGTGGCCCGCCAGGACTGG	18109
Db	32018	CCGCGGCCAGTCCGGGCTTCGGGAATCTGTCGAGCAGGAAGATGTACGCGCGCTCAGCG	32077
Qy	18110	AAAGGTTCGGACACGACTCGCGCTGCCCTCTCGCGCGCTGGACACGGTGTGCGCG	18169
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19070 ACACGAGNACCCAGACCAACTCCMAACTCTTCAACACCATCCCCCAACCAACCCCC 19129  
33014 AGTGGCCGATCGTACGCTTTGGCCGAAGTGTGTGGCAACATTCGGGATGATGCCCCG 33073  
19130 TCACCAACGTCATCCACACCGAGGCAATCTCGACAGCGCAACCCCTCAACCACTCAAC 19189  
33074 TGACCGCGGTGATGATCGCGCGGGGTGCTTGAAGTGTGGGACATGTGGGTGATGTGTT 33133  
19190 CCACCAACTCAACAAAGTCTCTCGCGCCAAAGCCCAACGCGCCCACTCTCCACCAAC 19249  
33134 TGACCGACTTCTGTTGGGTGCTGTGCGCGAAGCGAGGTGTGGCGGAATCTCGATGAT 33193  
19250 TCACCAACACACCCCTCAAGCCCTTGTCTCTACTCTCTCGCGCGCGCAACTCTCG 19309

Db	29003	CGAGGAAACAGCCAAATTCCTAGGCGCGGATGAGGAGCACTGTTGGTGTTCGGG 29062	QY	16034	GCACGGGCTGACGGCGCCCAACGGGCGGTCCACAGGAGCGTGTCTATCCGCTTGGCCCTGG 16093	
QY	14957	CCCATCGCGCGCTGTGCTGGGCGCAATGCCACTCCCGAAGTGATCGTTCGGAACAAGGCT 15016	Db	30143	CGAATGGCTTGACTGCGCGCAATGTCGTACACGAAAGGCTGATCACCAGGCACTCA 30202	
Db	29063	AGCAGTTTCGCGCGTGTGGGTATTCGGGTGCGGTGAGGTTGGGGCGACCGTGTCT 29122	QY	16094	CAACCGCGGACCTGACCCCGCGGACGTCGTGATCGGTGAGGCCCAACGGCACCGGACCA 16153	
QY	15017	TCAAGAGCTGGGTTTGATCTCTGCGCGCAATTCAGCTTCGTAAATCGACTGCTTGCTG 15076	Db	30203	CGAGTCCCGGCTGTCCGTGTCCGACGTGATGCTGTGAGGCGCATGGGACGGGCACGC 30262	
Db	29123	TCCGTGATCTGGGTTTGATTCGTTGCTGGCGTGAGTTGCGGAACCGCTTGCCGGGG 29182	QY	16154	CTTTGGGCGACCCGATCGAGGCGCCAGGCCCTCTCCGACACTACGACAGGAGCCGCCCG 16213	
QY	15077	AGTTTGACCTGCGGCTTCGGGCCACGCTGATCTTCGATACCCCACTCGATGGGCTTT 15136	Db	30263	GGCTTGGTGATCCGATCGAGGCGCAGGCGTTGATCGCTACGTACGCGCGGGATCGTGATC 30322	
Db	29183	TGCTGGGGTGGGTTGCGCGGCACTGCGGTGTTGCACTATCCGACGCGCGGGGCGTGG 29242	QY	16214	GCAACGAACCGCTGTGGCTGGGCTCGATGAAGTCAAGTCAATCGGCCACGCGCAGGTTGCCG 16273	
QY	15137	GCCAGTTCTCCGGCGGGCGATGCTCGAGCGGACACAGGCGACGACCACTCGTCTGCGCG 15196	Db	30323	CCGCTCGCGCGTTGTGGCTGGGGTCGGTGAAGTCGAATATTTGTCACACCAGCGGGCGG 30382	
Db	29243	CCGTTTCTCGATCAGGNACTGGCAGGCGAGGTGCGTCCAGTCCAGTCCGCGGTGACCA 29302	QY	16274	CAGGTGTGGCGGGGTCAATCAAGATGATGGCGCTCGGGAATGGTCTGTCTGCCGCGGA 16333	
QY	15197	TAACTGCGGTCCCCCGGACGAGCCGATGCCATCGTCGGCATGGCTGTTCGGTACCCCG 15256	Db	30383	CGGGTGTGCTGCTGATCAAGATGATGGCGATCGGCGAGGGGAGCTGCCGCGCA 30442	
Db	29303	GGGACGCGAGTCCGGAAGAGGATCTTGTTCGATTTGTCGGATGGATGCTGCTTTCCGG 29362	QY	16334	CGTTGATGTGGATGAGCGGTGCGCGCATGTGGACTGCTCCGCGGGGCGGTGCGAGTGC 16393	
QY	15257	GTGATGTACGAGCGGTGATGATCTGSCAGGTGTCAGTGGTGCCATGACGCGATCG 15316	Db	30443	CGTTGCACTGGAACAGGCCCTCCGCGCAGGTGGAATGCTCTGCGGGCACGCTCAACTCC 30502	
Db	29363	GTGGGGTGTCTGCGCGGAGGAGCTTTGGCGGCTGTGGCGCGCGCGTGGATGCGGTGG 29422	QY	16394	TGACGGAGACGCTGCTCGGCCCGCGGGGAGGGCGGCTGCGCGGGCAGGAGTGTCTCAT 16453	
QY	15317	GCGGATTCGCGAGAACCGTGGGTGGGACTCTGACACGCTGTACAAACCGGACCCGAGCC 15376	Db	30503	TCA CGGAGAACACGCCCTTGGCCCGACAGC---GGTCTGCTTCGCGGGGCGGCTGTCTAT 30559	
Db	29423	CTGGGTTCCAGACGATCCGCGCTGGATCTCGCGGGTGTGACGATCTGATCCCGATC 29482	QY	16454	CGTTCCGGCTCAGCGGCAACCAACGCCACGCTCATCTCTGAAGAGCAACCCGCCCAACA 16513	
QY	15377	ACCACGGAACAGCTACACCGGAGCGGCGATTCCTTTACGACGACGCAATTTGATC 15436	Db	30560	CGTTCCGGATCAGTGGGCAACCAACGCGCACTGATCTTTGAACAACCTCCG----- 30609	
Db	29483	GTCTCGGACCTCGTATGTTGTGAGGGCGGTTCTGCGGACGCGCGGAGTTCCGATG 29542	QY	16514	TCCCGTCAGACACACCCCGCGACGCGCCCGGGAGAGCAGCCCGCGACGATGTTCCGG 16573	
QY	15437	CCGACTTCTTCGTTATCAGTCGCGTAGGCACTGCGGATGAGAACCCGACGAGCGGCTGC 15496	Db	30610	-----CGA 30612	
Db	29543	CTGACATGTTCCGCACTACGCCCGCTGAGCGCTTGGCGATGATCCGACGACGCGTTGC 29602	QY	16574	GGGAAGCGCGCGGACGACGCGGTACCGGGGGAAGCAGTGGTCTCTGCTGCGGCA 16633	
QY	15497	TGCTGGAAACAGCGTGGGAGACATCGAACACGCTGATCAACCCCGACAGCCTCCGTTG 15556	Db	30613	GAGTCGAGCGCTCAACAGAGCGGATTCGG-----GTTCTGTCCGG 30655	
Db	29603	TGCTGGAGTCCCTTGGGAACCTTTGGAGCGGCTGGGATCGATCCGTTCTGTTGCAAG 29662	QY	16634	GTCCAGGGGTGTGCGCTGTGCTGCGGCAAGTCGACGCGGCTTCCGCGGCCAGG 16693	
QY	15557	GCACACCAACCGCGCTTCTCGCGGGCTGACCTACCAAGCTACGCGCGCGG---CTTTTC 15613	Db	30656	ATTTTCCGGTGTGCGGTGGATGTTGTCGGGCAAAACACCCGAAAGCGCTATCCGCGCAG 30715	
Db	29663	GCAGCGGACCGGTGTGTGCGGGCTTGATGTACCAAGCTATGCGGCGCGGATTCATTA 29722	QY	16694	CCCAGGCGCTGACGCGCCACCTCACCGACACCCCGGCTCGACCTCGCGGAGTGTGGGT 16753	
QY	15614	CCAGAGCTCCGCGAGGTTTCGAGGGGTATCTCGGCGACGGAAGCGAGCGAGTATCGCT 15673	Db	30716	CAGATGCAATGATGTCCTTCTGAGCAATCGCTTGTCTCCCGCGAGATATCGGTT 30775	
Db	29723	CCAGAGCACCGGAGGCTTCGAAGGGCACCTCGGAGCGGGCAATCGCGGGAGCGTGTGT 29782	QY	16754	ACACCTCGCCACGCGCGCGCTGTTTCGACCAACCGCGCCACCTCATCGCGCGGAC 16813	
QY	15674	CGGTCGTTGTCGCTACGCTCTCGGCTGGAGAGTCCGSCCTCACAGTCGACACTGCT 15733	Db	30776	ATTGCTTGGGTGACCGCTCGGGTTGGACACCGCGCTGTGCTGTGGTGGGATC 30835	
Db	29783	CGGTCGGGTTGCGTATTCGTTGTTGAGGGTCTGCGGTGACGGTGGATACGGCGT 29842	QY	16814	CGCACACTTCTCTGCAAGCACTCCAGGCACTCGCGGAGGCAACCCCAACCCCGCGTCA 16873	
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Db	29843	GTTCTGCTGCTGTTGTGCGGTTACACCTGGCGGCTCAAGCACTGCGGCGCGGTGAGTGG 29902	QY	16874	TCCACAGCAGCGCCCGAGCGGACCGGGAACGGGAGCGCGAGGAAGACCGCATTC 16933	
QY	15794	CCATGGCCCTCGCGGTGGGCTCAAGGTGATGTCATCAACCCCGCGCGGTTCGTGGAGTTT 15853	Db	30896	TCACCGGCACTCGT-----GCGGCTGGGCGGTCGATTCG 30931	
Db	29903	AATTCCGCTTGGCGGTGGGCTCAAGGTGATGTCAGCGCGGACGCTTCGTGGAGTTCT 29962	QY	16934	TCTGCTCGGACAGGCAACCAACGCGCGCATGGCCACGCGCTCTACACACACCCACC 16993	
QY	15854	CGCGACGCGGCGCTGCGGTTGAGGCGGCTGCAAGCGTTCTCGCAGCGGCTGACG 15913	Db	30932	TGTTCTCGGTCAAGTGGTCACTGTCGCGCGGATGGGAGCGGGTCTCACTCGGCGTTTC 30991	
Db	29963	CCGTCACAGGGTCTGGCTCGGATGGCGGCTGCAAGTCTGTCGCGCGCGCGCGGATG 30022	QY	16994	CCGTCTTTCGCGCGCACTCAACGACATCTGCACCCACTCGACCCCGCCACCTCGACACC 17053	
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Db	30023	GCACCGGTGGGCGAGGCTGCGGCTGCTGTTGCTGAGGCGGTTGTCCGATGCGCGC 30082	QY	17054	CCCTCTCCCTCTCTACCCAGGACCCCAACACCCAGGACACCCACCTCTCGAAGAG 17113	
QY	15974	GGCTCGGTCAACGAATCTCTCGCGGTGCTGCGGTGAGGAGTGGGTGATCAGGACGTTGCGA 16033	Db	31052	TGGCCCGCTACGAGATGTGTGTC-----CGGTTCCG 31084	
Db	30083	GCAATGGGCAAGAGTTCTGCGGCTGGTTCGCGGGTAGCGGCTGAACGAGGACGCGGCT 30142				

13034 AGGCTCAAGCCCTCGTCGAAGCCTACGGTCAGGACCGCCCCAACCGCGCCGCCCTCTGCG 13093  
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13094 TCGGAACCCCTCAAGTCCAAATCGGGCACTCANTGSCCGCTCGGGGTGFGGGGGGTCA 13153  
Db GGGAAATCGTCTGCCCGCACCGCGATCGTCAGCTGTTGGCACGTCGCGCGAGCGCC 26962  
13154 TC---AGATGGTGATGCGCTGCGGAATGTTCTGCCCGGAGCGTTGATGTGGAT 13209  
Db TGGTTGTGGCGGGTGGAGAACTGGCTTTGGAGCGCCCTGATCTCTGCCGATCATG 27022  
13210 GAGCGTTCGCCCGCATGTGACTGGTCCGGGGTGGCGTGCAGTGTGACGGAGACGGTG 13269  
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13270 CCTGGCCCGGGGAGGGGGGCTA-CGGCGGGGAGAGTGTGATCATTTCTGGGGTCAAG 13328  
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13329 CGGCACCAACGCCATCATCTCGAGGAGACCGCCGCCCAACATCCCGTCAAG--- 13385  
Db TGTCTTCTCCACCGTGGCGCGAGAACCATAGAGTGAACGATGGCCCGCGGAAATG 27202  
13386 -CACACCCCGGACGATCCCGGAGAAATCAGCCGCCGACGAGATGCCGTTAGTGGCG 13444  
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13559 -----GCTCGACCTCGCGGAGATCAGCCGCCGACGAGATGCCGTTAGTGGCG 13601  
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13602 CGCGGT-----GTTGACACCGCGGCAACCTCATTCGCGCGCGACCGGAC 13648  
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13649 CTTCTCTGC-----AAGCACTCCAGCACTCCGCGAGCAACCCACCGCGCG 13699  
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13700 TCATCCACA-----GCA 13711  
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13712 GCGCCCGAGCGGGAACGGGACCGGAGGCGCAGGAAGACCGGATTCATCTGTCGCG 13771  
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28103 AGGCGTTCGCGCGCGCTGCGAGCAGAGAACCGCAGCTGGCACTTCGCGCGCGCTGG 28162  
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28163 CGTGGTTCGCTGGTGGCGGACTCAAGTGGCGAGGGGTCTCTCCCGCAACTCG 28222  
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28223 ACACGAGCGGACCGTCTCTCATCAGGTTGACCGGTGGCAGCGGTGGTGGGGAGTGGTCC 28282  
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28283 GTCACCTGGTGGAGAGCAGGATTCGGCGTTTGGTGTGGCAGCGCGGTGGCTGGA 28342  
Qy ACTCCCCCACCAACCCCATCTCAACCAACT----- 14402  
28343 ATGCGCTGAGTCCACGAGTTGGTGGATGAGCTGGCGCGCGCGGTGGTGGAG 28402  
Qy -----CCACGACGACACCCAAACCCCTCA 14425  
28403 TGGTGGCTTGGATGTGCTGACCGCAGGATCTGGAGCAGTGTGCGCGCATTCGCG 28462  
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28523 GGTCTTGTGGCGGCGATGTGGCAGCGGTGTTGCCCGGAGGTGAGCGGGGATGGC 28582  
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28583 ATCTGACGAGTTGACCGCGGATCTGGATCTGCTGTTCTGTTCTTCTCTCTCTCT 28642  
Qy CCTTCAACCACTTCAACCAACCACTCTCCCAACACCGCGCACCAACCTCTCAACCTCA 14656  
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28703 CATTTGGCGGTATTCGCGGGCGGTGGGTGCTTGGGTGTTGTTGGTGGGGACTGT 28762  
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28763 GGGCGCAACCCAGCGGTATGACGAGTGGTGGAGCGCGGTGGTGGAGCGGTGGCGC 28822  
Qy -----AACCCACACCACTCTCGACTCGACTCCCGCACTCTCTCTCTCTCTCTCT 14797  
28823 GAGCGGCACTCGAGAACTTTCACCGAGGATGGAATCCGCTGTTGATGCGCGGTTCG 28882  
Qy AACACCACTACTTGGCTCCCAACACCGGCGAGCGCGAGCGGCTCACCGAGGAG 14857  
28883 CGAAGGACCGGGCTTGGCTGTTGGCTGCTGATTTGGAAGGAGGAGGAGGAGGAG 28942  
Qy GCGGTGAGCAAGCA-----CGACCCCATCAACCCCGCTCGTGTGATCTCTCTCTCTCTCT 14909  
28943 GACGATCGACCGGATTCGGCGGTGTTGAGCGGTGTTGTTCTGTTGCGCGGTGG 29002  
Qy -----CAGTCTCGCAGGAGCGAGACGAGAGCTGTTGGCGCTGTCGCA 14956







Db 20304 CC---GAGTGTGACCGTGTTCGTGCGGTGGGGTTCGTCTTCGGGATCAGCGGCACC 20360  
Qy 7513 AACGCCACGTCACTCTCGAAGACACCCGCGCAGACGTTTCGGGGGGACCAACCCGCC 7572  
Db 20361 AACGCACATGTGATCTCTGAAACAGCTAC-----GAAATCGGCCAGAT 20402  
Qy 7573 GCGGAGGTGACCGGGACGACGATGAGGTTGTCGCGGAGTCTTGGGGTGTGGCG 7632  
Db 20403 AGTACAGCGGAGACGGACAAACAGATCCGGATCTACTGTGATATTCGGTCTGCC 20462  
Qy 7633 TGGCTGTGTGGCCAAAGTCGACGCGGCTTGGCGCCGACCGCCAGGCCCTGCACGCC 7692  
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Qy 7693 CACCTCACCGACACCCCGGCTCGACCTCGGATGTGCGATACACCTCGCCACGCC 7752  
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Qy 7753 CGCGCGGTGTGACCAACCGGCCACCTCATGCGCGGACCGGACACGTTCTTGCAA 7812  
Db 20583 CGAGCGCGCTGATGAACCGGCTGCTGCTGCTGGTGGACCGCGGTGAGCTGTTGCT 20642  
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Qy 7873 GCGGGACCGGACCGGGGAGCGCCAGGAAAGACCGCATTCATCTGCTCCGGACAGGC 7932  
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Qy 7933 ACCAAACCGCGGATCGGCCACCGGCTTACACACCCACCCCGTCTTCGCGCGCA 7992  
Db 20739 GGTCAGTGTTGGGATGGGACAGCGCTCTACTCGAAGTTTCCGGTTCGCTGCTGCG 20798  
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Db 20799 TTGATGAGGCTTGGCGCGAGTTGAGGACATCTGGGGGAAGACCGCGGGTTTC----- 20853  
Qy 8053 ACCAAACGACAAACGACGAGACGCGCGCGCTCTCCAGACGACCGCTACGCC 8112  
Db 20854 -----GGATGTGTTCTTCGTTCCGATGCGGACGCTGCTGATGACGCTGTGGCG 20906  
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Qy 8410 GTCATGAGCGACCCCGCCACACCGTCCAAACACATCACACCTCTGCGACACAGGC 8469  
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Qy 8470 ATCAAAACAAACCTCCCAACCAACGACGCTTCCACTCCCGCCACACCAACCCCATC 8529  
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Db 21624 CGGACGAGACCGGTTGCTGATGACAGCCCTGGCGCATCTCCACACCGTGTGGTGAG 21683  
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Qy 8989 GC-----AGCGGACTCGACCCCAACCAACCAACCCCACTA 9021  
Db 21804 GACATCGCGAGGTGGGGAACAGTTCTGACCGCGGTTGACCAAGCGATCTGGCAAG 21863  
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Qy 9138 GGGCGCACCTTCTCGAACTCGCTTCAATGCGGGACATACGTGGGCTGCGACCGAGT 9197  
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Db 22164 GAGAGCTGACAGCGGCTGGCCAAATGCGCTGACGATGCGCGTCACTCGTGGGCTG 22223  
Qy 9337 GGTGCTGCTGCGGTGGGGTGTGGAAGTGT-----CATGCTCGGGGG 9379  
Db 22224 CTTTCGCTGTGGGGCTCGATGAATCGCTGCTCGGGATTCCTGCTTTCGCAACTGGT 22283  
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Qy 9500 GTGTTTGGGGC-----GTTGTTTTTGGGGCTGCTGCTGCTGCTGCTGCTGCTG 9549  
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Db 18576 ATACCTCGATGCGCGCGCGTCTGCCCATCTCTGGCTCT---GCAGGAAGTACTTGAACAG 18632  
Qy 5794 GAAAGCGCGTATGCTGATCGCCACATCGACTGAGCAAGATCGAAACA----- 5845  
Db 18633 GATGAGAGTGGGTGCTGATCGCTGATGTGAGCTGGAGCCGATTCGTTCCACAGTTGCC 18692  
Qy 5846 -----CCTCTCAGACCAAGCACTGTGTAGCGCGCGCGCGGAAAGGAGGACAGCT 5895  
Db 18693 GCGACTCGCGCACCCGTTGTTGACGAAGTGGCGCGCGGAGAAAGCGATGCCGCG 18752  
Qy 5896 GTCCAGCGCCCACTCCACCG---CGAGTTGCAAAACGCTGGCCCATCAGAGTCG 5952  
Db 18753 AATGGCGCGGCAAGACCAAGCGGCTCGCGGTTGCGCCGCAATCTCGCGAGCTGCGGAA 18812  
Qy 5953 GCGCAACCAAGCGCGCATGCTCGAGCTCGTACGAGCAATGTGCGCGGAGTGTCTCGG 6012  
Db 18813 GCGCAACCAAGCGCAACTGTGTGATCTGTGTGCGCGCAGGTGCAACGTGTCTCGG 18872  
Qy 6013 CACGCGAACCCGAAAGCCATCGCGCCGACCAAGTGTTCGTTGCACTCGGCTTCGATTCA 6072  
Db 18873 CAGGCACTGCGGAGGAAGTCCAGCCCGAGCGGGGTTCCGCGCGCTCGGGTTGACTCC 18932  
Qy 6073 CTCAGCGCGTGAAGTTCCGAACCTGTGATCAAGGCAACAGGACTCGCGCTTCTGTC 6132  
Db 18933 CTCATGGCGGTGGATCTGCGCAATCGTTTGAACACCGCCACCGGTTGCGCTGCGGACC 18992  
Qy 6133 TCGCTGCTTTCGACACCGGACCTCGCAAACTCGCGGTACCTCGCAGAACCACTG 6192  
Db 18993 ACACCGCTTTCGATACCCGATCCGGCCGCTTGGCCGCTCACCCTGCTCGAGAGCTG 19052  
Qy 6193 CGGGSACAGCAGCGAGGTGCGCTCTCTCAGCGGAGCGGTTTACCGCGGAGCTTCTGTC 6252  
Db 19053 GTGGG-----TGATGTCGCTGCGCTGCGGTGACCGTGCAGCGCGCCGCGAGT 19103  
Qy 6253 ACCGAGCGCATGCCATGTTGGCATGCGCTGTGTTTCCCGGCGGAGTGAACCTCGGCG 6312  
Db 19104 GACGAACCGATCGCATGCTCGCATGAGTGTGCGGTTTTCGGGTGGCGCGCACTCGCG 19163  
Qy 6313 GACGACTTCTGGGATCTGATCTCTCCGAGCAGGAGCGGATCGGCGGATTTCCCAACCGAC 6372  
Db 19164 GAAGACCTGTGGCGGTGTGTCGCCCGCGCAGGAGGTGATCGGCGAGTGTCCCTCTCCGAC 19223  
Qy 6373 CGCGCTGGGACCTGGACACGCTCTACGACCCCGACCCCGACACCCCGGCACTGTCTAC 6432

Db 19224 CGGCGCTGGGATGCGGAAGGCCCTTTACGATCCGATGCTTCCAGGCGCTGGAACGACGTAT 19283  
Qy 6433 ACCGAAACGGCGGATTCCTCTACGAGCGAGCGCACTTCCAGCGCGAATTTCTTCGGCATC 6492  
Db 19284 GCGCGGATGGCGGATTCCTCTACGAGCGCGGTGAGTTCGATGCCGACCTGTTTCGGCATC 19343  
Qy 6493 AGCCCCCGCAAGCCCTCGCATGAGACCCCGCAGCAACGACTCTCTCTCGAAACCGCTCG 6552  
Db 19344 AGCCACGTGAGGCTTGGCGATGGATCCGACAGCGGTGTTGCTCGAAATCGCCTGG 19403  
Qy 6553 GAAACCATCAACACGCGCGGATCAACCCCAACCTCCACGCGCAACCCCAACCGAGTC 6612  
Db 19404 GAAGCCCTCGAAACGGGCGGAAATCGATCCGTGTTCTTGAAGGCGCAGTGGGGTGGCAGC 19463  
Qy 6613 TTCAACGGCAACCAACGAGGACTACGCACTTCGCGTGCAACGCGGGCCAGTCAACC 6672  
Db 19464 TACATCGCGCTGGAAGCCCTGGGTACGCAAGGATGTGCGGAGTTCCTCGAGAGGCG 19523  
Qy 6673 GATGTTTTCGACTGACCGGAAACCGCGGAGCGTCACTCCCGGTCTATCTCGTACACG 6732  
Db 19524 GAGGCTACCTGCTGACGGGTACCTCGGCCAGTGTGCTGCGGTGCGGTGCGGTATTCG 19583  
Qy 6733 TTTGGTTTGAAGGTCCTCGGTGTCGTTGGAACAGGCTTGTTCCTCGTGTGGTGGCT 6792  
Db 19584 TTTGGTTTGAAGGTCCTCGGTGTCGTTGGAACAGGCTTGTTCCTCGTGTGGTGGCG 19643  
Qy 6793 TTTGATCTGCGCTGACGCGTTCGCGTGGGTGAGTCTCGATGGCGCTTTCGCGGGGT 6852  
Db 19644 TTTGATCTGCGCTGCGAGTCTGTTGCGGTTCGCGGAGTGTGATCTGGCGTTCGCGCGGT 19703  
Qy 6853 GTGACGCTGATGTCTCTCGGGTGCCTTCGTTGAGTTCGCGGCAAGCGGGTCTCGGCC 6912  
Db 19704 GTGACCTGATGTGACGCGCGGAGATGTTCTGTTGAGTTCCTCCGTACAGCGGTTTCGCG 19763  
Qy 6913 GCGAGCGGCAATTCGAAGGCTTCTCGCGCGCGCGGACGCGGACCGCTGCGGTGAGGCT 6972  
Db 19764 CCGATCGCGCGTGCMAAGTCTTCGCGGAGAGCGCGACGCGCACCGCTGCGGCGAAGGC 19823  
Qy 6973 GTGGGATGCTGCTGTTGTTGAGCGGCTCTCGAGCGCCATCGCAACGCTGTCAGCTGCTG 7032  
Db 19824 GCGGCGCTGTTGTTGTTGAGCGGTTGTGCGACCCCAACCGAATGGGATCGGGTGTG 19883  
Qy 7033 GCGCTGTGTGCTGCGGCTCAACAGGACGCTGCGAGCAACGCTCTGACCGCGCC 7092  
Db 19884 GCGTGTGTTCTGTTGAGTCAAGTGAATCAGGACGCGCGCTCGAAACGACTGCGCGCGCG 19943  
Qy 7093 AACGGCGCTCCAGCAGCGTGTCTCGCGAGGCGCTTCGCGAAGCGCGGCTTGTTCGCGC 7152  
Db 19944 AACGCTCCGTGCGAGCAGCGGTTGATCAACAGGCACTCGCAATGCGGCTCTTTTCGCGC 20003  
Qy 7153 GGTGATCTGACGCGGTGGAGGCCCGCAGCGACCGGCACTTTTGGCGACCCGATCGAG 7212  
Db 20004 TCCGATGTGATGCGGTGGAGGCAATGGCACCGGACCCAGGCTGGGTGATTCGATCGAG 20063  
Qy 7213 GCGCAGCGCTCTCTCGCGACTACGAGACGAGACCGTTCGCGGAGCGGCGCTGTGGCTG 7272  
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Qy 7273 GGTCTCGTCAAGTCAATGTGCGTCAACAGGCTGCGCGGCGCTGCGCGGGTGTATC 7332  
Db 20124 GGTCTCGTCAAGTCAATGTGCGTCAACAGGCTGCGCGGCGGCTGTTTCGCGGTGTATC 20183  
Qy 7333 AAGATGTGATGGCGCTCGGCAATGCTGTCGCGCGGAGTTCGATGTTGATGAGCGC 7392  
Db 20184 AAGATGTGATGGCGCTGCGGCAATGCTGTCGCGCGGAGTTCGCTGCGCGGATGAGCGC 20243  
Qy 7393 TCGCGCATGTGAGTCTGCTCGCGGCTGCGGTGCGAGTGTGCTGAGCGAGACGCTGCCCTGG 7452  
Db 20244 ACCTCGGAGTTCGATGCTGCTCGGGCGGCTCGGCTCTCTCGCGAAGTACTTGG 20303  
Qy 7453 CCCGCGGGAGGCGCGGCTACGCGCGGCGAGGTGTCACTTCCTCGGCTCAGCGGAC 7512















QY	20204	TCTACGACGACGACCTTCGACGCGCAATTCCTCGGCAATCAGCCCCCGGAGCCCTCG	20263	Db	30846	AACAACCAACCTCGGA	-----ACGAGCGAGATCGACCAAT	30891
Db	29772	TGACCGGTGCTGATCGGTTCGACGCGCGGTTCCTCGGCATCAGCCTCGGAGCGCGC	29831	QY	21344	GCGAGGAGGCTGCTCGCGGAGTCTCTGGGTGTGCGGTGTGCGCGCAAGTCCG	21403	
QY	20264	CCATGGACCCCGACGACGATCTCTCTCGAAACCGCTGGGAAACGATCGAACGCGC	20323	Db	30882	CGGATCGGCGGTCACTGCGCATCCAGCGGTGATCCCGGTGATGTTGTCGGCTAGGATC	30941	
Db	29832	CAATGGATCCGACGACGAGGTGTTCGTCGAAGTGGCGTGGAGGTTCGAAACGACG	29891	QY	21404	AGCGCGGCTTCGCGCGCCAGGCGCCCTGACGCGCCACCTCACCACGACCCCGGCC	21463	
QY	20324	GCATCAACCCCGACACCTTCACGCGACCCCGACCGAGTCTTACCGCGCACCAACGAC	20383	Db	30942	TCGACGCGTGCAGGCCCAAGCGCTGGCTGCAGGCCCGCTGACCGGGTCTCTGGG	31001	
Db	29892	GAATCGCTCGGTGCTGTGGGGTAGGAGCCGGTGTTCGCGGGGACCAATGGGC	29951	QY	21464	TCGACCTCGCGGACGTCGATACACCTTCGCGCAAGCCCGCGCGGTTCGACCAACCGC	21523	
QY	20384	AGGACACCGCGGACACATTCGTTCAGGCGCCCGAGCGGTACCGAGGATTCGTCTGACG	20443	Db	31002	CTTCTCGGCTGATTTGGGGTATTCATTCGCGACCACTCGTCTCTGTGTCGACGAACGC	31061	
Db	29952	AGGACACCGGTGCGAAAGTGGCT---GCCGCGCGAGCGCGGGTCACTCTCTGACCG	30008	QY	21524	CCACCTCATCGCGCGGACCGCGACACCTTCCTGCAAGCACTCAGGCACTCCGCGCAG	21583	
QY	20444	GGGACGACACGACATCGCTTCGCGCGCGCAATCTCTACATCTCGGTTGGAAGGCGCTG	20503	Db	31062	CCGTCGTGTGGGTGCGCATCGGAGGACCTGCTGTCCAGGCTGGCAGCTCGCCGATG	31121	
Db	30009	GAACCGCGCGAGTCTCTGCGCGCGCGCTTCTACACGTTTCGGCCTTGAGGGGCGCTG	30068	QY	21584	GCGAACCCCAACCCCGCGTCACTCAGACGCGCCCGAGCGGACCGGGAGG	21643	
QY	20504	CGGTCACTCTGACACAGCGTTCCTCTCTGCTGCGCTGCGCTGCACCTCGCTGCCAGT	20563	Db	31122	GCGGACGCGCGCGGGGTGATA-----ACGGCTCTCGGAAT	31160	
Db	30069	CGGTGGCGGTGATACCGCGTTCCTGCTGCTGCTGGTGGTTCGATTTGGCGTCCAGT	30128	QY	21644	CCGAGGAAAGACGCGATTCATCTGCTCGGACAGGGCACCCAAACGCGCCCGGATCGCC	21703	
QY	20564	CCCTCAGTCCGCTGAATGCAACATGGCTTTGGCGCGCGGCGCACGCTCATGACCAACC	20623	Db	31161	CCGCTGCGCGCATCGGATTCGTTTTTTCGCTCAGGGCAGTCAGTGGCTGGGATGGAA	31220	
Db	30129	CGCTCGCTTCGGGTGAGTGATATGCGTTGGCAGGTGGTGTGACGCTGATGTCGACAC	30188	QY	21704	ACGCGCTCTACCAACACCCACCGCTTCCTGCGCGCGCACTCAACGACATCTGCAACCCAC	21763	
QY	20624	CGATCACCTTCACCGAATTCGCCCGCCAAACGGGACCTCGCCCGCGAGCGGGTTCGAAGG	20683	Db	31221	AGCGCTTGTGCGCGCTTTCCCGCGTTTCGCGGACGCTTCAGGAAAGCTTCGACGCGC	31280	
Db	30189	CCCTGGCTTCTCTGAGTTCCTGCTCAGCGCGTTTGGCGCCAGATGGTCCGTGCAAGT	30248	QY	21764	TCGACCCCACTCGACACACCCCTCTCTCCCTCTCACCAAAAGACAAACGACGACG	21823	
QY	20684	CGTTCGCGCGGCTGACAGCTACCGCTACCGGTGAGGGTGTGGGATGCTGTGGTG	20743	Db	31281	TAAGCGACACCTGGGCGCGGACGTTCCGGGTGCTGTTGCTGCTGATGAGAGA---	31337	
Db	30249	CGTTTGGCGCGCTGCGGATGCGACCGGGTGGGGTGGGGTCCGCGCTGTTGCTGG	30308	QY	21824	ACAAAGGAGCGCGGCGCACTGCTCCAGCAGACCCCGTACGCCAGCGCCCTCTTCG	21883	
QY	20744	AGCGCTCTCGACGCGCGCGCAACGCTACCGTGTCTGCGCGTGTGCGTGGCGAGT	20803	Db	31338	-----TGCTCGACGCGAGCTGTGGGCGAGTCGGGGATCTTCG	31376	
Db	30309	AGCGTGTGCGGATGCTCGTCCGAATGCTACCGGGTGTGGCGTGTTCGCGGGTCTG	30368	QY	21884	CCTTCAGGTGCGCCTCCACCGCTCTCTCACCGAGGCTACCATCACCCCCCCTACT	21943	
QY	20804	CGGTCAACGAGACGCTCGAGAACGCTGTGACCGCGCCCAACGGGCGCTCCCGAGAC	20863	Db	31377	CGGTTCAAGTGGCGCTCTCGGATTTGCTGA---GGTCTGGGGCGTGGCGCGCGCG	31433	
Db	30369	CGGTGAATCAGATGCTGCTGCAATGGCTGACTGCGCGCAATGGTCCGTTCGAGCAGC	30428	QY	21944	ACGCGGACACTCCTCGCGGAAATCACCGCGCCACCTCGCGCGGATCTCACCCCTCA	22003	
QY	20864	CGCTCATCCGCGAGCCCTCGCAACCGGACCTGACCCCGCGAGCTGATGCGGTG	20923	Db	31434	TGCTGGGCACTCGGTTCGGGAGTTGCTGCTGGGCGACGCGGCTGGTGTGCTCTTC	31493	
Db	30429	GGGTGATTCGAGGCGCTCGCGAATCGGGGTGTGCGGCTCGATGTGATGTGTTG	30488	QY	22004	CCGACGCCACCTCATCAACCAACGCGCACCTCATGCAAAACCATGCCCC---CG	22060	
QY	20924	AGGCCACCGGACACCACTTTGGCGGACCCGATCGAGGCCCGAGGCCATCCTTCGCGA	20983	Db	31494	CGGACGCTGCAGGTTGGTTGCGGCTCGGGCCCACTGATGACGGCATTGCCACCGCGC	31553	
Db	30489	AGGCGCACGGGACCGGTACCGGGCTCGGGGATCCGATCGAGCGCAGCGCTGATCGGA	30548	QY	22061	GCACCATGACCACTCTCACACACCCCAACACACATCACCCACCATCACCGCCACG	22120	
QY	20984	CCTACGACAGGACGCTCCCGGCAACGGGCGTGTGTGCTGGGTCCGTCGAAGTCCAAACG	21043	Db	31554	CGCAATGCTCGCGGTGCGCACCCAGCGAGCGCGGTGCGAACCGCTGCTTTCGCGGGTGT	31613	
Db	30549	CATATGGGACGAGCGGATCCTGAGCGGGCCCTGTGGCTGGGGTTCGATCAAGTCCAACA	30608	QY	22121	AAACGACCTCGCCATCGCGCCATCAACACCCCACTCCCTCATCAGCGGACCC	22180	
QY	21044	TCGACACACACGCGCGCGGCGGTGCGCGGATGATCAAGTGGTATGCGCCCTCC	21103	Db	31614	CGGATCGGGTACGATCGCTGCGATCAACGGGCCCGGAGTGGTAGTGTCTCTCGCGGAC	31673	
Db	30609	TCGGCCACACGAGCGCGCGCGGTGTGGGGGGTTCATCAAGATGGTTCAGGCGCATGC	30668	QY	22181	CCACACCGTCCAAACATCACCACCTCTGCGCAACCAAGGATCAAAACCAAAACCC	22240	
QY	21104	GCCACCGGACACTCCCAACGACTCTCCACGCGGATGAGCGCTCGCGCATGTGACTGGT	21163	Db	31674	CGGATGTCTCGTGGAGCTCGAGGCGAATTCGATGCCCGGAGGCTTAGGACCAATGGT	31733	
Db	30669	GGCAGGGGAGTTGCTTCGAGCTTGCATGTGCACTGGAGACGCCACTTCCACAGTGGACTGGT	30728	QY	22241	TCGCCAACACGCGCTTCATCTCCCGCCACACCAACCGCATCTCAACCACTCCAC	22300	
QY	21164	CCGCGGTGCGGTGAGTGTGACGAGACGGTGCTCTGCGCGCGGGGAGGGGCGGC	21223	Db	31734	TGCGGGTCTCCCATGCTTTCCACTCGCACCGGATGGAACCGATTCGAGCAGTACGCG	31793	
Db	30729	CTGCGGGGCGGTTCGGCTCTCAACCGGAAACACGCCCTTGCC---CGAGAGCGCGCTC	30785	QY	22301	AGCACCCCAAAACCTTCACCTACACCCACCCCGCTCATCAGCGGCAACAC---	22358	
QY	21224	CGCGCGGAGGAGTGTATCATTTCCGCGTACGGGACCAACGCCACGTCATCTCTCG	21283	Db	31794	AAACCGCAGGTGCTGAGTTGGTGAACCGGTGGTGGATGCTCTCGCGCGGACCG	31853	
Db	30786	CTGCTGAGCGGGGTGTGCTGTTGGGATCAGCGGACCAACGACACCTCATCTCTCG	30845	QY	22359	-----CCACCGGACCAACTCTCTCAACCCCGCACTACTGGACCAACGACCGGCA	22408	
QY	21284	AAGAAGCACCCCGGACGACGCTTTCGGGGGGGACCAACCGCGGACGAGGATGCCGGTAGTG	21343					



Db 27606 ACTCACCAT-----CCGAACCGGT-----CGGCAATCCGCCGATC 27641  
Qy 18050 CGGCGGAGACGACAGGTGGAGTCCGGTCTCTGGAGCGGTGGCCCGCCAGGACCTGG 18109  
Db 27642 CCGCGCGCAGTCCGGCTTCTGGAACTCGTGGAGAGAGATGTACGCGGCTCAGCG 27701  
Qy 18110 AAACGGTCCGAGACCGTCCGGTCCGGTCCGGTCCGGTCCGGTCCGGTCCGGTCCGG 18169  
Db 27702 CCGCTCTGCACATTACCGGCGATCAGACGTGCGAGCGTCCCTCGGAATCGGTGGTCCGG 27761  
Qy 18170 CACTCTCCGCTGGACCGACCGACCAACAGACCAAGCCCGGATCAACACCTGGACCTACC 18229  
Db 27762 TCCTCTCTCTGGATCCCGGATCCGCAACGAATCCCTGGTGCACCACTGGCGGTACC 27821  
Qy 18230 AGGAACCTGGAAACCCCTCACCTCCCGCCACCAACCAACCCCAACCAACCTGGCTCA 18289  
Db 27822 GAATTTCTTGGCATAGCGGGGAGATTGGCCAGACCCCTCGTTGTGGGGGACATGGCTCG 27881  
Qy 18290 TCGCCATCCCGAAACCCAGACCCACCCACATCAACCAATCTCTCAACCACTCC 18349  
Db 27882 TCGTCTGCGGAGGGTGGTCCGGAGTCCGCAAGTTCTCGGTTTCAACGAGATGTTCCG 27941  
Qy 18350 ACCACACGGGATACCCCGATCCCGCTCACCTCAACCAACCAACCAACCAACCAAC 18409  
Db 27942 AGGAACGGGGTTCGCCGGCAGTCTGTTCAGCTCCCGGGGACAGCAGGAGGAGCCTGG 28001  
Qy 18410 ACTCCACACACCGACAAAGCCCAAAACCAACACACCGGACCCATCACCGGCTGC 18469  
Db 28002 CCG-----AAGATTCCGCTGTTGCTGTTGCTGAGGGGAATAAGCGCGGTG 28052  
Qy 18470 TCTCTCTCTCGCTTCGAGCAACACCCACCCACCCACCCACCCACCCACCCACCCGCA 18529  
Db 28053 TGTCTCTGCTGGCGCTGGATGAATCGCGTCTCTCGCGAAGCTGCTTTCGCGAATGGCG 28112  
Qy 18530 CCTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 18589  
Db 28113 CGCTGAACCTCGTTGGTACTGCTGCGAGCTCTCGGGGCGCGGATGTGTGGCGCCATTGT 28172  
Qy 18590 GGTAGCCACCAACCAAGCCACACCCACCCACCCACCCACCCACCCACCCACCCACCC 18649  
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Qy 18650 AAGCCCAAACTGGGGACTCGCGCACCAACCTCTCTGAAACACCCCAACCCCAACCGCG 18709  
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Qy 18950 CCACCAACCCCAACCAACCTCTCTCAACGAGCGGACCCGCGCCCAACCCCAACCCCAAC 19009  
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Qy 19430 GACTGGCGATGTGTCAGTCAAGTCAAGCAATCTCTCGCGCGCGCGGATGTTGCCATGCGC 19489  
Db 28998 GAATGGCGCGAGGTGAAGGGGCTGCAAGCTGCGCGCGCGCGCGCTGGTGGCAATGGCTG 29057  
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Qy 19550 TCGCGCATATGATCTGAAAGAAATTTGGGACCGGTTCTCTCA-----GCAAGTCTGGGTCT 19606  
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Qy 20144 CGCTCTACGACCCCGACCCCGACCAACCCCGGACCTGCTACACCCGAAACCGCGGATTC 20203  
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QY 15914 GCACGGCTGGGTGAGGCTGTCGGAATGCTGCTGTGAGCGGCTGTGGACGGCGCG 15973  
Db 25647 GCACGGGTGGCGGAGGCTGGCGTCTGCTGTGCTGAGCGGTTGTGCGATGCCCGC 25706  
QY 15974 GGTCTCGGTCAACCAATCTCTCGCGGTGGTGGTGGAGTGGCTCAATCAGGACGGTGCA 16033  
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QY 16094 CCAACGGCACTGACCCCGCGGAGCTGATGCGGTGAGGCCACCGCACCGGACCA 16153  
Db 25827 CAGGTGCCGGGTGTCCGTGTCGACGTGGATGCTGTGGAGCGCATGGGACGGGACGCG 25886  
QY 16154 CTTTGGGCAACCGATCGAGGCCAGGCCCTCTCGCCACCTACGACAGGACCGCCCG 16213  
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QY 16214 GCAACGAACCGTGTGGCTCGATGAAGTTCGAACATCGGCCACCGCAGGCTGCCG 16273  
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Db 26007 CCGGTGTGCTGTGTGATCAAGATGGTATGGCGATGGCGAGGAGCTGCGCGCA 26066  
QY 16334 CGTTGATGTGATGAGCGCTCGCGCATGTGACTGTGTCGCGGGGCGGTGAGTGTAT 16393  
Db 26067 CGTTGATGTGAGAGCCCTCGCGAGTGGATGTGCTCGGGGACGGTCCAACTCC 26126  
QY 16394 TCACGAGACGGTGTGCTGCGCGCGGGAGGCGGTGCGGGGCGGAGGAGTGTAT 16453  
Db 26127 TCACGAGAACCGCTTGGCCGACAGC- -GGTCTTTCGCGGGGCGGCTGTAT 26183  
QY 16454 GCTTCGGGTGAGCGCACCAACGGCCAGGTATCTGTGAAGAGACCGCGCCCAACA 16513  
Db 26184 CGTTCCGGATCAGTGCGCAACACGGCACCTGTATCTTTGAACAACCTCCG- - 26233  
QY 16514 TCCCGTCAGACACACCGCGCAGCAGCGCCCGGGAGAGCAGCGCGCAGCATGTTCGG 16573  
Db 26234 -----CGA 26236  
QY 16574 GGGAGCGCGCGGACGACGCGGTACCGGGGGGAAAGCAGTGGTCTGTGCGCGCA 16633  
Db 26237 GAGTCGACGCTCAACAGACCGGATTCGG- -GTTCTGTCCGG 26279  
QY 16634 GTCCAGGGGTGGCGGTGGTGTGTGGCCAAAGTCGAGCGCGCCCTGCGCGCCAGG 16693  
Db 26280 ATTTTCGGTGGTGGCGGTGGATGTGTGGGCAAAACACCCGAAGCGTATTCGCGCCAGG 26339  
QY 16694 CCCAGCCCTGACGCCCACTCAACGACCCCGCGCTCGACTCGCCGACGCTCGGCT 16753  
Db 26340 CAGATGCAATGATCTTACTTGAACAATCGGTTGATGCTTCCCGCGAGATATCGGTT 26399  
QY 16754 ACACCTTCGCCACCGCGCGGTGTTCGACACCGCGCCACCTCATCGCGCGGAC 16813  
Db 26400 ATTGCTTGGGTGACCGCTCGCGGTGGACACCGGCTGTGTGTGGTGGGATC 26459  
QY 16814 GGCACACTTCTGAAGACTTCAGGCACTCGCGGAGGGAACCCCAACCGCGCGTCA 16873  
Db 26460 GTGCCGCTGTGTCGGGCTTGAAGCGCTGGCGCTTAGTAATGACGCTGCGCAGGTGA 26519  
QY 16874 TCCACAGCAGCGCCCGCGGGACCGGGACCGGGAGCGCGAGGAAGACCGCATCA 16933  
Db 26520 TCACCGGCACTCGT-----GCCGCTGGGCGGTGCGATTCG 26555  
QY 16934 TCTGCTCCGACAGGGCACCCAAACGCCCGCGCATGGCCCTCTACACACCCACC 16993

Db 26556 TGTCTCCGGTCAAGGTGGTCAGTGGCCGGGATGGGAAGCGGGTCTCACTCGGGGTTTC 26615  
QY 16994 CCGTCTTCGCGCGCGCATCTCAACGACATCTGCACCACTGCACCCACCTCGACCACC 17053  
Db 26616 CCGTGTTCGCGCAGCGTTGACGAAGCTGCTGCGAGTGGATGCGATCTTCGGGCAGA 26675  
QY 17054 CCCTCTCCCTCTCTCAACCCAGGACCCAAACACCCAGACACCAACCCCTCGAAGAG 17113  
Db 26676 TGGCCCGGTACGAGATGTTGTCT-----CGGTTCCG 26708  
QY 17114 CGGCGCACTGCTCCAGAGACCCCGTACGCCAGCCCGCCCTCTTCGCTTCCAGGTG 17173  
Db 26709 ATACGAATCTTGACACAGACCTTGTGGGCGCAGCGCGCTGTTGCGTTGCAAGTCG 26768  
QY 17174 CCCTCCACGGCTCTCTACCGAGCGCTACACATCACCCCACTACTACGCCGACACT 17233  
Db 26769 GACT---CTGGGAGTGTGTGGGTTGTCGGGCGCTGTGGTGTGGGCCACT 26825  
QY 17234 CCCTCGGGAATACACCGCCCGCCACCTCGCGGCATCTCACCTCACCGACGCCACCA 17293  
Db 26826 CCGTCCGTGAGCTGGCGCGGGTTCGGGCTGGAGTGTGTGTTGGGATGCGGCTC 26885  
QY 17294 CCCTCATCACCAACCGCCACCTCATGCAAAACCATGCCCC---CGGCACCACTGACCA 17350  
Db 26886 GGTGGTGGCGGGCGTCCCGGTTGATGCAAGCCCTGCCAATCGCGGTGCCATGCTCG 26945  
QY 17351 CCCTCCACACACCCCGCCACCATCATCCACCTCACCGCCACCAAAAGACACTCG 17410  
Db 26946 CTGCGGTGCTGAGAGGAGCAGCTGCGCCCGTGTGTCGGCGACTGCGGTGATCGTGTG 27005  
QY 17411 CCATCGCGCATCAACACCCCGCCCTCTCATGAGGATCAAAACCAACCCCTCCCAACAAA 17530  
Db 27066 ATGACATTCGCGGTGCGGTGAGCGGCAAGGATCCCGTCCAGGTGTTGCGGGTTTCG 27125  
QY 17531 AGCGCTTCACCTCCCGCCACACCAACCCCTCTCAACCACTCACAGGACACCCAAA 17590  
Db 27126 ATGCGTTTCATTTCGATCGGATGGATCCGATGCTGGCGGAGTTCACCGAAATCGCCGGA 27185  
QY 17591 CCCTCACCTACACCCCGCCACCCCTCATCACCGCAACAC-----CC 17638  
Db 27186 CGGTGACATCCGCTGTCAGGGTTCGATGCTGTGACGTTGACGGTGAGTCTGATG 27245  
QY 17639 CACCGACCAACTCTCTCACCCCGCACTACTGGACCCCAACAGCCCGCAACCCGTCGACT 17698  
Db 27246 AGGTCCGATGCGCGCTACGCGGAGTATTTGGGTGCGCAGTGGAGAACCCGTCGCT 27305  
QY 17699 AGCGCACCAACCCCAACCCCTCCACCAACAGCGGCTCACCACTATCATGAATCTCGAC 17758  
Db 27306 TCGCGAGCGGTGTTGCTGCGCTCGCGGTACGCGTGTGAGACCGCTCTCGAGGTGCTC 27365  
QY 17759 CCGAACAACCTCACACCCCTCACCCACCACTCCCAACACCCCGCCACCCACC 17818  
Db 27366 CGGATGGGTTGTTGTCGGCGCTGTCGAGGAGTGGCGGCGGATCGATCAGGCGGAC 27425  
QY 17819 TCACCTCACCCACCCCGCCACCCCAACCCCAACCCCTCTCACCAACCTCGCAAAA 17878  
Db 27426 GGGTGGCGCGGTTCCGTCATGCGAGCAATCCGAGAGGCGCACACGGTGACACGG 27485  
QY 17879 CCACCACTGCGACCCCAACCACTACACCAACCAACCAACCAACCCCAACCA 17938  
Db 27486 CATTTGGCGAGATCATGTGCTGTGAGTGGAGTGGCGGTGCTGCTGCGGTGCTG 27545  
QY 17939 CC-----CAGCTCGACTCCCGCTACCCCTTCCACACAGCAGCTACTGCGTCTG 17989  
Db 27546 CCGGGGCAAGCAGGTGAGTGCAGCTGCCACGATGCTCTTCCACAGACGCGGTACTGCGT 27605  
QY 17990 AAGCACACAGCGGGTGCAGGATTCGGTTCCGGTTCGGGCGGCGGACGACTG 18049

Db 23367 CAACCGCAGGTTCCGACCCCTGGATGATTCCTGCGCGCGTGGACTCGGACGTTCTCTG 23426  
Qy 13892 CCTCTCACCAGGACCCCAACACCCAGGACACCAACCCTCGAAGAAG-----CGG 13945  
Db 23427 CCCGGGTTGGTGTGGTGGAGCTATGTGCGCCGAAGAGGTTCAGGGTGGATCCCTGC 23486  
Qy 13946 CGGCACTGCTCCAGCAGACCGGCTACGCCCGCCGCTCTTCCGCTTCCAGGTCGCC 14005  
Db 23487 GTCGCGCGCCCAAGAGTCGACCTCCGATCTGCTGGCTCTGTCAGTCGTCGGTTCGG 23546  
Qy 14006 TCCACCGCTCTCTCA-----CCGACGGCTACCAATACACCCCCCA 14045  
Db 23547 ACGAGCGGTTCCCGAATCCAGCTCTGTCGTCAACGTCGACGGTTCGCGCGACT 23606  
Qy 14046 CTACTACCGCGGACACTCCTCGGCGAATACACGCGCCGACCTCGCGGCACTCTCAC 14105  
Db 23607 CGGATTCGGAAGTCGCGGACCTGGTGGTGGTCTGCTGGGGTGTGTGAGTTGAGCCC 23666  
Qy 14106 CCTCACCGA-----GGCCACCAACCTCATCAACCAACGCGCCACCTCATGCAAAAC 14157  
Db 23667 AGTCGGAGAACCCGGGTGCTTCTGCTGGTGGACGTGGACGGCACACTGAGTCGTGGC 23726  
Qy 14158 ATGCCCCCGGACCATGACACCTCCACACCAACCCGCGACCAATCACC----- 14208  
Db 23727 AGGCGTTGCCGCGCGCTGCGAGCAGGAGAACCGCAGCTGGCACTTCGCGCGCGCGTGG 23786  
Qy 14209 -----CACCACCTCACCGCCACGAAACAGACCTCGCCATCGCGCA 14251  
Db 23787 CGCTGGTGCCTGGTTGGCGGACTCACGGTGGCGGAGAGGCTCTCCCGCGCAACTCG 23846  
Qy 14252 TCAACACCCCACTCCTCTGCTATCAGCGGACACCCGACACCTGTCACACATCAAC- 14310  
Db 23847 ACACGACGGGACCGTCTCTATCAGCGGTGGACCGGTGGTGGGGGAGTGGTGGCC 23906  
Qy 14311 --ACCTCTGCGAACAAAGAGCATCAAAACCAAAACCTCCCAACCAACAGCGCTTCC 14368  
Db 23907 GTCACCTGGTAGAGAGCAGCGGATTCGCGGTTTGGTGTGGCAGCGCGGTGGCTGGA 23966  
Qy 14369 ACTCCCCCACACCAACCCCATCTCAACCAACT----- 14402  
Db 23967 ATGCGCTGGAGTCACAGTTGGTGGATGAGCTGGCGCGCGCGCGCGGTGGTTGAGG 24026  
Qy 14403 -----CCACGACACACCCCAACCCCTCA 14425  
Db 24027 TGGTGGCTTGGATGCGTACCACCGATCTGGACAGCTGTGGCGGCCATTCGCG 24086  
Qy 14426 CCTACACCCACCCACACCCCTCTATCAGCGCAACACCCCAACCGACCACTCTCA 14485  
Db 24087 TCGACTGCGCGTGGCGGGGATCGTGCAATACCGCTGGGGTGTGTGGCCGACGGAGTGATCG 24146  
Qy 14486 CCCCCCACTACTGGACCCCAAGCCCGCAACACCGTACGACTACGCCACCAACCCCAAA 14545  
Db 24147 GGTCTTGTGGCGCGGATGTGGGACAGGTGTTGCCCGAGGTGACGGGGGATGGC 24206  
Qy 14546 CCTTCCA-----CCAAACGGGCTCACCACTATCATGAACTCGGACCCGCAACA 14596  
Db 24207 ATCTGACAGAGTTGACCGCGATCTGGATCTGTGTTCTTCTTCTTCTTCTTCTTCT 24266  
Qy 14597 CCTCAGCACCTCACCACGACAACTCCCAACACCCCAACCAACCACTCAACCTCA 14656  
Db 24267 CCGGATTTGCGGTTGCGGAGGCGGCAACTACGCGCGCGGCAACACTTCTCTGGATG 24326  
Qy 14657 CCCACCCCAACCAACACC-----CCCAACCCACCTCTCTCAACCACTCGCCAAAC 14708  
Db 24327 CATTCGGCGGTTATCGCGGGCGCGTGGCTCGCTCGGTGTTGTGTTGGGTGGGACTGT 24386  
Qy 14709 CACCAACCACTGGCACCCCACTACCAACCAACCAACCAAC----- 14752  
Db 24387 GGGCGCAACCAAGGTTATGACGAGTGGCTTGGACCGCGGCTGGTGGAGCGGTTGGCGC 24446  
Qy 14753 -----AACCCACACCAACCAACCTGACCTCCCACTTACCCCTTCC 14797  
Db 24447 GGACGGGCATCGCAGAACTTTCCAGGAGGATGGACTCGGCTGTTCGATGCGCGGTTTCG 24506

Qy 14798 AACACCACCACTACTGCTCCAAACACCCGCAAGCCGAGCGACCCGTCACCCAGCGAAG 14857  
Db 24507 CGAAGGACCGGGCTTGGTGGTGGCGCTCGATTTGGACAGGGCGCTGCTGCTCGGAACG 24566  
Qy 14858 GCGGTGAGCAAGCA-----CGACCCCATCAACCCGCTGCGTGATGTCTCTGTGG----- 14909  
Db 24567 GACGATCGCACCGCAATTCGCGCGCTGTGTAGCGGCTTGTCTCTGTGTCTGCGCGCGTGTGG 24626  
Qy 14910 -----CAAAGTCTCCGAGGACGAGACGAGAGCTGTTCGGCTGGTGGCGCA 14956  
Db 24627 CGAGAAACAGCCAAATTCACGCGCGGATGAGGACGCACTGTTGGTGTGGTGGGG 24686  
Qy 14957 CCATGCGCGCGCTGCTGCGGCATGCCACTCTCCGAAGTGAATGTTCTCCGAACAGGCT 15016  
Db 24687 AGCAGTTTTCGCGCTGCTGGTTATTCGGGTGGGTGGTGGGGGCGACCGTGTCT 24746  
Qy 15017 TCAAAGAGCTGGGTTTGAATTTCTCTCGCGCAATTCAGCTTTCGTAATTCGACTGTGCTG 15076  
Db 24747 TCCGTGATCTGGGTTTGAATTCGTCGCGGTGAGTTTCGGAACCCGCTTCCCGGG 24806  
Qy 15077 ACGTTGACCTGCGCTTTCGCGCACGCTGATCTTCGATTACCCCACTCCGATGCGGCTTT 15136  
Db 24807 TGCTGGGGGTGCGGTTGCCGCGACTCGGTTTCGACTATTCGACGCGCGGCGGCTGG 24866  
Qy 15137 GCCAGTTTCTCCGGGCGCGATCGTCGGAGCGGACACAGGACACCACTCGTCTGCGCG 15196  
Db 24867 CGCGTTTCTTCATCAGGAACCTGCGAGCGAGGTGCGGTCCACGTTCGACGCGGTGACCA 24926  
Qy 15197 TAACGCGGTCCCGCGAGCGAGCGCATCGCCATCGTCGGGATGGCTGTGCGTACCCCG 15256  
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Qy 15257 GTGATGTACGAGCGGTGATGATCTCTGGCAGGTGTCAGTGGTGGCATGACGCGATCG 15316  
Db 24987 GTGGGGTGTGTCGCCGAGGAGCTTTTGGCGGCTGGTGGCGCGCGGTGATGCGGTTGG 25046  
Qy 15317 GCGGATTTCCGACAAACCGTGGGTGGGACCTCGACACGCTGTACAAACCCGACCCGAGCC 15376  
Db 25047 CTGGGTTCCAGACGATCGCGGCTGGGATCTCGCGGCGTGTGACGATCTGATCCCGATC 25106  
Qy 15377 ACCACGAAACAGCTACACCGGAGCGCGGATTTCTTTTACGACGAGGCAATTCGATC 15436  
Db 25107 GTCTCGGACCTCTATGTGTGAGGCGCGGTTTCTCGGGAGCGCGCGGATTCGATG 25166  
Qy 15437 CCGACTTCTTCGTTATCAGTCCGCTGAGGACCTGCGGATGAGCCCGCAGCAGCGGCTGC 15496  
Db 25167 CTGACATGTTGCGCATCAGCCCGGTGAGGCTTGGCGATGGATCCGCGAGCGGTTGC 25226  
Qy 15497 TGCTGGAAACAGCGTGGAGAGCATCGAAACGCTGCTCAACCCCGACAGCTCTCGTG 15556  
Db 25227 TGCTGGAGTCCCTTGGGAACCTTGGAGCGGCTGGGATCGATCCGTTCTGTTGCACG 25286  
Qy 15557 GCACACCAACCGGCTTTCGCGGGTGAACCTTACACGACTACGCGCGCG-----CTTTC 15613  
Db 25287 GCAGCGGACCGGTGTGTTCGCGGCTTGTATGATACCACTATATGGGCGCGGATTCATTA 25346  
Qy 15614 CCACGCTCCGCGAGGTTTCGAGGGTATCTCGGGCAGGAGCGGAGGCACTCGGCT 15673  
Db 25347 CCAGACACCGAGGGCTTCGAAGGCACTTCGCGGACGCGGCAATGCGGGGAGCGTGTGT 25406  
Qy 15674 CCGGTGCTGCTGCTAGCTCTCGGCTTGAAGGTTCGGGCTCCACAGTCACACTGTGCT 15733  
Db 25407 CCGGTGCGGTTGCTATTCGTTTTCGAGGCTCTGCGGTGACGTTGATACGGGCT 25466  
Qy 15734 GCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15793  
Db 25467 GTTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25526  
Qy 15794 CCATGGGCTTCCGCGGTGGGCTGACGTTGATCAACCCCGCGGCTGCTGCTGCTGCTGCT 15853  
Db 25527 AATTGCGGCTTCCGCGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 25586

QY 11932 CCACCTCCGCGCGTATCCGTCGGGCGCTGTAGGACG--TGAATGCAATTGGCGAATGAAG 11989  
Db 21208 GGTGTGGCTCGGACCGGTCGCGCTCTGACCGGGTTGAGGCAATCGCGACGGCTG 21267  
QY 11990 CGAAGCTCTCGAATACCTCAAGCGCTACACGCGGACCTGGAC---CGCACTCGCCGT 12045  
Db 21268 CATGCGGCCGGAAGTGGTTTCGGGGTCTGTGGGGCTTGGTGGCCGCTGCGGTTCTGTGT 21327  
QY 12046 GCGCTGTACGAGTGGTTCAGCGGTGAGCAGGACCGATCGCGAATTTGTGGGATGCGGTGT 12105  
Db 21328 CTCGGGTTCAGGGTGTGAGTGGCGGGATGGCGCGGGCTCTACTCGGTGTTCGGT 21387  
QY 12106 GGTATACAGGGCGGCGAGCTACCCAGCGACTGTGGCATCTCGTCAAGTCCAGACG 12165  
Db 21388 GTTCGCCGACGCGTT- CGACGAGGCTTGGCGGAGTGGATGCACACCTGGCGCAGGAAC 21446  
QY 12166 GAGCTATCGGGGAGTTCCGACCGACCGT--GGATGGAACCTGGAGCAG-CTCTACGAC 12222  
Db 21447 TCGGGTTTCGGATGTGGTTCGGTTCCGAAGCGTGGTTGCTGATCGGACGGTGGG 21506  
QY 12223 CGGACCCCGACCGCTCAGGAACCAAGTTACACGCGCAGCGGAGGTTTCTCTATGACGCG 12282  
Db 21507 CGCAGTCGGTTTGTTCGGTTGCGATTGGCTTCTCGGGCTGTGGTTTCGGTGGTG 21566  
QY 12283 GCGGAC-----TTCGACGCGCGGTTCTTCGAGTTGTACC---GCGTGAAGCGC 12328  
Db 21567 TTCGCCCGGATGTGTGTGTGGGGACTCGGTGGGTGAGCTGGCTGCGGTGCATGCGGCTG 21626  
QY 12329 TGGCAATGGAACCGCAGCAGCGCTGCTCGAAACCACTTGGGAAACGTTTCGACAGG 12388  
Db 21627 GTGTGTTGTGTTCGAGGCGCGCGGTGGTGGCGGGTTCGCGCCCGGTTGATGTCAGG 21686  
QY 12389 GCGGAATCGAACCCGAGGTCCATGCGCGGAAGCCGGAACCGGGGTTTCGTGGGATCAATC 12448  
Db 21687 GCTTGCTTCGTGTGTCATGCTCGCGGTGCTACCGGTGAGTTTCAGGTTCGATCTC 21746  
QY 12449 CGGAGGA---CTACACACCGGATACACATCAGCCCTCAACGCACTGAGGGCTAC 12504  
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QY 12505 CTGCTACTGGCAGCGCGGCAAGCATTCGCTCAGCGCGTATCTCTACAACTTCGGGCTC 12564  
Db 21807 TGCTCTCTGTGACCGCGAGTGTCTACCGGATGCTGATCGGTGTCAGCATCAGGGGT 21866  
QY 12565 GAAGGCCC----- 12572  
Db 21867 GCGGACCCGGTGTGGGGTGTGCGATGCTTTCCATTGCCCCCATATGAGCGCGATGC 21926  
QY 12573 -TGGATCACTATCGACACCGGTTTCTCTCTGCTCGTCCGCTGATCTGCGCTGCC 12631  
Db 21927 TGGAGGAGTTCGCCCGAGATCTCCGAGGCGCGGAATATACGCAACCGGAATGCGCGATCA 21986  
QY 12632 AAGCGCTCCGTCGGTGA-----ATGCACCATGGGCTCGCAGGC 12672  
Db 21987 TCTGACCCCTGATCGGTGAGTGGACGGTGTGAGTGATGGGCATCTCCGAGTACTGGG 22046  
QY 12673 GCGGCTCCGTCATGGCCACTCCCTTCTCTTCAACGAGTTCTCTGCGCAACGCGGGCTG 12732  
Db 22047 TGGCTCAGGTGCGTGAGCCCGTCTGTTTCGCCGAGGTTCCAGCGCTTGTGCGTCAGG 22106  
QY 12733 GCGCAGACGCGCGGTGCA-----AGGCGTTTTCGGCGCGCGCGGACCGGACCG 12781  
Db 22107 GTGTCCGACGATTTGTCGAATTTGGTTCGGACGGGCGTTGTCGACGTTGGTCAGGAGT 22166  
QY 12782 GCTGGTCCGAGGTTGCGGATGCTGTGTGGAGCGGCTCTCCGACCGCCCGCGAACG 12841  
Db 22167 GTGTGGCGGAATCCGGCGGGTGGCCGGATTCCTGCTGATGCGCAAGACCGGACGAGG 22226  
QY 12842 GTCAACGCTGCTCTGGCGG----- 12859  
Db 22227 CGCGAACCGTCTGGCAGCTTTGGCGGAGATCCACACCGTGGTGGTGGAGTGGC 22286  
QY 12860 -----TGCTCCGCGGACGCGCGCTCAACCGAGGACGGCGCAAGCAACGCGCTGACCGCAC 12913

Db 22287 GGTGCTTTTTCGCGGTACTCCGGGCGAAGTCACTCCCACTTACGCTTCCAGC 22346  
QY 12914 CCAACGGTCTGTACAAAGTCAAGGTCACTCCGCAAGGCTTTGGCCCAACGCAACCTCTCCC 12973  
Db 22347 GGCAGCGTACTGGCTGCGATCCACCGGCGCTGCGGGTGAAGTACCGCCCGCGGATGG 22406  
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QY 13034 AGGCTCAAGCCCTCGTTCGAAGCCTACGGTTCAGAACCGGCCCAACGCGCGCCCTCTGCGC 13093  
Db 22467 TGCTGACCGGTTCGCTGTGACACGCGGTTTCGATTCGCTGGTTTCGCAATCACCGGCTGCTGG 22526  
QY 13094 TCGGAACCTCAAGTCCAAACATCCGGCACTCCATGCGCGCTCCATGCGGCTGCGGGTGGCGGGGTCA 13153  
Db 22527 GCGAAATCTGCTGCTCCCGGACACCGCGATCTGTCGAGTGGTGTGCACGTCGCGAGCGCC 22586  
QY 13154 TC----AAGATGGTGTATGGGCTCTCGGAAATGGTCTGCTGCCGCGGAGCTTTCATGTGGAT 13209  
Db 22587 TCGGTTGTGGCGGTTGGAAGAACTGGCTTTGGAAGCGCCCTGATCTTGCCTGATCATG 22646  
QY 13210 GAGCGCTGCGCGCATGTGGAATCTGCTCCGCGGTTCGCTGAGTCTGTGACGAGACCGGTG 13269  
Db 22647 GAGCGGTCAGGTTTCAAGTGTCTGGTGGGACCGCCCGGGAATCCGAGACCGGTCGGTGG 22706  
QY 13270 CCTGGCGCGCGGAGGCGGCGCTA-CGGCGGCGAGGAGTGTCTCATTTCCGCGCTCAG 13328  
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QY 13329 CGGCACCAACGCCCACTCATCTCTCGAGGAGACACCGCCCAACATCCCGTCAGA--- 13385  
Db 22767 TGCTTCTCCACCGTGGCGCGCGAGAACCATGAGCTGACCGCATGCGCCCGGAGATG 22826  
QY 13386 -CACACCGCGCAGCAGCTCCCGGAGAAATCAGCGCGCGCAGAGGATGCGCGGTAGTGGCG 13444  
Db 22827 CGACCGAAATCGATGACAGCGGGTCTACGATTTCTTGAAGGCGACGGTTTCGCGTACG 22886  
QY 13445 ATGAGGCTGTGCGCGCAGTCCAGGGTGTGGCGGTGGTGTGCGGCCAAGTTCGCGAGC 13504  
Db 22887 GACCGGCTTTAGATGCTCTCGCGGTGCTGGCGACGAGCGGGGAGGTGTTCGCCGAAG 22946  
QY 13505 CCGGCTTCGCGCGCCAGGCGCCCTGACGCCCACTCAGCGCACACCGCTCAGCGACACCGCG- 13558  
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QY 13602 CGCGCT-----GTTTCGACCAACCGCGCACCTCATCGCGCGCAGCGCGAC 13648  
Db 23067 TGGCGTTCTGCGGTGGGTGGAATTCGCGCACTGAAAGCGCGGTGTGCGGGCGC 23126  
QY 13649 CTTCTCTGCG-----AAGCACTCCAGCACTTCGCGCAGCGGCAACCCACCGCGCG 13699  
Db 23127 GCTCTCTGTTGACTTCGATGACGAACTGTGTTGGTTCGCGAGTGGACCCCGCTCGCAT 23186  
QY 13700 TCATCCACA-----GCA 13711  
Db 23187 TCGTGGCAACGGTTGATTCTGCTGTCGTCGACCGCATCTCCCGCGCAGCAGGTGAGGTCTG 23246  
QY 13712 GCGCCCGCAGCGGAGACCGGAGCGCGGAGCGCGCAGGAAAGACGCGATTCATCTGCTCCG 13771  
Db 23247 GCGCGATTCGGTGAATGCTCTGTTTCGAGTGGAGTGGCAACCGGAAGGCGTTTGTGGGAACA 23306  
QY 13772 GACAGGCGACCCCAACCGCGCATGGCCCAACCGGCTCTACCAACCCACCGCTCTTCG 13831  
Db 23307 CCGCGCGGACGACCTTGCATCTGTGTTGACCGGTCCAGTTGGCGGAAATGCGTGGCG 23366  
QY 13832 CCGCGCACTCAACGACATCTGCACCCACCTTCGACCCCACTTCGACCAACCCCTCTCTCC 13891

Db	18988	GAGGCCGAGCCGATTTGGAACACACCGCGGAAACAGCGGGCAAGGCAAAACCCGTTGAG	19047
Qy	10347	-----CGGTGCTGTGCTG	10360
Db	19048	CTGACGCAACAGCCTGCGCGGACTGTGCGGAAAGAAACGACGATTCGCGGTATTGATCTG	19107
Qy	10361	GTTCGGGCGTGTGATGTTGGCGCTGTGGGGCGG-----	10393
Db	19108	GTGCGGGCGAGACGGCGCTGTCTGGACGCGAGATGCCACGGCCCTGGCGCCATCG	19167
Qy	10394	-----TGGTGGCGTGTGTTGAGCGCGAGTTGGCGG	10423
Db	19168	CGCGGCTTCCAGGAACCTCGGATTCGACTCTTGATGCGGTGGAGCTGCGCAACCGGCTG	19227
Qy	10424	TGCGTGGGAGCGGTTGCTGGCGGACAGCCCTGAACGACTT-----	10464
Db	19228	AACACCGCACCGGATTCAGCTGCCCGCCAGACGATTTTCGACTACCCCAATGCCGAG	19287
Qy	10465	-----	10464
Db	19288	TGCTGTGCGGTCACTCTGCGCGAGCTTTTCCCAACGGAGACTACCGTGGACTCGGCC	19347
Qy	10465	-----GAGTCATCCGGTGATTTCCAGCCAGCGGTCCGGTGACACACGAGCC	10512
Db	19348	CTTGCCGAGCTCGATCGAATCAGACGAGAGCTCTCGATCTCACCGGGAAGCGCGGCA	19407
Qy	10513	CGCGGTCGAGCTGCCCGCAGCGCTCCGGTGGCGTCCCTGCTCGGGGTGCGTTGAT	10572
Db	19408	CGGGACCGAATCGGACACGACTGCGAGCCCTTCCACGAAAGTGGAACAGCGCAGCTGAA	19467
Qy	10573	GTATCGGGTCGGGAGGTGTGCGGTGTGTCGGGTGGGTGCT-----	10614
Db	19468	GTACCGACCGAGCCGATGTCTGAGCAGCTCGATTCCGCGACGACGACGAGATATTC	19527
Qy	10615	-----	10614
Db	19528	GAGTTATCGACAACAGAGCTCGACCTGTCTGAGCAGTTCTCTGCGAACTTCAAGCGCG	19587
Qy	10615	-----GTGTTGGTCAACGGGTGG	10631
Db	19588	AAATCGGGTGGAAATCACAATGGCCNATGAAAGAAAGCTTTCGGCTATCTGAAAGGT	19647
Qy	10632	GACGGGTGTGTTGGGTGCGCGGTGGCGGATCTGGCTGTGTGTGGGTGCGGGA	10691
Db	19648	AACTCGGACCTGCATCAGACCCGCGAGCGCTGTCTCGCGCGGAGAGCGGAGTCAGGA	19707
Qy	10692	TCGTCTGTTGGT- GAGCCGGCGTGTGTCGGATGCTCCGGGTGCGAGAGGTCTGCGGGCGG	10750
Db	19708	GCCGATCGCGATCGTCTCGCGAGCTGCCGACTGCCCGCGCGCTCGAUCTCTCCGAAAGC	19767
Qy	10751	AGCTGCCCGGTTGGGGCGGAGGTGCGG-----ATTGTTGCGTGTGATGTGGGGGAGCG	10805
Db	19768	GCTCTGGCAACTGTGTCGCACTGCGACCCAGCGCATCTCGAGTTCCCGCGCCGACCGGGG	19827
Qy	10806	GCGGAGGTGTTCCGGCTCTCGAGGGTGTCTCGCGGGTGTCCGCTGAGC-----	10857
Db	19828	CTGGGATCTCGCGGTTGTACGATCCCGACCGAAACACAGGGAAGCTGTACAGCGG	19887
Qy	10858	-----GCTGTGTCATCGCGGTGTGTGTGACGATGCGACGATCGCCCTCTCTAC	10910
Db	19888	GCCCGCGGTTTCTCGCAGGAGCGGGCGAATTTGCACCCCGCCATGTTCGGGATTTCCGC	19947
Qy	10911	GCCGAGCGGTGGGACACCGGTGTTCGCGCCAAAGTGGATGCGCTCTTTTCTGATGA	10970
Db	19948	GCTGAGGCGTTGGCGATGGAACCCGACGAAACGGTTGTGTGAGCTGTCTCTGGAGGC	20007
Qy	10971	GCTGACGCGGGGTATGGAGCTGTGCGGCTGTGCTGTGTTCTCTCGCGCGCGGGATCTCT	11030
Db	20008	CCTCGAAACGGCGGGCATAGACCCGACATCCCTGCGCGCAGCAAGACCGGTGTCTTCGG	20067
Qy	11031	GGGTCGCGCGGCGGCAACTACG-----	11057
Db	20068	TGTTGTACGCCCCAGGAGTACGGGCGTCTTTGAGGAGATGAGCCGAAACGCTGGGGG	20127
Qy	11058	-----	11057
Db	20128	TTTTGGACTACCGGCGGATGTGAGTGTGGCGTGGGTGGGTTCGGTATTTCGTTGG	20187
Qy	11058	---CGCGGCAATGCCCTCTGGACGCGCTGGGCTACCGGCGGCGGCGGTCTGCCC	11114
Db	20188	TTTTGAGGGTCTGCGGTGACGGTGGATACGGCGTGTCTGCTGCTGTGGTGGCCCTGCA	20247
Qy	11115	GGGGGTCTGCTGGCGTGGGGGTGTGGGAAGAGGCCAGCGGATGACCGGGCACCTGGC	11174
Db	20248	TTTGGCGTGTGAGTGTGCTTCCGCGAATGCGATCTCGCGCTGGCGCGGTGTGAC	20307
Qy	11175	CGGCA-----CCGACACCGGCGCATCATCTCCGTTCCGG	11207
Db	20308	GGTATGGCGACACCGGCGAGCTTCGTGGAGTTCTCCGCTGAGCGTGTGCTCCGGA	20367
Qy	11208	TCGCAATCCATGTGACACCGCGACGCACTGG-----CCCTCTTCGATGGGCGCTGGC	11261
Db	20368	CGGCGGTGCAAGTGTTCGCGCTGCCGCGATGGCACCGGTGGGTGAGGGTGGCGG	20427
Qy	11262	TCGACCGGCGGTCTGCTGCCCGCGACCTGCGTCCCGCGCGCCCTGCGCGCCCT	11321
Db	20428	TCGTTGTGCTGAGCGGTGTTCGATGCGCGCGGCAATGGGCACGAGGTTCGCGGT	20487
Qy	11322	GCTCAGGACCTC-----CTGCCCGCCACCC	11347
Db	20488	GGTGGGGGTAGCGCGGTGAACAGGAGCGGCGTCCGATGTTGACTGCGCGCAATGG	20547
Qy	11348	GCCCGCGACACCGCGCACCACTACCGT-----	11379
Db	20548	TCCGTCGAGCAGCGGTGATCACAGGCGTTGGCGAGTGGCGGTGTGCGTTCCGA	20607
Qy	11380	---GGTGGGCAACCGCGCCGCTGCAAGCTCCGCTCCGATCGCCACCGTCTGGGCCACAC	11435
Db	20608	TGTGGATGCGGTGAGGACATGCGGACCGGACCACTGTTGGTATCCGATCGAGGACAC	20667
Qy	11436	ACAGCACACACCTCTCGCTCGCTCGCTCCGCTCCGATCGCCACCGTCTGGGCCACAC	11495
Db	20668	GGCCCTGATCGCCAGTACGGGACGGCGCGGAGAGGATCGGCGGTGTGTTGGGTG	20727
Qy	11496	CACCGCGACACCATCCCCCGGCGGCTTCGGGAGCTTCGGGTTCGATCTCTCTAC	11555
Db	20728	GCTCAAGTCCAACTCGTTCACAGCAGCGGCGCTGGCGTTGCGCGGCTCATCAAGAT	20787
Qy	11556	CGCGTGGAACTAGCAACCGGCTCTCCCGCACAC-----CGGACTCGGCTC	11604
Db	20788	GGTCTTGGCGATGCGGACGCGGCTGCCCGCACGTTGATGTGATGAGCCACGTC	20847
Qy	11605	CCGACACCTCTGCGCTTCGACACCCCAACCCGACACCTCTACCCACCTCCACACA	11664
Db	20848	GGCGGTGAGCTGTGCGGCGGTTCGGTCCGCTTCTCAGCGAGAACACGCGCTGGCGGA	20907
Qy	11665	CAATCTCAGCACAAACCGGACACGCTGTGCGCGCGCTGTTGGCGGAGCTC-----	11715
Db	20908	CAGTGGTCTCTTCCCGGTGGGGTGTCTGCTTCGGGATCAGCGGACCAACGACACA	20967
Qy	11716	-GACAACTCCAATCCGCTCTCGGCTTCGACAAACCGACACGCGGCGGCGGAGGAAAG	11771
Db	20968	TGTGATCTCGAACAGTCTCCAGTCTGAGAGGGGGAACCGGCGCGGTGAGAGGGA	21027
Qy	11772	-----AGTCAACCTGCGGCTGAAGTCACTCATGTTGAGGTGGAAACGACCCCA	11819
Db	21028	CGGGGACCGGATGTAGCCGTCCCGTGGTCCCTTGGGTGCTGTGCGGTAAAGACACCGGA	21087
Qy	11820	GCATCCGACACCGGAAGCGCTGATGACGACGAGAAGTTC-----ACATCGGCAACA	11871
Db	21088	GGCTCGCGGCGGACGCGGATGCGATTCGATATCGAGGACCGCGCGGCGCTGTC	21147
Qy	11872	GAGCTGAGATTTTCAAAATTCATGACAAACGACCTCGGCGCTGCTGTAACCGGAGCGCTG	11931
Db	21148	CGCGGTGAGTGTGCGTATTCTGCTAGGATGACACGCGCGCGCTGGATGACCGCGCAGT	21207



[illegible]

14677 GTGGG-----TGATGTCGCTCGGCTGACCGCTGCGAGCGCGCCCGCGAGT 14727  
Db  
6253 ACCGAGCGATGCCCATCGTTGGCATGGCTGCTGCTTTCCCGCGGCGAGTGACCTCGGG 6312  
Qy  
14728 GACGAACCGATCGCGATCGTCGCGATGAGCTCCCGGTTTCGGGTGGCGGCACTCGCG 14787  
Db  
6313 GACGACTTCTGGGATCTGATCTCTCCGAGCAGGACGCGATCGGCGGATTTCCCAACCGAC 6372  
Qy  
14788 GAAGACCTGTGCGGCTGCTCGCGCGCGCACGAGGTGATCGGCGAGTTCCCTCCGAC 14847  
Db  
6373 CGCGCTGGGACCTGGACAGCTCTACGACCCCGACCCCGACCAACCCGCGACCTGCTAC 6432  
Qy  
14848 CGGGCTGGGATGCGGAAGCGCTTTACGATCCCGATGCTTCCAGGCTCGGAACGACGAT 14907  
Db  
6433 ACCGAAACGGCGGATTCCTCTACGACGCGAGCGCACTTCGAGCGCGAAATTCCTGGGCATC 6492  
Qy  
14908 GCGCGATGGCGGATTCCTCTACGACGCGGTGAGTTGATGCGGACCTGTTCGGCATC 14967  
Db  
6493 AGCCCCCGGAAGCCCTCGCCATGGACCCCCAGCAACGACTCTCTCTCGAAACCGCTGG 6552  
Qy  
14968 AGCCACAGTGAAGCGTTGGCGATGATCCGACGACGCGTTGGTCTCGAAATCGCTGG 15027  
Db  
6553 GAAACCATGCAACGCGCGGATCAACCCCCACACCTCCAGCGACACCCCGAGTGC 6612  
Qy  
15028 GAAAGCCCTCGAAACGGCGCGGAATCGATCCGTTGCTTTGAAGGCGAGTGGGTCGCGACG 15087  
Db  
6613 TTACCGGCAACCAACGACGAGACTACGCATCTCGCTGCGCAACACGCGGCGAGTCAACC 6672  
Qy  
15088 TACATCGGGCGTGAAGCCGTTGGTACGCGACGGAATGTCGGCAGTTTCCGAGAGGG 15147  
Db  
6673 GATGTTTCGCACTGACCGGAACCGCGGACGCTCATCTCGGTCGTATCTCTGTACACG 6732  
Qy  
15148 GAGGGCTACTCTGACGSGTACTCGGCGAGTGTCTGCTGGGTGCGGTGCGTATTGG 15207  
Db  
6733 TTTGGTTTGAAGGCTCTCGGTCGTGCGTGGACAGCGCTTGTCTCTGCTGTTGGTGCCT 6792  
Qy  
15208 TTTGGTTTCGAGGGTCTCGGTCGACGCTGGTGGATACGGCTTGTCTGCTGTTGGTGGCG 15267  
Db  
6793 TTGCATCTGGCTGTGACGCGTTGCTGCGGTCGAGTGTCTGATGGCGCTTCGCGGGGT 6852  
Qy  
15268 TTGCATCTGGCTGTGAGTGTGCTGCGGCGAGTGTGATCTGGCGTTGGCGGTTGGT 15327  
Db  
6853 GTGACGTGATCTGCTCTCGGTCGCTTCTGTTGGAGTTTTCGCGACGCGGGTCTGCGCC 6912  
Qy  
15328 GTGACGTGATCTGACGCGCGGATGTTCTGTTGGAGTTTCTCCGTCAGCGGTTTGGCG 15387  
Db  
6913 GCGGACGGGATTTGCAAGCGCTTCTCGCGCGGCGGAGCGGACCGCTGGGTCGAGGTT 6972  
Qy  
15388 CCGGATGGGCGGTGCAAGTCTGTCGCGAGAGCGGACCGGCTGGGCGGAAGGC 15447  
Db  
6973 GTGGGGATGCTGCTGTTGGAGCGGCTCTCCGACGCCATCGCAACGCTCACCGTCTGCTG 7032  
Qy  
15448 GCGGGCTGTTGTTGTTGGAGCGGTTGTTCGACGCGCCACCGGAATGGGATCGGGTGTG 15507  
Db  
7033 GCGGTGTTGTCGCGAGTTCGCTCAACAGGACGCTGCGAGCAACGCTCTGACCGCGCC 7092  
Qy  
15508 GCGGTGTTGTCGTTGGGTGACGCGGTGAATCAGGACGCGGCTCTGAAACGACTGCGCGCG 15567  
Db  
7093 AACGGGCGTCCGAGAGCGTGTATCCGCGAGGCGCTCGCCAAACGCGGCTTGTGCGGC 7152  
Qy  
15568 AACGGTCCGTCGACGAGCGGTTGATCAACAGGACCTCGCGAATGCGGCTCTTTTCGCG 15627  
Db  
7153 GGTGATGTCGACGCGGTGAGGCCACAGCGACCGGACCATTTTGGGCGACCGATCGAG 7212  
Qy  
15628 TCCGATGTGGATTCGTTGGAGGACATGGGACCGGACGAGGCTGGTGTATCCGATCGAG 15687  
Db  
7213 GCGGAGGCTCTCTCGGACCTACGGAACGACCGTGGCGGAGGCGGCTGTGGTGTG 7272  
Qy  
15688 GCGGAGGCTTATCGCAACGATATGGGACGGCCCGGAGCGGATCGGCGCTTGTGGCTG 15747  
Db  
7273 GCGTGGTCAAGTCCMATGTCGGTCAACAGAGTGGCGGCGGCTGCGCGGGGTGATC 7332  
Qy  
15748 GGGTGGTCAAGTCCGAACATCGGTATACGCGAGGCGCGGCGGCTGTTGCGGCTGTGATC 15807  
Db

7333 AAGATGTTGATGGCGCTGCGGATGTTGCTGCGCGGAGCTTGTCATGTGGATGAGCCG 7392  
Qy  
15808 AAGATGTTGATGGGCAATGCGGACGCGGAGCTGCCCGCTCGCTGCACGCGGATGAGCCC 15867  
Db  
7393 TCGCCGATGTGGACTGGTTCGCGGGTGGGTGAGTGTGTCGAGTCGTCGAGAGACGGTCCCTGG 7452  
Qy  
15868 ACGTCGAGGTTCGATTTGTTGTCGCGGGCGGTCGCGCTCTCGCGCAACAGGTACCTTGG 15927  
Db  
7453 CCCGGGGAGGGCGGCTACGGCGGCGAGGAGTGTCACTATTCGGGTCAGGGGACCC 7512  
Qy  
15928 CC---GGAGTCTGACCGTGTGTCGGGTGGGGTTCGTCGTTTCGGGATCAGCGGACCC 15984  
Db  
7513 AACCCCACTGATCTCTGAAGAAACACCGCCGACGACGTTCCGGGGGAGACCAACCGGCC 7572  
Qy  
15985 AACGCACATGTGATCTCTGAAACAGCTAC-----GAAATGCCCGAGAT 16026  
Db  
7573 GGCAGGGTACGCGGGACGACGATGAGGCTCTGCGCGGACGTCCTGGGGTGTGGCG 7632  
Qy  
16027 AGTACAGCGGAGACGGAACAAAACAGAAATCCGGATCTACTGTGATATTTCCGGTCTTCCC 16086  
Db  
7633 TGGTGTGTGTCGGCCNAAGTCCGACCGCGCTGCGCGCCAGGCCCGACCGCCCTGCACGCC 7692  
Qy  
16087 TGGTTGGTGTGCGGAAGACGACGGAATTCCTGCGGGGACAAAGCCGAACGAGTCTTGTCT 16146  
Db  
7693 CACCTCACCGACACCCCGCTCGACTCTCGCGGATGTGGGATACACCTCGCCACAGGCC 7752  
Qy  
16147 CAGTCTGAGTCCCGCGCGGACGAGCTTCGCTGATGTGTGCTACTCGCTTGTCTTGGC 16206  
Db  
7753 GCGCGGTGTTTCGACACCGCGCACCTCATGCGCGGAGCCGCGACAGCTTCTTGCAA 7812  
Qy  
16207 CGAGCGCGCTGGATGAACGCGCTGTGCTGCGGTGCGGACCGCGGTGAGCTGTGCT 16266  
Db  
7813 GCATTCAGGCACTCGCGGAGGAGCGCCACCCCGCGTCATCCACAGAGCGCCCGC 7872  
Qy  
16267 GGAATGCGCGGTTGGCGCGCGTTCGAGAGGCTTCTGGGGTGATCAGCGGAAT- 16320  
Db  
7873 GCGGGACCGGACCGGGAGCGCGAGAAAGACCGCATTCATCTGCTCGGACAGGGC 7932  
Qy  
16321 -----CGTGTCTTCTGCTCGGTTCGGTTCGTTCTCGGGCAGGGT 16362  
Db  
7933 ACCCAACCGCGCGATGCGCCACAGGCTCTACACACCCACCCCGCTTTCGCGCGCGCA 7992  
Qy  
16363 GGTGAGTGTGGGATGGGACAGAGCTCTTACTCGAAATTTTCGGGTTCGCTGCTGCG 16422  
Db  
7993 CTCAGGACATCTGACCCCACTCGACCCCGCTCGACACCCCGCTCTCCCTCTCCTC 8052  
Qy  
16423 TTTGATGAGGCTTGGCGCGAGTTGGAGGACATCTGGGGGAGACCGCGCGGTTTC- 16477  
Db  
8053 ACCCAAAACGACAAACGACAGGAGCGCGGCGCACTGCTTCAGAGACCCGCTACGCC 8112  
Qy  
16478 -----GGATGTGTTCTTGGTTCGATGCGGAGTGTGATCAGACGCTGTGGCG 16530  
Db  
8113 CAGCGCGCTCTTTCGCTTCCAGGTGCGCTCCACCGCTCTCTCACGAGCGGTACAC 8172  
Qy  
16531 CAGTGGGTCTTTCGCGCTGCAAGCGGCTCTTGGGCTGCT---GGTTCGTGGGCG 16587  
Db  
8173 ATCAACCCCTACTAGCGCGGACACTCCCTCGCGGAAATCAGCGCGCCACCTCGCC 8232  
Qy  
16588 GTTCGGCGGATGTGTTGATGGGCAATTCGGTGGGGAGTTGGCGCGCGCTTTCGGGCT 16647  
Db  
8233 GGCATCTCTACCCCTCACGAGCGCACCACTCATACCCAAACGCGGCCACCTCATGCAA 8292  
Qy  
16648 GCGGTGTGTGTTGGGATGCGGCTCGGTGGTGGCGCGCGCGCGGCTGTGATGCAA 16707  
Db  
8293 ACCATGCCCCC---CGGACCATGACACCTCCACACACACCCCGCCACCATCACCCAC 8349  
Qy  
16708 GCCCTGCTCTGACGCGCGGATGTGGCGGTGCTGTGTTGAAAGACTTGTTCGGGCA 16767  
Db  
8350 CACTCAGCGCCACGAAACGACCTCGCCATCGCGCCATCAACACCCCGCTCCCTC 8409  
Qy  
16768 TTGTGGCGGTCGGGAGGAGTCCGTGAGCTGCCCGCGCTCAATGCCCGCGGTTTCGGTG 16827  
Db



10531 GACACCGCGCCACCGCGCAGAGAAAGGTGTGAAAGGCTATCTCGGAACCGGCAATGCG 10590  
1897 GGCAGCGCTCTGTCGCGCGGTATCGCTACAGCTTCGCGCTCGAAGCGCGCGATCAC 1956  
10591 GGAAGCGTCCCTCTGCTCGGTTGCGTATGCGTTCTGCGGTTCGAGGGCCACGCGTGAGC 10650  
1957 GTGACACGGGGTGTCTCGGATCGCTGCTGACGCTGCACTCTGGCGTGCAGCTGCGTGGG 2016  
10651 GTAGACACGGCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10710  
2017 TCGGCTGAGTGACAGCTCGCGCTGCGCGCGCGCGCTCTCGGTCATGTTCACCCCTCGGATG 2076  
10711 CAGGCGGAGTGTGATCTGCGCTGCGCGCGCGCGCTGCGGTCATGTTCGACGCGGAGAG 10770  
2077 TTTCATCGAGTCTCTCCCGCAGCGCGCGCTGCTGCGGTCAGGTCGAGCGTACTCG 2136  
10771 TTTCGTTGAGTCTCTCCGTCAGCGTGTCTGCGCACCGGATGCGGCTGTAAGTCTGTCGG 10830  
2137 GCTGACGCGGACCGGACCGGCTGCGGCGAGGCGCTCGGATGCTGTGTGTGAGCGGTTG 2196  
10831 GCGGCTGCGGATGGAACCGGTTGGGTCGAGGTCGCGGTTGCTGTGCTGAGCGGCTG 10890  
2197 TCGGATCGGTCGCGCTGCGGCGATCGGTCGCTGCGGTCGCTGCGGTCGCTGCGGTCGCTG 2256  
10891 TCAGACGCGCAGCGGAAACCGGCTCGGCTACTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 10950  
2257 CAGGACGCTGCTGCAATCGGCTGACGCGCGCGGCTGCGGCTCAGGAGCGGCTGATC 2316  
10951 CAGGACGCTGCTGCAATCGGCTGACGCGCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 11010  
2317 CCGCAGGCGCTGCGGAAACCGGCTGCTGCGGCGGATGCGGTCGCTGCTGCTGCTGCTGCTG 2376  
11011 CAGCAGGTCCTCAGCAGTTCGCGGCTGTCGCGCTCCGATGTGCGAGCGCAT 11070  
2377 GGGACGGGACACGCTGCGGTCATTCGATCGAGGACACAGGCGTGTGCTGCGCAGTACGGG 2436  
11071 GGAACGGGTACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11130  
2437 CAG---CGGCGCGGTGACAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2493  
11131 CAGGATCGGGAACCGGACCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11190  
2494 ACCATGCTGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2553  
11191 ACCGAGCGGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11250  
2554 GTGTTGCGCGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2613  
11251 GAGCTGCGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11310  
2614 GCGGTGCGGCTGCTGACGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2673  
11311 GCGGTGCGGCTGCTGACGAGGACATCCGCTGCGCAGGACCGGCTGCTGCTGCTGCTGCTGCTG 11361  
2674 CCGCGGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2733  
11362 CCGCTGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11421  
2734 GCGCGGCGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2793  
11422 GACCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11436  
2794 GCCATTTGCGTGGCTGAGTGGTGGCGCTCCAGTGGCTGTGCTGCTGCGCGGTCGCTGAG 2853  
11437 -----ACCGAGAACGAGGAA 11451  
2854 TCGGTGCGGTCGCGGTGCGGTCGCGGTTCCTGTCGCGGTCGCGGTGCTGAGGCT 2913  
11452 GCAGCGAGTCCCGACGACCTGGGATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11511  
2914 GGGTTGCGGCGGCGGAGGCGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2973  
11512 GCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11568

2974 CTTCCGATGTTGGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3033  
11569 CCGTTCATGTCGTTCTTCTACTGCGCGCCACGCGCAGCGCTTGGAGACACCGAGCGGTG 11628  
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3094 CCGATCGCGGCTGACCAAGGCTCATGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3153  
11689 CCAGCGTTCGATGCTGTTGAGGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11739  
3154 GTGTTTCCCGGACAGGCTGCGGCTGCGGATGCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 3213  
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3214 CCGTGTTCGCGCGCGGATGCGGCTGCGGAGGCTGCTGCGGCGGCTGCGGCTGCGGCTGCGG 3273  
11800 CCGAGCTTCCGCGCCACATGCGAGTGCAGGTCGCGGCTGCGGAGTACGTGCGGCTGCGG 11859  
3274 TCTGTGTGACATCTCTGCGCGCGGACGCGGCGGATGCGGTCGCGGAGCGGCTGCGGCTGCG 3333  
11860 TCGTTGTGTCAGCTGCTGCGCGGAGCGGAGAACTCCCAACCGCTGCGGCTGCGGCTGCGG 11919  
3334 GTCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3393  
11920 CTCCAGCGCGGCTCTTCCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11979  
3394 ATCGAAACCGGACGCGGCTCTTGGCCATTCAGGCGGAGATGCGGCGGCGGCTGCTGCTGCTG 3453  
11980 GTGAGGCGCGGCGGCTGCTGCGGCGACAGTCAAGGCGAAATCGCGCGGCTGCGGCGGCTG 12039  
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3514 GCTGTGCGGCGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3573  
12100 GACATTTCCGCGCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12159  
3574 CTATGTTGAGCGGCTGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3633  
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3634 ACCGCGCTGCTGCGGCGGATCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3693  
12217 GTGTTGTTGCTCGGCGATCTGGAAGCGGCTGCGGAGTCTGCTGCGGAGTGTGCTGCTGCTG 12276  
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12277 GACATGCTGACGCGCTATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12336  
3754 CTGCGGAGGAGTGTGCTGAGCTGCTGCGGAGATACAGCCCGGAGCTGCTGCGGCTGCTGCTG 3813  
12337 GTTCCGAGCGGCTGCTGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12396  
3814 TTCTTCTCCAGGTGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3873  
12397 TGGTGTGCGAGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12456  
3874 TACCGCAACTGCAACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3933  
12457 TATCGGAACCTCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12516  
3934 GGACACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3993  
12517 GGATTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12576  
3994 ACCACCGAGACCGCGGAGAGTCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4053  
12577 ACCGTGCGGAGTGGAGACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12636

Db	44620	CGAGGGGATCTCTGCTCGGCGCCATGAGCTCTCGAGCGGATCGACCGGCTCTTCGCGCCCAA	44679
Qy	29562	GGGGAGCGCTGCGCTCTCTTCGACAGCTGACGCGCGGGGACAGAGCTGTCTCGGCTTTTGGT	29621
Db	44680	GATCGATGCGCGCTGGCACTTGTGATCAGCTCACCCAAAGATAAGCCCTTGGCGCTTCAT	44739
Qy	29622	CATGTTCTCTCTCGGCTCGGCGGTGTGGCTGCGCCGCGGAGGGCAACTAGCGCGCGCG	29681
Db	44740	CCTCTTCTGCTCGCTCGCGCGGTCTCTCGGACGTCAGGTCACTCAACTACGCGCGTGC	44799
Qy	29682	CAACGCGCTCTCGACTTCTTGTCTCATCGCCGCGCGGAGGGGCTGCCGCGGCTCTC	29741
Db	44800	GAGGCGCTTCTCGATGCGCTTGGCACCACCGGCGCGCGCAGAGGCTCCCTGCTCATC	44859
Qy	29742	TCTCGCTGGGGCTGTGGAAAGAGGGCA CAGGGATGACGGGCCACCTCGACGTCGACGA	29801
Db	44860	GCTCGCTGAGGCCACTGGGCGAGCGACGCAATGACAGACAGCTCAGCGCGCGCG	44919
Qy	29802	CAATGCGCGGATCAGCGCGCGGGAATGGCGGCGCTGCGGACTGCGGAGGCTCTGGCGCT	29861
Db	44920	CGCCCCCTCGCATGGAGCGGCGCGG --- CCTTCCCTCGACCTCTGAGGAGAGGCTCGCCCT	44976
Qy	29862	GTTTCGACGGGGCTTGGCGCAGCGGAGCGGCTTCTGATGCGCGCTCGGCTCGACCTCAC	29921
Db	44977	CTTTCGATGCGGCGCTCTTTCGAACCGAGACCGCCCTGTCTCCCGCGCGCTTCGACTTGAG	45036
Qy	29922	GGCGGTACGCTGTGTGTCGCGCTCGCACCGGTGCGCGCGCTGTCTGAAGTCTGCTTCA	29981
Db	45037	CGCGCTCAGGGGAAACGCGCGGAGC - - - - - GTCCCCCGTTGTTTCCAAAGTCTCGTCCG	45090
Qy	29982	GCTGCCTCGGTCCGCTCGGCGCGCGCGGCCCCCGGCACATGGGGCCCCCGGCGGCGAGCA	30041
Db	45091	CGCTCGCACCGGTACGCAAGGCGCGCAGCAACACGCCC - - - - - A	45129
Qy	30042	GGCGGCGCTGCGCTGAGCGTCTGSCCGGCGAGAGTGCCGTGAGCGCAGCGAGGCGCT	30101
Db	45130	GGCTCTGTGCTTACAGAGCGCTCTCAGCCCTCCGCGCGCGGCAACGAGCGTGCCCT	45189
Qy	30102	GCTGCGCCTGTGCGGTGCATGTCTCGCGCGGTGCTCGGCCATAGCGGTGCGCAGGAAT	30161
Db	45190	GCTCGATCTCATCCGACACGAAGCGCGCGCTCTCGGCGCTCGGCTCTCTTCTGAATCGCT	45249
Qy	30162	CGAGCATCGCGGGCTTCCGCGAGCTGGGTTTCAGCTCGCTCAGCGCGGTCTGAGCTGCG	30221
Db	45250	CGATCCGATCGGCTCTCTCAAGAGCTTGGCTCTCGACTCCATCATTCGCGCTCGATCTCCG	45309
Qy	30222	CAACCGTCTCACGGCGCGACGGGCTCGGGCTGCGGGCGAGCTGGGCTCTCGATTTCCC	30281
Db	45310	AAATCGGCTCGCGCGCCACCGGCGTGGAATCCACGCAACCTCTCTTCTGAGCATCC	45369
Qy	30282	GACCCCGGAGCGCTGGCCG	30301
Db	45370	AAACCCAGCTGGGCTCGCAG	45389

RESULT 12	
AAF88313	
ID	AAF88313 standard; DNA; 50000 BP.
XX	
XX	AAF88313;
XX	
XX	28-AUG-2001 (first entry)
DT	
DT	
XX	
DE	S. spinosa DNA fragment_SEQ ID 2.
XX	
XX	Forosamine; trimethylrhamnose; polyketide synthase; biosynthesis;
KW	spinoseyn; polyketide aglycone; transgenic plant; insect resistance;
KW	macrolide; insecticidal; ds.
XX	
XX	Saccharopolyspora spinosa.
OS	
XX	
XX	DE19957268-A1.
PN	
XX	
XX	

08-MAR-2001.  
29-NOV-1999; 99DE-1057268.  
27-AUG-1999; 99DE-1040596.  
(FARB ) BAYER AG.  
Eberz G, Moehrl V, Froede R, Velten R, Salas JA;  
WPI; 2001-267102/28.  
New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for  
recombinant production of insecticidal spinosyns and their derivatives  
-  
Claim 7; Page 31-49; 354pp; German.  
This invention describes a novel method nucleic acid (I) and its encoded  
polypeptide (II) containing at least one region that encodes an enzymatic  
activity involved in biosynthesis of spinosyns. (I) are used (i) to  
identify, inactivate or modulate genes involved in the biosynthesis of  
(II); (ii) to generate a library of polyketide synthases; (iii) for  
adding forosamine or trimethylrharnnose to a spinosyn or polyketide  
adlycone; and (iv) for recombinant production of the corresponding  
enzymes, which are used for production of (II), their precursors or  
derivatives, including production of transgenic plants that express (II)  
and thus have increased resistance to insects. (I) are also useful as  
markers for sequencing of the Saccharopolyspora spinosa genome. (II) are  
macrolides with insecticidal, but not antibacterial, activity, and can  
also be used to raise specific antibodies, useful for identifying  
expression clones in a gene bank. Cells transformed with (I) may produce  
(II) at significantly increased levels or produce new derivatives of  
(II). This sequence represents a genomic DNA fragment of the S. spinosa  
genome which contains the coding regions for proteins involved in  
forosamine, trimethylrharnnose and polyketide synthase biosynthesis.  
Sequence 50000 BP; 6867 A; 14165 C; 19274 G; 9694 T; 0 other;

Query Match	10.2%;	Score 3142;	DB 22;	Length 50000;
Best Local Similarity	49.2%;	Pred. No. 0;		
Matches 15063;	Conservative 0;	Mismatches 12830;	Indels 2753;	Gaps 147
Qy	1417	CACGGAGGACGGACGGCGGAGACCCGATCCCATCATCGCATGGCATGCCGTTTC	1476	
Db	10123	CACGAGCGGAGTTCGGGAGAGCGGGAACCCATCGCATCTGGCGATGGGCTGCCGGTAC	10182	
Qy	1477	CCGGGCGGAGTCCGGTCCCGAAGACCTGTGGGAGCTGGCGGCTCCGGGCGGAGACGCC	1536	
Db	10183	CCGGGTGGGTGCAGGACCCGGNAGGGCTGTGGAACTGGTTCGCTCCGGTGGCGACGCC	10242	
Qy	1537	ATCGGCGGTTTCCACACGACCGCGGATGGGCCACGGAACTGCTACGCCACGAGACGCC	1596	
Db	10243	ATCGGTGAATTCCTCCGCTCATCTGTGGTGGCACTCGACAGAGCTCTACGATCCCGACCCG	10302	
Qy	1597	ACGACCGCGGACGTTCTATCCGACGGAGGCGGTTCTTACAGCGCGGCGCATCTTC	1656	
Db	10303	GATCAGCCCGGAACCTGCTACACCGGACCGCGGCTTCCTCCACGACCGCGCGAGTTC	10362	
Qy	1657	GACGCGGCTTCTTCGGAAATCAGTCCACTGAGGCACCTGGCGGATGGATCCGACGACGGG	1716	
Db	10363	GACGCGGATTCCTTCGACATCAGCCCCGTGAGGGCTCGGATGGACCCGACGACGGG	10422	
Qy	1717	CTGCTCTGGAGACGTCTCTGGAGCGGCTTCGAGCGGGCGGGAATCGATTCGCTTCGGTA	1776	
Db	10423	CTGCTCTGGAATCTCTCTGGGAGACCGTCGGAATCCGTGGGATGGACCGGAGTCCCTTG	10482	
Qy	1777	CGCGGGTCCCGTACGGGCGTCTTCGCGGGCGCTCTCTCTTCGACTACGGCCCGGATG	1836	
Db	10483	CGGGGAGCCGACCGGGGTGTTTCGGGATTTGATGTACGAGGGCTA-----T	10530	
Qy	1837	GACACCGGTCGTTCGGAGGGGCGCGGACGTGGAGGGGCCATCTCTCACCGGTACCACG	1896	







QY	22969	CACCAACCCACCAACCTGGCTCATCGCATCCCGAAACCCAGACCCACCAACCCAC	23028	Db	39485	GGATACGCGCGGAAACGCTTCTCGAGCCCTGGCCGACACGCGCGAGTCTTGA	39544
Db	38426	GCGACCTGGCGGACCTGGCTCTCGTGTGGCGCGCTCTGGACGACGCGCTC	38485	QY	24106	CTTCCCGGGGATCGATCGCTGGGGCCCTGGGCGGAAGGCGATGTCCGCGGTGAT	24165
QY	23029	ATCACCAATCTCTACCAACCTTCACACACGAGGATCACCCCATCCCTCTCACTGTC	23088	Db	39545	CAGCCGACACGTCGCTGGGGCGCTGGGGCGCGGCGGTGATATTCACGGGG	39604
Db	38486	CCCTCCGCGCTCACGAGGCTTCGCGCGCGCGCGCGGCTCTCGCGCTGGCGCTG	38545	QY	24166	CGGCTCATGTATTACTGGAAGCGGGCATTTCTGCGATGGAGCCACGATGGCGCTC	24225
QY	23089	AACCAACCCACCAACCCCAACCTCCACACACACCTCCACACACCCGACACAA	23148	Db	39605	CCCTGGCAGCCAGCTGGAGCAAGCTGTGTGCGCGATGGCCCTTCGCTGGCGTG	39664
Db	38546	AGCAGGCCACCTGACGCGGAGGCTCTGCGGAGCACTTGGCGCAGGCTTG-----	38598	QY	24226	CGGCAATTCATGTGTGCGCGGCGAGCGCGCAATTCACACTGATCATCGCGACATC	24285
QY	23149	GCCAAACACCAACCCGAGCCCATACCGGCTGTCTCTCCCTCTCGCCCTCGACGAA	23208	Db	39665	CGGCGCTCGCGCAAGCCCTGGAGCACGACAGAGA---CCACCGTCACCGTCCGCGACATC	39721
Db	38599	-----CGCGAGACCGCGCGCTCGCGGCTGTCTGTCTCTCGCCCTCGAGGAA	38650	QY	24286	GACTGGGAGCGCTGTCTCCCGCTTACCGCTCGAGCGCACAGCCGCTCATCGAGGAC	24345
QY	23209	ACACCCACCCACACCCCCACACACACCGGACCCCTCTCTCAACCTCAACCTCCCC	23268	Db	39722	GACTGGGCGCGCTTGGCGCTTCGATCAGCGTGTGTCTCCCGCGCTCTCTCGCGACT	39781
Db	38651	AGTCCCTTCGCGACCATCGCGCGTGTGCGCGGAGCTCGCTTCTCGCTCACCTCTGTC	38710	QY	24346	ATTCCGAGGTTTCGCAAGCGCTCAGGAGCTGGAAGCAGCTGTGTGTGTGTGTGTGTGT	24405
QY	23269	CAAAACCCACCAACCCACCAACCCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	23328	Db	39782	TGCCCGAGCGCGCCCTCGAAGACAGAGAAGCGCGCTCTCTCTCCGAGCACGCGCCGG	39841
Db	38711	CAAGCCCTCGGAGCATCGCCCTTCGAGCGCCCTTGTGTGTGTGTGTGTGTGTGTGTGT	38770	QY	24406	ACCAAGCTCAGCGGATTCGAGCTCTCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	24465
QY	23329	ACCACCCACCCACCCCTCTCACACACCCCAAGCCCAACCTGGGAGCTTCGCC	23388	Db	39842	CCCCCGAC-----CTCCTCGACAAAGTCCGAGCGCTCGGAGAGC	39883
Db	38771	TCCGTGGGACATCCGACCCCATCGCATCGAGCAGCGATGACCTGGGCGCTGGGC	38830	QY	24466	AAGCAGAACAGGTCGTCTCGGCTGATTTCGAGACAGCATCTGCACGTTCTTCGGCCTT	24525
QY	23389	CGGACACCTCTCTGAAACACCCACACACCGCGGGAATCATCGACCTCCCGACAC	23448	Db	39884	GAGCAGTCTCTGTCTCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	39943
Db	38831	CGGCTCTCGGCTCGAGCACCCCGAGCGTGGGAGGCTGTGTGTGTGTGTGTGTGTGTGT	38890	QY	24526	CGTAATCCGGAAGGATCGAGGACCAACGAGCTTCGCGAGCTTCGCGTTCGACTTCGCTG	24585
QY	23449	CCACCCCCACACCTCTCACACACCTCACCAACCCCTCACCAACCCACCAACCAAC	23508	Db	39944	GAGGCGCTTCCAGCTCGACCCCGACAGCTTCTTCGACCTTCGATTCGATTCGATTC	40003
Db	38891	ATGACCGAGCGCGCTGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	38950	QY	24586	AGCTCGGCTCAGTTTCAGCAAGAACTCGCCAAAGAAACCGGACTTCGCACTCCCGCTCC	24645
QY	23509	CAACTCGCATCGCACACCGGACCCACACCGCGCGCTCTCACCCCAACCCCTCAC	23568	Db	40004	ATGACGTCGAGCTTCGTGGCGCTTGTCAACAGGCGCACCGCATCAAGCTCCCGGCGAC	40063
Db	38951	CAGCTCGCTCTCGCGCGCGCGGTTCTAGCTTCGCGCGCTCTGTTCGCGCTCGCTCG	39010	QY	24646	CTGTCTTCGACTATCCACCCCGCAGGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT	24705
QY	23569	CCACACACCAACCCACCCCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG	23628	Db	40064	CTCGCTTCGACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	40123
Db	39011	GAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG	39070	QY	24706	GACCTAGACGACGAGGAGCGGCACTGTGCAATGTCTCTCCGCAAGTGGCCCATCGG	24765
QY	23629	GGCGCGCTCGCACACCTCACCCACCTCACCCACCCACCAACCCCAACCAACCTC	23688	Db	40124	CAGCGCTTCGACGAGGCTCTCCGCGGAGCGA-----CGCGCGCGCTCCGCGC	40174
Db	39071	GGCGCGCTCGGCGCTCACGTGCGCGGATGGCT---CGCTCGAGAGCGCGAGCACCTC	39127	QY	24766	GTACCGCTCGAGGAGCAACCGATCGCCATCATCGGTATGGGATGTGGTTCGCGCGGCG	24825
QY	23689	CTCTCACGAGCGAAACCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	23748	Db	40175	CGCGCTCGAGCGACGAGCCCATCGCCATCGTGGCATGGCGCTCGCGCTTCGCGGCGCG	40234
Db	39128	GTCTCTCATCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	39187	QY	24826	GTACGTTCTCGGAGGCTGTGGGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	24885
QY	23749	CAACAAAGGATCTACCTCACCATCAACCTCGGACACCGAGCAACCCAGACCACTC	23808	Db	40235	GTGCGGATGTGACGCTCTTTGGGAGTTCTTCCACAAAGGCGGCGAGCGGTCGAGGCC	40294
Db	39188	ACGGCCCTGGGCGGCGGCGTCACTTTCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGT	39247	QY	24886	TTCCCGACCGGCGGCTGGGACCTGGACACGCTTACGACCCCGGACCCCGACCCACCC	24945
QY	23809	CAACAACTCTCAACACCATCCCGCACACACCC---TCACACCGTCTATCCACAC	23865	Db	40295	ATTCAC---AGAGCGCTGGGACCGCGGTGCCCTCTACGACCCCGACCCCGACCGGAC	40351
Db	39248	GCCACGCTTCTGAGGAGCTGACGCGGAGGCTCGAGGTTCGAGTTCGCGCGGCTGTTC	39307	QY	24946	GGCAGCTCTACACCGGAAACCGCGGATTCCTCTACGCGGCGAGGCACTTCGACCGGAA	25005
QY	23866	GCAGGCGTCAATCTTTCGCGCGCGGCTGTGGAAACCGATGCGGAAATCTTCTCTCC	23925	Db	40352	GCCAAAGCTACGTCGCGCATGCGCGATGTCTCGACACAGATCGACCTCTTCGACCTGCC	40411
Db	39308	GGCGGATCGGGGCGGCGCTCGCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG	39367	QY	25006	TCTTTCGATCAGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	25065
QY	23926	ACGGAGCGGAGGAGGCGGCGGCGGATTCGATGATGTGTGTGTGTGTGTGTGTGTGTGT	23985	Db	40412	TTCTTCGATCAGCGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	40471
Db	39368	GTCTCTGCAAGGTCTTAGGCGGAGGAACTCTCACGA---CCTGTCTGCTCTCGACCC	39424	QY	25066	GAACCGGCTGGGAAACCATGAAACACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	25125
QY	23986	CTTGAACATTCATCTTCTCTGCGCGCGGCGGCTTGGGAGCGGCGGAGATCAGTGC	24045	Db	40472	GAATCTGCTGCTGCGGCTCGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	40531
Db	39425	CTGAGCGCTTCTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	39484	QY	25126	CCACCGGAGTCTTCGCGGAAATCAACGCTCAAGACCAAGCGCGCGGCGGCGGCGGCGG	25185
QY	24046	GCATACTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	24105				

Db 36281 CGAGGACACGGGCTCTCGCCCTCTGTCGCGGACCGCCATGAACATGACGCGCGTGG 36340  
Qy 20827 AACGGTCTACCGCGCCCAACGGGCGCTCCACGACGCGGTATCGCGCAGGCGCTCGCC 20886  
Db 36341 AGGGGATACCGCGCCCAATGGACCTCCACAGAGGTCTTCGCGCGCGGTCCAC 36400  
Qy 20887 AACGGGACCTGACCGCGCCGACGTCGATGGGTGGAGGCCAACGGGACCGGACCACT 20946  
Db 36401 GACGCCCATATCGGGCGCTCCGACGTCGACGTCGTGCAATGCATGGCACCGGCACTCC 36460  
Qy 20947 TTGGGCGACCGATCGAGCGCCAGGCGCATCTCGGACCTACGGACAGGACCGTCCGCG 21006  
Db 36461 TTGGGAGACCCCATCGAGGTCAAGCCCTTGGCGCGCTACGCCGATGGACAGCCGCT 36520  
Qy 21007 AACGGGCGCTTGTGGGTGGGCTCCGTCAAGTCAACGTCGACACACACAGGCGCGGG 21066  
Db 36521 GAAAGCCTCTCTTCTCGCGCACTCAAGACCAATTTGGGCACTCGAGGCGCGCTCC 36580  
Qy 21067 GCGTGGCGGAGTGAATCAAGATGTGATGGCCCTCGCCACCGGACACTTCCACCGACT 21126  
Db 36581 GGCCTCGCGGCGTCCGCAAGATCGTCGCTCCCTCGGCCATGACGCGCTGCCCCCACC 36640  
Qy 21127 CTCGAGCGGATGAGCGCTCGCGCATGTGGACTGTCGCGGGTGGCGGTGAGTGTCTG 21186  
Db 36641 CTCACACGACCCCGCGCAATCCCTGATCGAGTGGGATGCGCTCGCCATCGACGTCGTC 36700  
Qy 21187 ACGGAGACGGTCCCTGGGCGCGG---CGGGAGGGCGGCGCGCGGAGGAGTGTCA 21243  
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Db 36761 GCGTTGCGACTCTCGCGCACCAACGCCCACTGTTCTCGAAGAGGCTCCCG- - - - -C 36813  
Qy 21304 GTTCGGGGGACACCGCGCGACGAGGATGCGGTAGTGGCGAGGAGGCTGCTCGCGC 21363  
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Qy 21364 AGTCCTGGGGTGTGGCGGTGGTGTTCGGCAAGTCGACGCGGCGCTCGCGCGCCAG 21423  
Db 36868 AGCC- - - - -TGCGCGTGTCTGTTCGGCGAGGAGCGCGCGCGTGGCGCGCCAG 36919  
Qy 21424 GCGGAGGCGTCAGCGCCACTACCGACCAACCGCGGCTCGACCTCGCGGACGTGCGA 21483  
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Qy 21484 TACACCTCGCCACGCGCGCGCGTGTTCGACACGCGGCGACCGCTATCGCGCGAC 21543  
Db 36980 TACTCGCTCGCCACACCGCGGCTACCTTCGAGCACCGTGGCGCTCTCGTGTCCACGAC 37039  
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Qy 21784 CCGCTCTCTCCCTCTCTACCCAAACGACACGACCAACGACGAGGAGCGCGCGGCA 21843  
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Qy 21844 CTGCTCCAGCAGACCGCGTACGCCACGCGCGCGCTTTCGCGCTTCGAGGTGCGCGCTCAC 21903  
Db 37307 CCGGTGCGAGTGGTCCAGCGCGCGCTGTTCTCGATGATGGTCTGCTGCGCGCGCGCTG 37366

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Qy 21964 GAAATCACCGCGCGCCACTCGCGGCACTCTACCTTCAACGAGCGACCAACCTCATC 22023  
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Qy 22024 ACCCAACGGGCA- - - - -CCCTCATCAAAACCATGCCCCCGGACCATGACACCTCCAC 22080  
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Qy 22432 ACCCAACCCCTCCACCAACGCGGTACACCTTACATCGAACTCGGACCGCGCAACAC 22491  
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Qy 22492 CTCACCGCTTCAACCAACCACTCCCAACACCGCGCGCGCGCGCGCTCACCGTCA 22551  
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19705 TCACGTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 19764

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20767 AACGCTCAACGCTGCTCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 20826



Db	32072	CCTCGCGCGCGCGTGTTCCTCGTTCGGGTCTCGGCAACAACGCCCATGTCATCTC	32131	Qy	17572	CTCACCACG-----ACACCCAAACCTTCACTACCAACCCACCCACCCCTC	17622
Qy	16492	GAAGAAGACACCGCCACAAATCCGTCAGACACACCCGCGAGACGCCCGGAGAA	16551	Db	33077	CTCGCGCAGGTCTAGCCAAATCATCGTCTCGAGGTGGAGTCCCTTTTATTGACC	33136
Db	32132	GAAGAGCTCCGCGGCCA-----	32150	Qy	17623	ATCACCGGCAACACCCCAACCGCAACTCTCAACCCCACTACTGACCCCAACGAC	17682
Qy	16552	CGACCGCGCGACGATGTTCCGGGGGAAGCGCGCGAGACGCGCGGTACCGCGGGAA	16611	Db	33137	GTCAACCGGACACGAGCTCGAGGTTCGAGCTCGAGCGCGGTACTGGTATCGAAACCTC	33196
Db	32151	-----CGCGGGCGGAGTCAGGCGCTTCA CAGCGTGCATCGACGCGCTCCCGCGCGGTG	32205	Qy	17683	CGCAACACCGTTCGACTAGCCACCAACCAACCTTCAACCAACAGGGGTCAACAC	17742
Qy	16612	GGCACTGGTCTGCTCGCGGAGTCAGGGGTGTGGCGTGTGCTGCGCCAGTCG	16671	Db	33197	CGGAAACCGCTGTCTTCGAGCGGACCGAGCGGCTCTCGAGATGGGCAATCGCTTC	33256
Db	32206	GCCCTCGTCC-----TGTCGCGCAGGAGC	32230	Qy	17743	TACATCGAACTCGGACCGGCAACACCTCTAC-----CACCTTCAACCAACCAACCTCC	17799
Qy	16672	CAGCGCGCTCGCGCGCGCAGGCCCGAGCCCTCGACGCCACCTCACGACCAACCCCGC	16731	Db	33257	TTCTGTCGAGGTACGCTCTCATCCGTCGCTCAGCTGCGCTTCCGCGAGACCTGCGAGCG	33316
Db	32231	GAGCGCGCTCGCGCGCGCAGGCTTAAGGCTTCGCGAGCACTGCTGCGCCCAAGCGAC	32290	Qy	17800	AACACCCCAACCAACCTCTCACCCCTCACCCACCCCAACCAACCCCAACCCACCTC	17859
Qy	16732	CTCGACCTCGCGCGCTCGGGTACACCTCGCCCAACCGCGCGCGTGTTCGACCAACCG	16791	Db	33317	TCACCGCTCGATCCGTCGCTCGCTCATTCGAGCGAGGAGGCACTCCCGCT	33376
Db	32291	CTCACCTCGCGGATGTGCGCTATTGCTGGCCACCAACCGCGCCCACTTCGAGCAACCG	32350	Qy	17860	CTCACCAACCTGGCCAAACCAACCAACCTGCGACCCCGCACCACTACCCACCAAC	17919
Qy	16792	GCCACCTCATCGCGCGCGACCGGACACCTTCCTGCAAGCACTCGAGGACTCGCCGCA	16851	Db	33377	CTCTTGTCTCTTGGGCGGAGCTTATGCGCGGCTCTACGCGCGAGTGGAAAGCCTTC	33436
Db	32351	GCCGCTCTGTAGCCCAACGACCGGACGAGCTCTCTCGCGCTGACTCGCTCGCCGAG	32410	Qy	17920	AACCAACCCCAACCAACCTCGACCTCGACCTCGCCACCTTCCCAACCAACCAAC	17979
Qy	16852	GGCGAACCCACCCCGCTCATCCACGACGCGCCCGAGGCGGACCGGACCGGGAG	16911	Db	33437	TTCTGGGCTTCTGCTCCGCAAGTCTCATCTCCCACTAGCTTCCAGGCGAGGCT	33496
Db	32411	GACAAGCCGACCGAGACCTCTCTCGACGAGCGAAG-----	32451	Qy	17980	TACTGGTTCGAAAGCACACAGCCGCGGTCCGGATCCGGTTCGCGGTTCGCGGCGG	18039
Qy	16912	GCCTGAGAAAGACCGCATTCATCTCTCGGACGAGGACCCCAACGCCCGGCTATGCC	16971	Db	33497	TTCTGGTTCGACGCGCCCAACGCAACCCCGAA-----GGCGTCTCGCTCGG	33547
Db	32452	---CCACGCAAGGTCTCTGCTCTTCTGCGCAAGCTCGACTGGGAGGATGCC	32509	Qy	18040	GCAGGACTGCGGGGGAACGCGAGAGTGGAGTGGGTTCTGGGACCGCGTGGCCCGC	18099
Qy	16972	CAGGCTCTACCAACCAACCGCTCTTGGCGCGGCACTCAACGACATCTGCAACCAAC	17031	Db	33548	CCGATCGATGGGCGGTTTGGCAAGCCATCAACGCGGCGGACCTCGACGCGCTCAG	33607
Db	32510	CTCTCTCTGCTGACTCTCTCGCCCTCTTCGACACACAGCTCGAAGCATCGAGCGCG	32569	Qy	18100	CAGGACTGGAAACGCGTGGGACCACTCGCGGTGCGCCCTCGCGCGGCTTGACACG	18159
Qy	17032	CTGACCCCGACCTCGACACCCCTCTCTCGCCCTCTCACCCAGACCCCAACACCCAG	17091	Db	33608	CAGCTCC-----ACGCGACCGGCAACGAGAGCGCGCGCTCTCGCCCTG	33652
Db	32570	CTCGTCTCAGCTGAGTGAGCTGCTGCGCGTCTGCGCGCGAGAGGCGCGCC	32629	Qy	18160	GTGTGCGCGCATCTCTCGCTGCGACCGCACCAACCAACGACCAAGCCCGCATCAAC	18219
Qy	17092	GACACCAACCTCTGAAAGAGCGCGCATGCTCCAGCAGACCCCGTAGCGCCAGCGCC	17151	Db	33653	CTCTCTCCACCTCTCGAGCTTTCACACACGCGCCAAAGAGAGACAGCTGACAC	33712
Db	32630	TCCCTCGACCGGCTCGAGTCTG-----CAGCCCGCTCTTT	32668	Qy	18220	TGGACCTACAGGAAACCTTGAAACCCCTTACCTCTCCCGACCAACCCAC	18276
Qy	17152	GCCCTCTTCGCTTCAGGTGCGCTCTCACGCGCTCTCTCAACGAGGCTACCAATCAC	17211	Db	33713	TGGCGCTACCGCATCATCGTGGAGGCTCTTGACCAACCGCGCGCGCGCTCGCC	33772
Db	32669	GCGGTATGGTCTCCCTGGCGCGCTCTGGGCTCGCTCGG-----TCGAG	32716	Qy	18277	CAAACTGGCTCATCGGCATCCCGAAACCCAGACCCACACCCCAACATCACCAACATC	18336
Qy	17212	CCCCACTACTACGCGGACACTCTCTCGCGGAAATCACCGCGCCACCTCGCGGCTATC	17271	Db	33773	GGCACTTGGTCTCTGTCGCTCGCTCGGCTCGGCGAGAGCGGCTCTCTGCGACGCTC	33832
Db	32717	CCCCGCGGCTGTCGGCAACGACGAGGCGAGATAGCGCGCTTCTGTCGAGGCGCT	32776	Qy	18337	CTCACCACTCTCACCAACCGGATCACCCCATCTCCCTTACCTTCAACCAACCAAC	18396
Qy	17272	CTCACCTCTACGAGCGCACCACTCTATACCCAAACCGGACCCCTCATGCAACCAATG	17331	Db	33833	ACCGATGCGCTTACCGCGCGCGGCTGCTCTCTCGCTGCGCTTGGCTGAGCCAGCTTCA	33892
Db	32777	CTCTCTCTCGAGGACGCGCGCGCATCGCGCTCTGCGAGCAAGCGTCAACCGCTCG	32836	Qy	18397	ACCAACCCCAACCTTCCACCAACCGGACCAACGCGCCCAACCAACCAACCGGACCC	18456
Qy	17332	CCCCCGGCAATGACACCTCTCAACACACCCCGGACGATCACCCACCTTAC	17391	Db	33893	ATAGGCGCGCGGCTCTCACCGAGCACCTGCGGAGGCTGTTGCGGAGCTGCC---CCG	33949
Db	32837	CCGGCAACCGGCGCGCTCGAGCTCGCGGCTCTCGACCTCCGACCTCAACCTTACCTG	32896	Qy	18457	ATCACCGGCTGCTCTCTCTCTCGCTGAGCAACACCCCAACCCCAACCCCAAC	18516
Qy	17392	GCCACGAAACGACCTCGCATCGCGCATCAACACCCCGACCTCTCTCTGTCATCAGC	17451	Db	33950	ATTGCGGCGGCTCTCTCTCTCTCTGAGGCGCCCTCTGCGGACCATGCGGCC	34009
Db	32897	CCCTGGGCGGACAGGCTCTCATTCGCGCGCTTCAACGCCCCAGGCGCACGCTGATCC	32956	Qy	18517	ACACCCACCGGCACTCTCTTCAACCTTCACTCCCAACCCCAACCCCAACCCCA	18576
Qy	17452	GGCAACCCCGCACCGTCAACATCAACCTCTCTGCAACCAACCAAGGATCAAAAC	17511	Db	34010	CTGCGCGGCGCTTGGCTCTCTCTCTCTCTGCTCTCAAGCCCTCTGCGGACCTCGCC	34069
Db	32957	GGCGAGCCCGCGCGCTCGACGCGTGTGACCTGCTGCTCACCGGAGCGAGTCTTCGCG	33016	Qy	18577	CCAAACCCCTCTGTTAGGCAACCAACCAACCCCAACCCCAACCCCAACCCCA	18636
Qy	17512	AAACCCCTCCCGACCAAAAAGCTTCTTCACTTCCCGGACCAACCCCAACCCCA	17571	Db	34070	GAGCTCTCTGTTGCTCTTCAACGCGGCGCGCTCTCTGATTTGGACATCTCCGACCACTC	34129
Db	33017	CGAAGAGTCCGCGTTCAGTACGCTTCCCACTCAGCCCAAGATGGAGCGCGCTCAAGACG	33076				



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29604 CACCCGCGACGGCGTGCCTCGCGGTGCTGCTGCGACGCGCGAGGCGCGGACCGCGAGGG 29663
29349 TCGCGCGGAGTTGCGGGCGGAGCTCGGTGGGTTCGGCGCGACGGTGGAGTGTGTCGCTG 29408
29664 CCGCCAGGACCTGATCACCGAGTTCACCGGAGGCGCGGAGCTGCTGCTGCGCTG 29723
29409 CGACGCGGCGGACCGCGACGAGCTGCGCGACCTGCTGACACAGATCCCGACGATCGGCC 29468
29724 TGACGTCCTCCGATCGCGACGAGTGGCGCGCTGCTCGCGGCTCCCGGAC----- 29775
29469 GGTGACCGGTGCTGTCACAGTTCGGGCACTCTGAGACGCGGTGATACAGTTCGCTGTC 29528
29776 -CTGACCGGGTGGTGCACACCGCGCGGTCTTCGAGGACGCGGTGATCGAGCGCGTGC 29834
29529 GCGGAGCGGCTCGGGCGGTCTCTCGGGCCAAAGCGGAGCTGCGCTCTTCTCGACGA 29588
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29955 GGGTGTGCGGTCAAGGCCCTGACGCGCGCGGAAACGCTTCTCTGAGACGCGCGATGCG 30014
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29769 CACAGGATGACGGGCGACCTCGAGTTCGACACCATGCGCGGATCAGCGCGCGGAAT 29828
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29829 GCGCGCGTGCAGATGCGCGAGGCTCTGCGGTGTTGACGCGCGCTTGGCGCGAGCGGA 29888
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30195 GTGCTGCTGTCGCGCATCAAGCTCGACTCGCGCGGTGTTGACCTCGCGGTGCGGCGAG----- 30242
29949 ACCGTTGCGCGCTGCTGCAAGTCTGCTTCAGCTGCTCGCTCCGCTCGCGCGCGCG 30008
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30009 GCGCGCGCGCATGGGCGCGCGCGCGGACGAGCGCGGCGCTGCGGTGAGCGTCTGCG 30068
30303 GTTCACTGTGACCGGGGCGCTGCG-----CGGCGCGCTCGC 30338
30069 CCGGCAGAGTGCCTGTGAGCGAGCGAGCGCTGCTGCGCTGCTGCGGTGCGATGTCG 30128
30339 CGGGTTCGCGTGGCGGCGGCGGCGGTGCTGCTGACCTGCTGCGCGGCGAGTCTGCG 30398
30129 GCGGTGCTCGGCGCATAGCGGTGCGGACGGAATCGACGATCGCGGGGCTTCCGCGAGCT 30188
30399 GTGCTGCTGCTGCTAGCAGCGCGCGGAGCGCTGCGCGCGGACACGCGGTTCAGGAC 30458
30189 GGGGTTGCACTGCTACGCGCGGTGAGTGGCGCAACCGCTTCACGCGCGCGGAGCGGCT 30248
30459 CGGGTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 30518
30249 GCGGCTGCGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 30308
30519 CAACTTCCCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 30578
30309 GCGGAGGCTGCTGCTTCCGACGAGGCGCACGCGCGCGGAGCGGCGGATGCGCTCTC 30368
30579 GGGCGCGCGGTGCTGCTGCGGACGCGGACCGCGGACCGGACCGGACCGGATGCGCAC 30638
30369 CCGCGCGC 30375
|||

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Db 30639 CGAAGAC 30645

RESULT 11

AAV05287

ID AAV05287 standard; DNA; 49377 BP.

XX

AC AAV05287;

XX

DT 21-MAY-1998 (first entry)

XX

DE The soraphen biosynthesis gene cluster from *Sorangium cellulosum*.

XX

KW Polyketide synthase; PKS; biosynthesis; soraphen; SorA; SorB; SorC; SorM; biosynthetic module; beta-ketoacyl synthase; acyltransferase; ketoreductase; beta-ketone processing domain; cytosolic agent; an antimicrobial agent; phytopathogenic fungi; transgenic plant; biological control; ss.

KW

XX

OS *Sorangium cellulosum*.

XX

XX

EH Location/Qualifiers

FT CDS

FT 383..760

FT /\*tag= a

FT /product= SorR

FT /note= "gene product highly homologous to the reductase domains of type I PKSs such as eryA from *Saccharopolyspora erythraea*"

FT CDS

FT 927..19874

FT /\*tag= b

FT /product= SorA

FT /note= "gene product is highly homologous to type I PKSs that are known to be involved in the synthesis of polyketide compounds"

FT misc\_feature

FT 942..7115

FT /\*tag= c

FT /note= "module 1 of SorA"

FT misc\_feature

FT 7203..12884

FT /\*tag= d

FT /note= "module 2 of SorA"

FT misc\_feature

FT 13455..19616

FT /\*tag= e

FT /note= "module 3 of SorA"

FT misc\_feature

FT 19871..46318

FT /\*tag= f

FT CDS

FT 19871..46318

FT /\*tag= g

FT /product= SorB

FT /note= "gene product is highly homologous to type I PKS genes"

FT misc\_feature

FT 19870..24556

FT /\*tag= h

FT /note= "module 1 of SorB"

FT misc\_feature

FT 24638..30820

FT /\*tag= i

FT /note= "module 2 of SorB"

FT misc\_feature

FT 30881..35446

FT /\*tag= j

FT /note= "module 3 of SorB"

FT misc\_feature

FT 35528..40114

FT /\*tag= k

FT /note= "module 4 of SorB"

FT misc\_feature

FT 40190..46318

FT /\*tag= l

FT /note= "module 5 of SorB"

FT CDS

FT 46851..47891

FT /\*tag= m

FT /product= SorM

FT /note= "gene product is homologous to the methyltransferase from *Streptomyces hygroscopicus* that is involved in the synthesis of the polyketide rapamycin"

FT

XX

Qy	27129	CGCTACTGTTACCGCAACCTCCACAGCCCGCTTCCGCTTACGCCACCGCCATCCAGACCCCT	27188
Db	27828	CGGCTACTGTTACCGCAACCTTGGCAACACAGGTGCGGTTCGGTCCGCGCGTCCGAGGCT	27887
Qy	27189	GACCGACGAGGACACCGCGCTTATCGAATACAGCCCGCCACCCACCCCTCGTCCCGCG	27248
Db	27888	CGTTCCGACGAGGACACCGCGGTGTTGTCGAGGTGAGCGCGACCCGGTGCTGTCAGCC	27947
Qy	27249	CATCGAAGACACCAACCGAAACACACCGAAACATCACCGCACCGGACGCTCCGCGCG	27308
Db	27948	GCTCAGTGAATCAGCGACGAGCG- - - - -GGTGGTGACCGGGTCTGCGGCG	27995
Qy	27309	CGGCGACAAACGACACCGCTTCTCACCGGCTTCCACCGGCTCGCCACACCCACACACCGGAT	27368
Db	27996	CGAAGACGGTGGCTGCGCGCGCTGCTGAGCTGATGCGCGAGCTGTACGTGACGGGTGT	28055
Qy	27369	CGGCGACACCAACCTTGGCACCACTACACCAACACCCACCCACCCCAACCCCA	27428
Db	28056	CCCGCTCGACTGACCGCGGTCTTCCGCGCGGAC- - - - -	28088
Qy	27429	CACCCACTCGACCTGCGCCACTACCCCTTCCAAACACGACACTACTGGCTCCAAACAC	27488
Db	28089	CGGCGGGTCGACCTGCGGAAGTAGGCTTCCACCAACCGGCACTACTGGCTGCGGCGCG	28148
Qy	27489	CACCAACAAACGACCTCAACCAACCGGCTTACCCCAACCCACCAACCCCTCTCTCAC	27548
Db	28149	CGAGTCCGACACGACCGGCTTCCGTGGCGCAGGCGCGCGGACCAACCGCTGCTGGG	28208
Qy	27549	CGCACACTCACCTTCCGCGACACACACACACTACTCACGGCGGCTCTCCCTACG	27608
Db	28209	CGCGGTCTGAGCTGCGGAGTCCGACGCTCCGACGCGCTGGTGTTCACCTCGCGGCTGTCGTGG	28268
Qy	27609	CACCCACCTCTGGCTCACCGACACACCGCTCGCGGATGGTCTCTCTCGCGGCGCACCGC	27668
Db	28269	GAGCACCTGCTGGCTGCGGACACGCGGTGCGTGGGCTGGTATCTCTCCCGCTCCCG	28328
Qy	27669	GCTCTCGAATCGCTTCCAAACCGCGCAACCGGTGAGTGCCTCTGGGTGAGGAAC	27728
Db	28329	GCTGGCGAATCGCGCTTCCGCGCGCGGACGAGCGGGTGACCGCGGTGACCGCTCCAGAGCT	28388
Qy	27729	GACCTGCAACGACCGTGGTGATCCCGGACACCGAGGACGTGACGTTGAGGTACCGT	27788
Db	28389	GATCATCGAAGCTCCGCTGGTGGTCCGCGCGGCGGCGGCTCCAGGTGCGCTT	28448
Qy	27789	TCGGGACGCGATGAGAGTGCCATCGCGCTTCCGATCCACTCGTACTCCGCGCACCGC	27848
Db	28449	GAGCGGCGGACGAGACCGGCTCGCGACGAGTGAGCTTACTTCCAGCGCGACCGCGG	28508
Qy	27849	GTGCTCGGCGGACCGGAGTGAGCCCGTCAACCGCAACCGGCTCTCTCACACACACCGCA	27908
Db	28509	CGCG- - - - -GGGACGTGGACGCGGACGCGGCGGCTGCTGTCGACGCGCCCGCG	28559
Qy	27909	CACCGATCAGCGTCCGACACGACACGAGCGGTGCTTGGCGGAGCTGGCGCCCGCG	27968
Db	28560	TCAGGAACCGGAGTTCGACTTCCACG- - - - -CTGGCGCGCGCG	28598
Qy	27969	CGGCGCGAGCCCATCGAATGGGCGAGCTTACGCTCGTATGGCGCGGACTCGGACAT	28028
Db	28599	GGATCCGAGCGGATCGAGCTGAGACCTTCTACCGGACCTGGCGAGGCTGGTTA- - -	28655
Qy	28029	CGCTACGGGCGGTCTTCCAGGGGCTGACCGCGCTTGAGGTTCGGCGACGATGCTCT	28088
Db	28656	CGGCTACGGGCGCGGTTCAGGGGCTGCAAGCGGTGTCGCGGCTGACCGCGACGCTCT	28715
Qy	28089	GGCGGAGGTGCTGCGGAGAGGCTCTGCGGATGCTCCGCGCGCGGCGCTTCGGTGT	28148
Db	28716	CGCGAGGTGCGCTGCGCGGAGGACCTTCCGCAAGGAC- - - - -GCGGGCGGTTCGGCGT	28769
Qy	28149	TCACCGCGCTTCTGACGCGCGCTTCCAGCGGCTCACCGGCTCACCCCGACGAGCGGGA	28208
Db	28770	CCACCGCGCTGCTCGACGCGGCTGTCAGGCGCGCACCGCGCTGGGCGGCGACGAGCC	28829

Db	25674	CGACAGCCTGTACGACCCCGAATCCGGCCCGCGGCAAGACTACACCCGCGACGGCGG	25733
Qy	24972	ATTCTCTACGGCGCAGGCACATTGACGCGGAATTTCTTCGGCATCAGCCCGCGGAAGC	25031
Db	25734	CTTCTGCGAAGACCGGGCTTTGACCGGGCTTTCTTCGGGATCTCGCCACGCGAGGC	25793
Qy	25032	CCTCGCATAGACCCCGACCAACGACTCTCTCTCGAAACCGCTGGGAAACCATGAAACA	25091
Db	25794	CGTCGCATAGACCCCGACGAGCGGTCTGCTGGAGGCTCTCTGGAGGCCATGGAAGA	25853
Qy	25092	CGCGGCATCAACCCCGACACCCCTCCACGCGACCCCGACCGAGTCTTCGCGGGAATCAA	25151
Db	25854	CGCCGGGTCGACCCCACTTTCTGTAAGGGCAACGACGTCGGCGGTGTTTCAACCGCATGTT	25913
Qy	25152	CGCTCAAGACCGCGCGCATATCCGCCAAGACCGTGTGAGAGACCATCAGAGGGTA	25211
Db	25914	CGGCCAGGTACGTGCG-----TCCCGGGACAGCGTCTGACGCCGAGCTGGAGGGTTT	25970
Qy	25212	CGCCCTGACCGGCAGTTTCGGGAAGTGTGGCGTCCGGCCGGGTGGCTACACGCTCGGGCT	25271
Db	25971	CGGGGACACGGGGGTCTCGAGTGTCTGGTCCGGCCGCGTGTCTGAGTGTTCGGGTT	26030
Qy	25272	CGAAGCCCGCGGTGTGCGTGTGATACGCGGTGTCTGTCGTCTGTTGGTGGCGTTCGATFG	25331
Db	26031	CGAAGCCCGCGGTGACGATCGACTCGCGGTGCTGCTCTGCTGCTGCGATGCACCT	26090
Qy	25332	GGCGGCGAGGCTTTCGTCGGGTGAGTTCGATGGCGCTTTCGGGGGTGACGCT	25391
Db	26091	CGCCGCGAGTCTGCTCGGCGAGGCGAGTGTCTGATGGCTTTGGCGGCGGCGACGCT	26150
Qy	25392	GATGTCGTCTCCGGGTACGTTTGTGAGTTCTCACTCAGCGGGTCTGGCCCGCGACGG	25451
Db	26151	GATGGCAACCCCGGCGCATTCGTGGAGTTCTCGCGGACGCGGGCTCGCCGTGACCGG	26210
Qy	25452	GGGTGCAAGGCGTATTTCGGCGGTCTGACGCGTACCGGTGGCGGAGGGTGTGGGAT	25511
Db	26211	TGCGTCAAGGGGTTTCGCGCGCGCGCGACGCGCACCGGTGGCGGAGGGCGTGGTGT	26270
Qy	25512	GCTGCTGGTGAAGCGCTCTCGACGCGCGTGCACACGCTCACCGTCTCTGGCGGTGT	25571
Db	26271	GGTCACTCTCGAGCGGCTGTGCGTGGCGCGGAAACCGCGCCACCGGATCTCTGGCGGTGT	26330
Qy	25572	GGGTGCGAGTGGGTCAACACGAGCGGTGCGAGCAACGCTGTGACCGCGCCCAACCGGCC	25631
Db	26331	GGCGGCGAGCGGTCAACACGAGCGCGCTCTGACACGCGCTGACCGCGCGAAGCGGGC	26390
Qy	25632	CTCCAGCAGCGTGTATCCGTCAGGCCCTTGCCCAATCGGACTGACCCCGGCCGATGT	25691
Db	26391	GTCCGAGCAGCGGTGTATCCGCGGGCGCTGGTGAAGCGCGGGCTGGCACCGTCCGATGT	26450
Qy	25692	CGACGAGTGAAGGCGCACGCGACCGGACCACTCTGGGGGACCGGATCGAGGCCAGGC	25751
Db	26451	GGACGCTGTCGAGGGCGCACGCGACCGGACCACTGCTGGGTGACCCGATCGAGGCGCAAGC	26510
Qy	25752	ACTCTGGCGGCTACGAGCAACACCGCCCGCCACACCGCCCTTGTGGTGGGATCCCT	25811
Db	26511	TCGTGTGGTACTACGCGCAAGGACCG-----CGAGTGGCGGCTGTGGCTCGGTCTCGT	26564
Qy	25812	CAAATCCAAATCTGGGCGACGACAGCGCGCGCGCGGTGGGCGGAGTGCATCAAGATGTT	25871
Db	26565	GAAATCGAATCTCGGCGACGCGCAGCGCGCGCGGGGTGCGCGCGGTCTCATCAAGATGTT	26624
Qy	25872	GATGGCTTCGCAACGGGCTGCTGCGCACAGACCCCTCCACGTGAGAGCGACCCACCCCGA	25931
Db	26625	CCAGCGCTTCGGGCGAAGTCTCTCGCGCGGACCGCTGACGTCGACCGGCTTACCCCGA	26684
Qy	25932	GCTGACTGCTCACAGGGCGAGTACAACTCTCTGACACAAACCGGTGCTTGGCCCGCGGA	25991
Db	26685	GCTGACTGCTCGCGCGGTGCTGAACTGCTGAGAGAGCCCGGAGTGGCGCGCGAA	26744
Qy	25992	CCCGGCCCGCGCACGCGACCGCGGTGTTCATCTTCGCGGTGTCAGCGGCACCAACGC	26051
Db			
Db	26745	-----CGGGCGCCCGCGCGCGCGGGTCTTCGCGTTCGGCGTTCAGCGGCACGAACGC	26798
Qy	26052	CCACATCATCTCGAAGAAGCACACCATCTCCCGAGGACGATATCCGACGACGAACCGCC	26111
Db	26799	GCACCTGATCTGAGGAGGCGCCGC-----	26825
Qy	26112	TGCCAACGACCAAGCCTTGCCCATCTCCCTCTTCCTTCCTGCGGTGTTCGGCGAGTCT	26171
Db	26826	-----CGAAGAGCGGTGCCACACCGAGGTTCCCTGCTGCGGTGCTGCTTCGCG	26879
Qy	26172	TGAGCCCGGTTCGGGGCGAGGACAGCGGTTCGCCAGTACGTGGGACGCCCGCCGGA	26231
Db	26880	CGGAGCAGGGCGTCTTCGGCGGTTCAGCGCGGTGCGCTTCGCCGATTCGTGGCGGGTGA	26939
Qy	26232	CATGTCACCTCCGACATTTGTTGCGGGTCTGGCGCGCGCGGCGGTACTGGAACACCG	26291
Db	26940	CGGTCTTCGGCGGTGTGGCCCGGGCGCTGTGACGAACCGGGCCGCTGACCGAGCG	26999
Qy	26292	CGCGTCACTCTGGCGCGGACCGCGAGAACTTGCGCAGGCACTGACAGCCCTGGCAGC	26351
Db	27000	CGCGTCACTGCTGTTGGCTCTCGGAAGAAGCGGTGACGAACCTGGAAGCGCTGCGCG	27059
Qy	26352	CGGGAACCCCAACCCCACTACACAGGCGCACACCGGGGGCGGTGACCGCGGGCGGT	26411
Db	27060	CGGGAAGACCGCGCGGTGTACCGG-----CGGGCGGGTTCGCGGGCAAGCT	27113
Qy	26412	CGTCTGCTCTCCCGACAGGGCGCGAGTGGCGGCGGATGGCGCTGACCTGCTCAC	26471
Db	27114	CGTCTGGGTCTTCGCGCGCAGGGTCTGCACTGATCGGATGGCGCGGAACTCTCTGA	27173
Qy	26472	CTCTCACTCGTGTTCGCGCAACATCGACGCACTGCGAGAAAGCCCTTCACCCCTGGGT	26531
Db	27174	CTCTCGCGGTCTTCGCGAGCGGTTCGCGAATGGCGCGCGCCCTTGGAAACCTGAT	27233
Qy	26532	GCCCTGCTCTGACGACATCTTGCAACCGCGACCCCGACGCCCGCATGGCAACAAGC	26591
Db	27234	CGATTGGTCACTGCTCGACGTGCTCGCGGGGAGTCCGACCTGC-----TGGACCGGT	27287
Qy	26592	CGAGTGTTCAGCGCGGTCTTCAGCATCATGCTCTCCCTCGCGCGCTGTTGGCGCTC	26651
Db	27288	CGAGTGTGAGCGCGCGCGCTTCGCGATGATGCTCGGCTTGGCGCGGTGTGGCAGTC	27347
Qy	26652	CTACGGCATCGAAACCGACCGCGTCTTCGCGCACTCCAGGAGAGAAATCGCGCCGCA	26711
Db	27348	GGTGGTCTCGCGCGGATGCGTCTCGGCACTTCGCGAGGCGGAGATCGCGCGCGCTG	27407
Qy	26712	CATCTGGCGCGCATCTGACCTGAAAGACGCGCGCAAAACCTTGCACTGCGGAGCGCGC	26771
Db	27408	CGTCTCGGGCGGTGCTGCTGCGAGGACCGCGCGAAGGTGTTGCTTTCGCGAGCCAGGC	27467
Qy	26772	ACTGGCGCGTACGAGCGCGGGGCGCATGGCTCTACTGCCCCCTGCCCCCAGGAGCT	26831
Db	27468	GATCGCAACCGGTGCGCGCGCGCGCGCGCATGGCTTCGTTGCGGTTGAGCGAAGAAG	27527
Qy	26832	CGAGCAGCTCATTTCCGAAACGCTGGGAAGGCGAGTGTGGGTGGCGAGCCCTCAACCGGCC	26891
Db	27528	CGGACCGGTGGTGGCGCGGTGGCGGACCGGGTCCAGGTGGCGGGTCAACAGGCC	27587
Qy	26892	CACTCCACCACTCTTCGCGGACACAAAGCGGTGATGAGTGTGGCGCATGTCAC	26951
Db	27588	TGCTCTCGTGTGATCGCGGGGAAGCCAGGCGCTCGACGAGGTGCTGCGACGGGTTGTC	27647
Qy	26952	CGACCGGCTACGGGCGAAACGATCCCGTTCGACTACGCTCCCTCCCTGCCCCCAGCT	27011
Db	27648	CGGTGAGGAAGTTCGCGGTGGCGGGTGGCGGTGAGCTTACGGGTCCTCCACCAACAGGT	27707
Qy	27012	CCAAACCTCTCAACGACGAACTCTGCACTCTCTGGGAGACATCACTCCCGCCAGCGCTCAC	27071
Db	27708	CGAAGCATCGAGATCTGTGGCGGAGACCTTGGCGGCGATCGAGGCGGAGGCCGAA	27767
Qy	27072	CGTCCGCTTCTTCTCCACCGGTGGAAGGACCTGG---CTGGACACCAACCTTGGAGCG	27128
Db	27768	GGTCCCTTCTACTCGACCTGATCGGTGACTGGATCGGTGACGCGCGGGATCGTCAGCG	27827



QY	22804	-----GAGGAAGACCTTCAGAGCCCTCGCCGAAACCCCT	22835
Db	23595	CACGGTCGAGGTGTATTTCGAGCTCGAAGCGCCGGAAGACTGGATCGGAACGCCACCGG	23654
QY	22836	CGACATCGAGCCCTCTGTCTTCGACACAGTGTGTGCCGACATCTTCGGCTTCGGACACCGCCA	22895
Db	23655	GCACCTGTTCGGACACGGCTTCGGCGCACGAGGCCCTTCGACTTTCACCGCTTCGGCGCCGGC	23714
QY	22896	CCAAACGACCAAGCCCGCATCAACACCTGTGACCTTACGAGGAACCTTGAAACCCCTCAC	22955
Db	23715	CGGAGCCACGACGTCGACGGCTCTGGCGCGCGCGGACGAGATCTTCGCGGAGGTGCG	23774
QY	22956	CTTCCCCACACCCACCAACCCCAACAACTGTGTCATCGGCATTCGCCGAACCCAGAC	23015
Db	23775	CTTCGCGGAGGAGCTGGACGCGCGCGGCTTCGGCATTCACCCCTCTCTCTGTGGAGCGGGC	23834
QY	23016	CCACCAACCCCAACATCAACCAATC-----CTCAACCAACCTCCACACACGAGGATCAC	23069
Db	23835	CGTGACGCGGTCCTTCGCGGACGACGAGCAGCGCGGAGTGTGGCGACCTGTGCTCTGCA	23894
QY	23070	CCCATCCCCCTCACCTGTCAACACACACCCACCAACCCCAACACCTCCACACACACCT	23129
Db	23895	CGCGCGGGTGCTTCGGCGCTGGCGTGGCGGTGTGCCGGGTGCCCTCCCAAGCGGC	23954
QY	23130	CCACCAACCCGACAAAGCCCAAAACACACCAACCGGACCCATCACCGGCCTGCTCTC	23189
Db	23955	GGACGAACACCGCGGCTGTCTCTACGGCGGATTTCGTGGCAGCGCGGAACTCTCGGC	24014
QY	23190	CTCTCTCGGCTTCGACGAACACCCACCCCAACCCCAACCCCAACACCCACCGGACCT	23249
Db	24015	CGGGAAGACCGCGCGGATCGCTGTACCGGGTCGACTGGACCGAAGTGTCCATTGACA	24074
QY	23250	CTCTAACCTCACCTCCCCCAAAACACACCAACCAACCCCAACCCCAACCCCTCTGTGA	23309
Db	24075	CAGTGGGTGCTGGGCCAAATCGAGGTGCTGAGGCTTTCGGTGAAGAGCCCT---GGA	24131
QY	23310	CGCCACCAACCGCACCAACCCACCCCAACGACCCCTTCACACACCCCAACCCCAAGC	23369
Db	24132	ACTGACCGCGGGTCTTCGAGGCTGTGCAGACCTGGCTCGTCAACCGCGCGCAGCATGC	24191
QY	23370	CGAACTGGGACTCGCCCGCACACCTCTCTCGAAACCCCAACCCCAACACCGCG---	23425
Db	24192	CGCGCTGTGTGTGTGACCCCGGGCGCGTGTGGCGAGGTGACCGACCCCGCGGTGGCGC	24251
QY	23426	----GAATCATCGACTCCCCACACCCCCACCCCGCACCCCTTCACACCTCACCCCA	23480
Db	24252	CGTGTGGGCTGTTCGAGCGCGGACGGGAGAAACCCCGGTTCGATCTTCCTGATCGA	24311
QY	23481	AACCTTCACCAACCCCAACCAACCCCAACCTTCGCATTCGCACACACCGCACCCACAC	23540
Db	24312	CACCGAGGGAGATCCCGGCCCTTGACCGGTTCAGAGCCGAGATCGGTGGCGGGCG	24371
QY	23541	CGCGCGCTCACCCCAACACCTTCACCCCAACACCAACCAACCCCAACCCCAACCCCA	23600
Db	24372	GAAATTTCTGTGTCCCGCATCACTCGCGGAGCGGAGCGGAGCGGCGGTTCGCGCC	24431
QY	23601	CGGAACCACTCATCACCGGGGAACCGGGCCCTTCGCCACCCACTCACCCACCACT	23660
Db	24432	GGACGGGACGTGCTGATCTCGGGCGCGGTTCGCTCGGTGCGCTTGGTGGCGCGCGTCT	24491
QY	23661	CACACCCCAACCAACCAACCTCTCTCTCAACAGCCGAAACCGGCCCCCAACACCC	23720
Db	24492	CGTCGAACGCCACGGGTGGGAACTCTGTCTGGGTCCCGCGCGGCGCGAGACCGCA	24551
QY	23721	CCACGACAAACCTCACCAACCCAACTCCCAAAAGGCAATCCACTCAACATCACAC	23780
Db	24552	CGCGTGGGGACCTTGTTCGCGGACCT-----GGCGCGGACGTGTCCGTGTGGC	24602
QY	23781	CTCGGACACCAACCCAGACCACTCCAACTCTCTCAACCACTCCCAACCACTCCCAACCA	23840
Db	24603	TTCCGACGTCTCCGATCGCGCCACGAGTGGCGGCCCTCTGCTCGAC-----GAGCA	24650

Qy	23841	CCCCTCACCA	CGGTATCCAC	CAGCAGCGAGG	GTCAATCTT	CTCGCCCCCGT	TCGGAAC	23900		
Db	24651	CGGGCCGAC	CGCGGT	CGTGACAC	CGCGGGGT	CATCGAC	CGGGGTGAT	TCGAGACGCT	24710	
Qy	23901	CGATGCCGA	ATCCTTCT	CTTCGGTTA	CGGCAGCGA	AGGCAAC	AGGCGCGGCGAT	CTTCGCA	23960	
Db	24711	GGACGGGAC	CGCGCTTG	GGCCACGGT	TTTGGCGCGA	AGGTTCAG	CCGTGCGCTTAC	CTCTCGGTCGGC	24770	
Qy	23961	TGAGTTGCT	GTCTGGAC	CACTGAAAC	CTTTGAAC	CACTTCA	TTCTTCTCTGT	CGGGCGCGG	24020	
Db	24771	CGAGCTGAC	CCCGCGAC	CGCGA---	---CCTCGAC	CGCTTCTG	CTCGTCTAC	CTCTCGGTCGGC	24827	
Qy	24021	CGTTTGGG	CACGGGAAT	TCAGTGGCA	TATCTGGCGG	CCAAAGC	ATACCTTGGAC	CGCGCT	24080	
Db	24828	CGTGTTCAT	GGCGGGG	CAGCGGCAG	TTCGCGCG	CAGCAAC	CGCTTCTCTG	AGCGGCT	24887	
Qy	24081	CGCGACG	ATCGTCAG	ACATGGA	CTTCCTCCG	GGGCATCG	ATCGCTTGGG	GGCCCTCGG-	24139	
Db	24888	GATGGGAA	ACCGCGGG	CGGGGCTT	CGCGGCTT	CTGCTGG	CGTGGG	CGCTTGTGGGA	24947	
Qy	24140	-----	CCGGA	AAAGGG	CA	TGCGCGG	GTGATGCGG	CTCATGTTTAC	CTTGGAAAAAGCG	24191
Db	24948	CCAGACAC	CGGTATGG	CGCGCGG	CAACGAC	AGGCCAC	CCCGGGCG	CGGATGAGC	CGCGCG	25007
Qy	24192	CGGCATTT	CGCGATGG	AGCCAC	GATGGCGT	TCGGGCA	TTCATCTG	TCGCGGGCGCA	24251	
Db	25008	CGGTGCTT	GCAGATCAT	GACGAG	CGCGGAGG	CACTGTTT	TCGACG	CGCGGCTGTC	25067	
Qy	24252	GGGGCGA	ATTTCCAA	CTGATCAT	CGCGGACAT	CGACTTGG	AGCGCTTCG	TCTCCGCGCTT	24311	
Db	25068	GTGCGCG	AGTGCCTGT	GTGCCCG	CAAGCTCG	ACTGTGG	GGGTGCGCG	CGCGCGC	25127	
Qy	24312	CACCGCT	TCGACG	CCACAG	CGCCCTCAT	CGAGGAC	ATTCGG	AGGTTTCGGCA	AGCGGTCA	24371
Db	25128	CGCGCGG	CGGGGTCT	GTGCCG	CAAT-----	---GCTGCGT	GGCTTGGT	CTCGCGGGCGG	25181	
Qy	24372	GGAGCTG	GAAGCAG	CTGTGCT	GCAGCGG	CAAGAC	AGCACAG	CTCAGCGAT	TCGCA	24431
Db	25182	GGCGAGG	CGCGCGGG	GTCCACTG	-----	-----	-----	-----	TCGCAACGG	25217
Qy	24432	TCTCGT	GAGCGAT	TGGCCG	CACTGACGT	CTCTCA	AGCAGAAC	CCAGGTGCT	CTCGGCT	24491
Db	25218	GCTGGC	CGGACGGCT	GGCGGGCT	CGCCCCGG	CGGAC	CAGCTC	AGCTTCTCT	CTGGA	25277
Qy	24492	GATTCG	GACAGG	CATCTG	CACCGTTTCT	CGGCGCTT	CGTTAAT	CCGGAAG	GCATCGAGG	24551
Db	25278	GGTCCGG	CGGAGGT	CGGGCGT	GTCTGGG	GCACG	CCGACG	GGAGCGCGT	CTCGGCTG	25337
Qy	24552	ACGAGCT	TTCCGCG	ACTCGG	CTTCGACT	TCGCTG	ACGT	CGGT	CTCAGTT	24611
Db	25338	CACGGCT	TTCAAG	GACCGCG	CTTCGACT	CTGCTG	ACCGCG	GTTCGAG	CTGCGCA	25397
Qy	24612	CGCCAAG	GAACCG	GACTG	CCACTCC	CGCGT	CTCTGT	TTGACT	ATATCC	24671
Db	25398	GCGACCG	CGACCG	GGCTGA	AGCTG	CGCGG	CAAGCT	CTGCTT	TCGACT	25457
Qy	24672	GGAATG	CTGCC	ATCTG	CGCACAC	AACTCT	CTGAC	CTCTAG	ACGACGA	24731
Db	25458	GGCGCT	CGCGCG	CACTGCG	-----	---CGACG	AACTCTGGT	GTGGCG	CGCCAGCGC	25508
Qy	24732	ACTGT	CGAATG	CTCTCC	CGCAAG	TGGCC	CAATG	CGGCTA	CCGTTCG	24791
Db	25509	GGTGAC	CAACAG	CGGCGCG	GAAG-----	-----	---CCGAC	CTTCGAC	GAGCCGAT	25553
Qy	24792	CATCAT	CGGTAT	TGGCAT	GTGCTT	CCCGG	CGGCGT	AGCTTCT	TGCGCG	24851
Db	25554	CATCGT	CGGGAT	TGGGTG	CGCTT	CGCGG	CGGGGT	TCGCG	GGGCGCG	25613
Qy	24852	ATTGCT	CTCGTTCGG	GTAAAG	CACTAT	CGGGT	CTTTCC	CGAC	CCGAC	24911
Db	25614	GCTGGT	CGCGAG	GGCGG	GACGCGGT	GTCTG	AGCTT	TCCCG	ACCGAC	25673
Qy	24912	GGACAG	CGCTTAC	GACCCCG	ACCCGAC	CCAC	CCCGG	CACTG	CTAC	24971

Db	21384	GGACGGCCGGGTCAAGGGCTTCGCGACGCGCGGACGCGACCGTCTCTCCGAAAGGGGT	21443
Qy	20727	GGGGATGCTGCTGGTGGAGCGCTCTCGACGCGCGCCCAACAGGTTCAGGCTGCTGGC	20786
Db	21444	CGGATGCTGCTCTGAAACGGCTTCGCTGGCGCCGCGAACCGGGTCTGCTGCTG	21503
Qy	20787	CGTGGTGGCTGGAGTGGCGGTCAACAGGACGGTTCGAGCAACGGTCTGACCGCGCCAA	20846
Db	21504	CGTCTCGCGGAGCGCGGTCAACAGGACGGCTTCGAGCGGCTGACCGCGCCAA	21563
Qy	20847	CGGGCCCTCCAGAGCGGCTCATCGCCAGGCGCTTCGCAACAGCGGACCTGACCCCGC	20906
Db	21564	CGGGCGCTCGCAGCAGCGGCTGATCGCAGCGCGCTGGCGGGCGGAGTCAACCGCTC	21623
Qy	20907	CGACGTGATGCGGTGGAGGCCACGCGACCGGACCGGACCTTTGGGCGGACCGATCGAGC	20966
Db	21624	CGAAGTGGACGTCTCGAAGCGCAGCGGACCGGACCGGCTGGGCGGACCGATCGAAGC	21693
Qy	20967	CCAGGCCATCTCGGACCTACGAGCAGGACCGTCTCGGCAACGGCGGCTTGTGGCTGG	21026
Db	21684	CCAGGCCCTGCTGCCACCTACGGCAAGCC-----GCGAGACGCGGTTGTGGCTCG	21737
Qy	21027	CTCCGTCAAGTCAACGTCGAGACACACAGCGCGCGGGCGGTGGCGGAGTGATCAA	21086
Db	21738	GTGCTGAAGTCAACATCGGCCACACCGAGCGCGCGGCGGTGGGCGCGTGATCAA	21797
Qy	21087	GATGCTGATGGCCCTCGGCCACCGGACCTCCACCGACTCTCCACGGGATGAGCGCTC	21146
Db	21798	GATGCTCAGGGCGCTGGCGCAGGACACCTGCGCGGACCTCCACGTCGAGAAACCCAC	21857
Qy	21147	GCGCATGTGACTGGTCCGCGGTGGCGTGCAGCTGTGACGAGAGCGGTGCGCTGGCC	21206
Db	21858	CAAGCAGGTGACTGGTCCGCGGTGGCGTGCAGCTGTGACCGAGCGCGGAGTGGC	21917
Qy	21207	CGCGGGAGGGCGCGCGCGGCGAGGAGTGTCATTCATTCGCGCTCAGCGGACCAA	21266
Db	21918	CGCG---AAGCGCCACCGCGCGCGGTGCTCTGCTGCTGCTGCGCATCAGCGGACCAA	21974
Qy	21267	GCACCATCTATCTCGAAGACGACCGCGGAG--AGGTTCGGGGGACCGCCG	21324
Db	21975	CGCGCATCTATCTTGAAGAGGCGCGCGCGGACACCGCGGAGCGGCGTGGCCGA	22034
Qy	21325	GACGAGGATGCGGTAGTGGCGAGGAGGTGTGCGCGGAGTCTCTGGG-----	21373
Db	22035	CGCCGTGTGCTGGTGGTGAATCTCGCGGAGACCGGATCCCTGGCGGGCGAGCGCG	22094
Qy	21374	-----TGTCGCGGTGGTGGTGGCGCAAGTTCGAGCGCGGCTTCGCGCCAGGCCA	21428
Db	22095	ACGCTGGCGGCTTCTCGACGAGAGCGTCCCGCTGACCGCGTGGCGGCTGCTGCT	22154
Qy	21429	GGCCCTGACGCCACCTCAGGACACCGCGGCTCGACCTCGCGGAGTTCGAGTACAC	21488
Db	22155	GTGACCGCGGCGACGCTGACCGACCGGCGGCTGCTGTCGCGGCTGCGCGGAGGCG	22214
Qy	21489	CC-----TCGCGCACCGCGCGCGCTGTTCGACAC-----CGCGCACCGCTC	21531
Db	22215	CGGGCGGGGTGACCGGCTGGCCGCGGAGAGCGGAGCGGCTTGTGACCGGTAC	22274
Qy	21532	ATGCGCGCGGACCGGACCACTTCCTGCAAGCACTTCAGGCACTCGCGGAGGCAACC	21591
Db	22275	CGCAGGATCGCGGCAAGAGCGTCTGGTGTTCCTCCCGCGGAGGCGGAGTGGCGGG	22334
Qy	21592	CACCCCGCTCATCCAGCAGCGCCCGAGCG-----GGACCGGAGCGGGGA	21641
Db	22335	CATGGCGGGAGTCTCTCGAAGCGTCCCGGTGTTCCCGGAGCGCATGAGGAATGCG	22394
Qy	21642	GGCGCAGGAAGACCGCATTCATCTGCTCGGACAGGCGACCGCAAC---GCCCGCGAT	21698
Db	22395	GGCGCGTGCAGCGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	22454
Qy	21699	GGCCACCGGCTTACACACACCGCGCTTTCGCGCGCGGACTCAACGACATCTGAC	21758
Db			
Db	22455	GCTGATCGGTGCAAGTGTCTGACGCGCGGTGTTCTCGGCTGATGTTGGGCTGCGCGC	22514
Qy	21759	CCACTGACCCCGACCTCGACACCGCCCTCTCTCCCGCTCTCTCACCACAAACGACAA	21818
Db	22515	GCTTGGGCTCTGGTGGCGGTCTGTCGCGGACGCGGTCTCTGGGCTCTCTCCAGGGG	22574
Qy	21819	CAAGCAACAGGAGCGCGCGCTCTCTCAGCAGACCGCTGACGCGCGCGCGCTCTCT	21878
Db	22575	TGCGCGCGCTCTGGTGGCGGTCTGTCGCGGACGCGGTCTCTCGAGGACGAGTCTG	22634
Qy	21879	CTTGGCTTCAGGTGGCGCTCTCAGCGCTCTCTCAGCAGCGGTACACATCACCACCG	21938
Db	22635	CGCAGCGAGCGATCGCGCGGAGCTGTGCGGCGCGCGGCGATGCGGTCTGATCAGT	22694
Qy	21939	CTACTAGCGCGACATCTCTCGCGGAAATCACCGCGCGCGCTGCGCGCGCTCTCT	21998
Db	22695	GAGCACACAGAGGTGGTGGCGCGCTGCGCGCTGCGCGCGCGCTGCGGTGAGATCG	22754
Qy	21999	CCTCAGCAGCGCCACCTCTCATCACCAACGGCGCACCTCTCTCTCTCTCTCTCTCT	22058
Db	22755	CGTCAACGGCTCGCGCTCGGTCTGATCGCGGTGACCGCGAGCGCTCACCGAGGCGT	22814
Qy	22059	CGGACACATGACCTCTCTCAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22118
Db	22815	CGAAGTCTCTCGCGGTGCGCGGTGCGGTGAGCTTACGCGTCCACACCGCGCGCG	22874
Qy	22119	CGAAGACGACCTCGCGATC-----GCGCGCATCAACACCGCGCGCGCTCTCT	22166
Db	22875	GGACATTCAGGACACCTTGGCGGAGCTTCTGGCGGAGTCTGGCGGAGGCGCGCG	22934
Qy	22167	CATCAGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22226
Db	22935	GCCTTCTCTCTCAGCGTGGCGGAGTGTGATCAGCGATCGCGGCGCGCGCGCGCG	22994
Qy	22227	CAAAACAAACCTCTCCACCAACAGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT	22286
Db	22995	GTACTGTGTACCGAAGCTTGGCGGAGTGGCTTGGCGCGCGCGCGCGCGCGCG	23054
Qy	22287	CAACCACTCAGCAGACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22346
Db	23055	CGACGAGGCGCGCGGCTGTCGAGGTGATGCGGATCCGCTGCTGCTGCTGCTGCTG	23114
Qy	22347	CACCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22397
Db	23115	CAGCGAGTCTACCGATGGGTCTGTCACCGGAGCTTGGCGCGCGCGCGCGCGCG	23174
Qy	22398	ACAAGCGCGAACCGCTGAGTACGCGACACCAACCAACCTCTCTCTCTCTCTCTCT	22457
Db	23175	GCGGCTGTGACCTGATGCGGAACTGTTCTGTCGCGGTGTCGCGGTGCGCGCG	23234
Qy	22458	CACCACTACATCGAACTCGGACCGGACACCGCTCAGCGCTCAGCGCGCGCGCG	22517
Db	23235	GATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23294
Qy	22518	CCCCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22577
Db	23295	GCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	23354
Qy	22578	CTCTCTCAGCACTCGCGCAAAACCAACCAACCTGCGGACCGCGCGCGCGCGCG	22637
Db	23355	GCTGCTGGGCGGCTTCTCTCGGTCGCGGAGTCCGAGCGGCTGCTGCTGCTGCTG	23414
Qy	22638	CCACAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	22697
Db	23415	GTCGCTCGGACGATCTGCTGGTGGCGGAGTGGCGCGCGCGCGCGCGCGCGCG	23474
Qy	22698	CCACTACTG-----GCTCGAACTACCGAGCGCGCGCGCGCGCGCGCGCGCG	22744
Db	23475	GGCGTGGCGCGCGGTGACGAGCGGCTTGGCGGCTCTCTCGCGCGCTGACCGT	23534
Qy	22745	GGGCTTCTCGCGCTCGGCTTCCAGACACCGCGGAGTTCGAGTTCGCGGCGGTG	22803
Db	23535	GCTGCTGCTGTCGCGGAGCGGTGGCTTCCAGGTGATCTGAGCGCGCGCGCG	23594





Qy	14412	CACCCAAACCTTCACTTACACCCACCCACACCCCTCTCATACCGCAACACCCACC	14471
Db	14997	CGCGAAGACGGCGACACCGCGTCTGCTCGCGACTCCCTCGCGCGGTCCCGCAGC	15056
Qy	14472	CGACCACTCTCACCCCTACTTGGACCCCAACAAAGCCCGCAACCGTGCATAGC	14531
Db	15057	CGAGCAAGACCGCATCTCTGTAAGTGTCTCGCGCCACGCTTCGACGGTGTCTCGGCA	15116
Qy	14532	CACACACCCAAACCTTCACCAACACGCGCTCACCACTATACGAACCTCGAACCCGA	14591
Db	15117	CAGGGCGCGAAGGCATCGGCCCGCCAGGGTTCAGAGAGTTCGGCTTCGACTCGCT	15176
Qy	14592	CAACACCTTACACCTTACCCACACCAAACTTCCCAACACCCCAACACCCCTCAC	14651
Db	15177	GGCCGGGTCAACTCCGCAACAGCTGACCGCGCCACCGGGCTGCGGCTGCGCGCAC	15236
Qy	14652	CTTACCCACCCCAACCAACCCCAACCCCACTCTCTCAACCACTCTGCCAAACAC	14711
Db	15237	GCTGATCTTGTACTACCCACCCGAGGCGTGTGCTGCTACCTGCGGTGCA-----	15291
Qy	14712	CACCACTGCAACCCCAACCACTACACCAACCAACCAACCAACCAACCAACCAACCA	14771
Db	15292	-----CTCTCGGGAGGCCAGACGGCTTGGAGCGGGCGGAAGACACTCTCG	15341
Qy	14772	CTTCGACCTCCCACTACCCCTTCAACCAACCACTACTGGCTTCAACCAACCCGCA	14831
Db	15342	GCAGTCTCTCGCGCGTGTGCGTTC-----GCCGGTTCAGGAGCGGGCGTGTGAC	15396
Qy	14832	CGCAGGACCGCTTACCGAGCGAGCGGTGAGGAGCAACGCCCATCAACCCCGCT	14891
Db	15397	ACCTGCTGGCGCTCGCCGACACCGGACACGAAACCGGACCGGACCGGACCAACCA	15456
Qy	14892	GCCTGATGCTCTGTGGGCAAGTCTCCGACGAGCGAGACGAGCTGTTCGCGCTGT	14951
Db	15457	GC-----GCCCGCGCGCGACGACGAGCAACTGATCGACGCACT	15497
Qy	14952	GCSCACCAATGCGGCGCTGTGTGGGCCATGCCACTCCCGAAGTGAATTCGGAACAA	15011
Db	15498	GGACATC-----TCCGCTCTGTGCAACGAGCCCTCGGGGACGAGCTGACCGCGAT	15051
Qy	15012	GGCTTCAAGAGCTGGGTTTGAATCTCTCGCGCAATTCAGCTTCGTAATCGACTGCT	15071
Db	15552	GGCAACCAATCTGGAGGAAGAACATGTCCGCGCGAACGAGC-----	15595
Qy	15072	TGCTGAGTTGACTGCGCTTCGGCGACGCTGATCTTCGATTACCCACTCCGATGCG	15131
Db	15596	-----AGATGTTGACGACTGCGCGCTCGCTGGAAGGAGACGTCGCGCTTCAGAGAA	15050
Qy	15132	GCTTTGCACTTCTCGCGCGCGCATCTGTGGAGCGGACACAGGCAACCACTCGTCT	15191
Db	15651	GAACAGCGCGCTC-----	15663
Qy	15192	CGCGCTAACCTGCGGTCCCGCGACAGCGGATCGCCATCTGCGGATGCGCTTCGCTGA	15251
Db	15664	-----GCAGCGCGCGCGCGGACCGCTCGCGATCTCTTCACTGCGCTTCGCTGA	15713
Qy	15252	CCCGGTGATGATCGGACGCTTCAATCTCTGGCAGGTGCTGAGTGGGCGCATGAGC	15311
Db	15714	CGCGGGGGATCCGCGCGCGGAGCACTTCTGGCGGGTGGTTCGGAAGGGCGCGAGCT	15773
Qy	15312	GATCGGCGGATTCGCAACGAGCTGGGTGGGACCTCGACAGCTGTACAAACCCGAGCC	15371
Db	15774	CTACACCGGCTTCCCGGAGACCGCGCTGGGAGCTCGAAGGCTTACACCCCGGACCC	15833
Qy	15372	GGACCAACCGAAGCTTACACCGGAGCGCGGATCTCTTTACGACGCGAGCAATTT	15431
Db	15834	CGACAAACCGGACGACGATGCTGCGGGAGGCGCTCTTCTGACGAGCGCGCGCACTT	15893
Qy	15432	CGATCCGACTTCTTGGTATAGTCCGCGTAGGCACTGGCGATGGACCCCGCAGCGG	15491
Db	15894	CGACGCGGGTCTTCTGGCATCTCTCGCGCGAGGCGCTGGCCATGGACCCCGCAGCG	15953





Qy	10034	TGCGGGGGTGTGTGTGCGGTGCCCGGATGCCGGTCCCGTGGCGGTGCGGTGCG	10093	Qy	11112	GCCGGGGTGTGCTGCTGCGGGGTGTGGAGAGGCGCAGCGGGATGATCCGGGACCT	11171
Db	11498	GCCTGTCCGGACGGCGGTGCAAGGGCTACCGGAGGGCCGACGCGACGGGCTGG	11557	Db	12381	CGTGACCGGACG-----GCGGGCAAGCGGCAAGGTCTCTGGGTCTTCCCGGCGAG	12435
Qy	10094	GTGGTGGCGGTGTGTGGGTGAGGTGTGTGGTGGGGTGTGGGTGTGGTGTGGTGTGG	10153	Qy	11172	GGCGGGACCGACCAACCGGGCGCATCATCGTTCCGGTCTGCATCCCATGTTCGACCCCGGA	11231
Db	11558	CCGAGGGCTCGGTGTG-----TCGTCTCGAAGCGCTTTCCG	11596	Db	12436	GGCTCGAGTGGATGGGCGGGACCTCTGAGACTCTCTGCGGGTGTTCGCGCGG	12495
Qy	10154	TGGGCTGGAGCGGTTCGGGGTTCGGCGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG	10213	Qy	11232	CGCATCGGCTCTCTTCATGCGGCTGCGTCTTGAGACCGGCGGCTCTGCTGCGCGCGGA	11291
Db	11597	TGGCAACGCAACGTGGCCACCGGGTGTGGCGGTCTCTGCGGCGACGCGGTGAAACGAG	11656	Db	12496	CGGA-TCAGGAATGCGCTGCGGCACTGGAAACAGTGCAGCTGGTCTGCTGGAGCT	12554
Qy	10214	CCGGCCCGAGACGCGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG	10273	Qy	11292	CTGCGTCCGCGCGCGCGCTGCGCGCTGTGTGAGAGACCTCTGCGCGGACCGCGCGG	11351
Db	11657	ACGGTCTTCAACGGCTGTACCGCCCCGAAACGGGCGGTGTGGTGTGGTGTGGTGTGG	11716	Db	12555	GCTCGCGGCGACCGCACCTGTGTGACCGGGTGTGGTGTGGTGTGGTGTGGTGTGG	12607
Qy	10274	CGGCGAGGCTGAGCATCCGGAACCGGTTCCTCTCGACCTCGACACCGACACCGGA	10333	Qy	11352	CCGACACCGCGCACACCATCTACCGGTGTGGGCAACCGGCGCGGCTGTGCACGCGCG	11411
Db	11717	GCGCGTGGCGAGCGCGGGTGGCACCGTCCGATGTGGACGTGTGGAGGGCCACGGGA	11776	Db	12608	-----GCTTCGCGATGATGGTGG	12626
Qy	10334	CC--GACCTCGACACCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG	10391	Qy	11412	GCTGGCGGCGAGACACACGAAACACACACCATCTCTCGCCCTGGTCTGCTCCCA	11471
Db	11777	CCGGACCGCGTGGGTGACCGATCGAGGTCCAGGCTGTGTGCGCACCTTACGGGCGAG	11836	Db	12627	GCTCGCGGGTGTGGACCTCGTGGGGGTGACCCCGGATGGGTGTGCGGCCACTCCCA	12686
Qy	10392	GGTGTGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG	10451	Qy	11472	CATCGCACCGTCTGTGGGCGACACACCGCGACACCATCTCCCGCGCGCGGTTCG	11531
Db	11837	AGCGGMAACAGCGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG	11896	Db	12687	GGCGAGATCGCGCGG---CGTGTGTCTCGGCGCTGTGTGTGGACGACGCGGGA	12743
Qy	10452	CTGAAACGACTGTGATCATCCGTTGATTTCCAGCCCGAGCGGTCCGTTGACACAGAGC	10511	Qy	11532	CGACTCGGTTGACTCTCTCACCGGCTCGAAGTACGCAACCGGCTCTCCCGCACAC	11591
Db	11897	CGCGCGGTGTGGGCGTATCATGATCATGATCATG-----	11931	Db	12744	GGTGTGCGGTGTGCGACCGAGCGGATCGCGGGGAGCTGGCGGGCGCGCGGGATGGC	12803
Qy	10512	CGCGCGGTCCGAGTCCCTGCCAGCGCTCCGTTGGCGTGCCTGTCTGCGCGGTTCGTTGA	10571	Qy	11592	GGGACTCGGCTCCCGCACCTCTCGACTCGACACCCCAACCCCAACCCCTCACCCA	11651
Db	11932	-----GCCATGCGCCACCGCGCTCATCGCGCCACCGCTGCACGTGGA	11972	Db	12804	GTGCGTGCACGTGAGCAAGAGGACGAGTCCGCGGCTGACGCG-----	12848
Qy	10572	TGTATCGGTCGGGAGGTGTGCGGTGTGCGGTGGGTGGTGTGGTGTGGTGTGGTGTGG	10631	Qy	11652	CCACTTCCACACACACTCCAGCACAAACCGGCAACCGGTGTGCGCGCGGTGTGGCGGA	11711
Db	11973	CG---AGCGACGAGCCAGTGTGCTGCTGCGGGCGCGCATGAGTGTTCAC-----	12023	Db	12849	-----GTGGGCAACCGGTCGAGTGGCGCGGTCAACACCGGTC	12890
Qy	10632	GACGGTGTGCTGGTGTGCGCGGTGTGCGCGCATCTGGTGTGTGTGTGTGTGTGTGTGT	10691	Qy	11712	GCTGACAACTCGAATCCGCGCTCTCGCGCTCGACAAACCGACGCGCGCAAG	11771
Db	12024	---CGAGGCGCGGAGTGGCGCGCACCGGACCTCGCGCGCGGGTGTCTCTCT	12079	Db	12891	CTCGGTCTCATCTCGCGGAGACGCGAGCGCTCGAAGAGCCCTCGAAGCCCTGCGCGG	12950
Qy	10692	TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	10751	Qy	11772	AGTACCTCGGCGGTGAAGTCACTCATGTTGAGGTGGAACGACACCCAGCATCCGACAGC	11831
Db	12080	TCGGCGCCAGCGCACCAACGCGCACCTGATCATC-----	12114	Db	12951	CGAGGTGTCTGGGTTCGCGGTCGCGGTGGAATACGCTCCACACCCCGGACGTGGA	13010
Qy	10752	GCTGGCGCGTGTGGGGCGAGGTGCGGATTTGTTGCTGTGATGTGGGGAGCGCGGA	10811	Qy	11832	CGAAAGCGCTGATGACGACGAGATTTCATATCGGCAACAGAGGTGAGATTTTCAATT	11891
Db	12115	-----GAGGAGGTCCCGCGAGAGGCGCTGACGAGAGGTGGCTC	12158	Db	13011	GGCGATCGCGAAACCTTGGCCAGACCTTGGCGGGATCGACG-----	13055
Qy	10812	GTGGTCCGCTGTCTGAGAGGTGTCTCTCGCGGTGTCTGCTGACGCGGTGTCTGTGATG	10871	Qy	11892	CATTGACAAACCTCTGCGCTGTCTGNAACCGGACGCTGCGACTCGCGCGTATCGCT	11951
Db	12159	CGTGTGCGCTGTCTCTCGCGCGAGCGCGGTGTCTGCGCGG-----	12206	Db	13056	-----GCGGTTCCGGGATTCGCTTTTATTCAC	13086
Qy	10872	GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	10931	Qy	11952	GGGCGCTCTAGGACGTGAATGCAATTGGCGAATGAGCGAAGTCTCTGGAATACCTCA	12011
Db	12207	-----GCAGCGCGGCGCTGCGCGCGGTCTCTGAGAACGATCTGTGCGCGGT	12257	Db	13087	G-----	13087
Qy	10932	GTTCGCGCGGAGGTGTGTCGCTCTTTTGTGGATGAGTGAACGCGGGTGTGAGCT	10991	Qy	12012	CGCGTCTACTCGGACCTGGACCGGACTGCGCGCTGCTGTGACGAGGTGTGAGCGTGA	12071
Db	12258	GGCGGTGCGCTGTCTCGCGCGCGGACGCTGTACAGAGCGCGGTGTCTATCG-----	12313	Db	13088	-----TCTTGGGACGTGGATCGAGAGGCGCTGTGACGCGGGTACTGTGTACCGGA	13141
Qy	10992	GTGCGGCTGTGCTGTCTCTCGCGCGCGGATCTCTGGGTGTGCGCGCGGCGGA	11051	Qy	12072	GCAGAGCGGATCGGATTTGGGATGGCTGTGTTTACCGAGCGGGGCGAGCTAC	12131
Db	12314	-----CGGGCTC	12320	Db	13142	ACCTCGCGACAGGTGCGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGG	13201
Qy	11052	CTAGCGCGGCGCAATGCGCTCTGAGCGGCTGCGGTACCGCGCGGGCGCGGCTCT	11111	Qy	12132	CACGCGACTGTGGCATCTCTGTCAGTCCAGACGAGCATCTCGGGGAGTTCCCGACCGA	12191
Db	12321	CCGCGACGAGGCGCCAGGACCGCTGTGAGGACTTGGCCCGCGCGGAGAAACGCGCGCT	12380	Db	13202	C-----GCTGTCTGTGGAGATCAGCGCCA	13226
				Qy	12192	CGTGTGAGAACTTGGAGCAGCTCTACGACCCCGGACCCCGACCGCTCAGGAACCACTTA	12251

Db	9429		CGGTTTCGGTCCGGC-----GTCTGAC	9452
Qy	7881	CGGGACCGGGAGCGCGCAGGAAAGACCGCAITTCATCTGCTCCGGACAGGGCACCACACG	7940	
Db	9453	CGGAAC---GCCGTTGACGGCAGCTGCGCGTCTCTTACACCGCCAGGAGCGCAGTG	9509	
Qy	7941	CCCCGGCATGGCCACCGGCTTTACACACCCACCCCGTCTTTCGGCCGCGCACTCAACGA	8000	
Db	9510	GGCCGGGATGGCCGCTGAACCTCCCGAGAGCTTCCCGGTCTTCCGGACGCCCTTCGAGGC	9569	
Qy	8001	CATCTGCACCCACTCTGCACCCCGCACTCGACACCCCTTCCTCCCTCTCCTCACCCAAA	8060	
Db	9570	CCGCTGCGAGGCGGTGGACACACCTCGCTGAGCGTCCGCTGCGCGAGTCTGTTGGA	9629	
Qy	8061	GCACAAACGAAACGAGGACGCGCGCGCACTGTCTCAGACAGACCCGCTAGCCACCGCGC	8120	
Db	9630	CGACA-----GCGCGTCTCGACACAGATGTACACCCAGGGCGC	9671	
Qy	8121	CCTCTTGGCTTCCAGTCCGCTCCACCGCTCTCTCACCGACGGCTACCAATCACCC	8180	
Db	9672	CTGTTTCGCGTGGAGACCGCTGTTCGGCTCTT---CGAGTCTTGGGGTGTGGGCC	9728	
Qy	8181	CACTACTACCGCGGACACTCCTCGGGGAATACCGCGGCCACCTCGCGCGCATCCT	8240	
Db	9729	GGGTCTCTCGCGCGTCACTCGATCGGGAGCTCGCGCGCGGCACTGTTCGGCGTCT	9788	
Qy	8241	CACCCTCACCGACGCCACACCTCTATCACCCAAACCGCCACCTCATGCGAAACCATGCC	8300	
Db	9789	GGACCTGGCGGACCGGGGAGCTGGTCCGCGCGCGCGCGCGCTGTATGACAGGCCCTGCC	9848	
Qy	8301	CCC---CGGCACATGACACACCTCCACACACACCCCCACACATACACCCACCACTCAC	8357	
Db	9849	CGCGGCGCGGATGGTCCGCTCCAGCGACCGAGGACGAGTCCGCGCCCTGCTCGA	9908	
Qy	8358	CGCCACGAAACGACTCGCATCGCGCCATCAACCCCGCACTCCCTCGTCAATCAG	8417	
Db	9909	CGGCACGG-----TCTGGCTCGCGCGGTCAACGCTCGGACTCGGTGGTCTCTC	9959	
Qy	8418	CGGCACCCCCACACCGTCCAAACATCACACCTCTGCCAAACAAAGGATCAAAAC	8477	
Db	9960	CGGCACCGAAGCGCGCTGCTCGCGTCCGCGATGAATGGGTGGTCCGCGCGTAAGAC	10019	
Qy	8478	CAAAACCTCCCAACCAACCGCTTCCACTCCCGCCACACCAACCCCACTCTCAACCA	8537	
Db	10020	CGACGGCTGGCGTGAGCACGCTTCCACTCGCGCTCATGGAACCGATGCTCGACA	10079	
Qy	8538	ACTCCACAGACACCCAAACCTCACTACACCCACACCCCGCTCATACCGC	8597	
Db	10080	CTTCCGCGGTGCGCGAAGCGCTGACGTACCGGCGCGGTTCCGCTGCGCGTCTCGAC	10139	
Qy	8598	CAACACC---CCACCCGACCACTCTCACCCCGCACTACTGGACCCCAAGCCCGCA	8654	
Db	10140	GCTGACCGGGAACTTCGCGGGCTCGACAGCCCGGACTACTGGGTTCGCGCAAGTGGCGAA	10199	
Qy	8655	CACCGTACGTACGCGCACACACCCAAACCTCCACCAACAGCGCGTCAACACTACAT	8714	
Db	10200	CGCGTGGGTTACGCGAGCGGTACCGCGTGGGCGCCCAAGCGGTCGAGTTCT	10259	
Qy	8715	CGAATCGGACCCGCAACACCTCAACCCCTCAACCCACCAACCTTCCCAACCCCGC	8774	
Db	10260	CGAGTCCGCGCGGGCGGTGGCTCGCGCGATGGCGCTCGGCACTCGCGGACCGCA	10319	
Qy	8775	CACACACACCTCAACCTCAACCCCGCAACCAACCCCGCAACCTCTCTCAACCA	8834	
Db	10320	GCAGAGTCTGCTGCGACCTCGCGCAAGAACGGGCGCGAGTGGCGGACCTCTCACCGC	10379	
Qy	8835	CCTGCCAAAACCAACCACTGCGACCCCGCAACCTTACACCAACCAACCAACCAAC	8894	
Db	10380	GCTCGCGAATCGACAGTCCGGGGCGTGGCGTTCGACTGAGCGAGCTGCTCGAGAAC	10439	
Qy	8895	CCACCCCAACCACTCGACCTCCCACTCCCACTTCCCAACCAACCAACCACTAGCT	8954	
Db	10440	GGCCACCGCGTCCGGACCCGCTCTGCCACCTACCGGTTCAGCACCAACGCGCTTCTGGGT	10499	
Qy	8955	CGAAAGACACACAGCCCGGTGCGGCAACGCTGTACAGCAGCGGACTCGACCCACCAACA	9014	
Db	10500	CGACGTGACAAACAGCGGCGCTCAGGCTCACCCCGCGCGGAGGAGCGATCGTGA	10559	
Qy	9015	CCCCCTACTCGCGCCCAATTTGAACTGGCACTGAACGTTGAGAGCGCTTCTTGACGGCG	9074	
Db	10560	CGCGCGGTGAGGACGCTGTGGAGCTGGTCCGGAGAGCGCCGCGTGGTGTCTCGGCA	10619	
Qy	9075	CTTGTCTTGAAGTGCATCCGTTGGCTGTGACCATGCTCGCGGCGCAACGTTCTGCT	9134	
Db	10620	CC-----GGGACCGCGGAGTTTCGACCTCGACCGGCTCTTCAA	10658	
Qy	9135	GTCCGGCGCCACCTTCTCGAACTCGCCCTTCATGCGGGACATACGTTGGGCTCGACCG	9194	
Db	10659	GGACACCGCTTCACTCGCTCAGCGGTCAAGCTGCGCAACCGTCTGCGGACTTCAC	10718	
Qy	9195	AGTGGATGAGCTGACGCTGCAATGCGCGCTGGTGTCTCTGTGATGGGGGTGTGAGTGT	9254	
Db	10719	CGGCTGGAGCTG---CCAGACACCTGATCTTCGACTACCCGAACCCGCGCTCTCGCGG	10777	
Qy	9255	GCAGTTGGGGTTCCGGCTCGGATGGGAGGGGCGCGTTTGTGTGATGTGTATGCGCG	9314	
Db	10778	ACCACTCGGGCGCAACTGTCTCGCGAGCGCCCGCGCGCGCGCGCTGACGAGG	10837	
Qy	9315	GGGTGGAGTCTTGTGTGGGGTGTGCTCGGTTGGGTGGAGTGTGATGCTCATGCTC	9374	
Db	10838	ACGTCTCGAGAGCCGATCGGATCTGCGCATG-----AGCAC	10877	
Qy	9375	GGGGTGTGCTTGAAGTGTCTGCTGGTGTGTGGTGTGATGCTTGGCGGGGTGTG	9434	
Db	10878	CCGACTCGCGGGTGGCGCGACAGCCCCCGAAGACTGTGGAAGCTCTCGCGGAGGACG	10937	
Qy	9435	GCCCGCGGGGTTCGGTGGCGGTGATGATGATGATGATGATGATGATGATGATGATG	9494	
Db	10938	GGACCGCTGTCCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTCG	10983	
Qy	9495	TGGTTGTGTTTGGGGCGGGTGTTCGCGGCTCGTTCGCGTTCGCGTTCGCGTTCGCG	9554	
Db	10984	-----GGCTCTTACACCCCGACCCCGCCACCGCGGACCGA-----GCTA	11024	
Qy	9555	TTTGTGCTGAGTGTCTTTCGCGAGAGGGGTGGGGTGTGATGCGGCTGGTTTGGGCT	9614	
Db	11025	CACGCTTCGGGGCTTCTTCGACGACGCGGCCAGTTCGACCGCGGGCTCTTCGGAT	11084	
Qy	9615	GCATCCGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	9674	
Db	11085	CTCACCGCTGAGGCCCTGGCCATGGAACCGCGACGAGCGGCTGTCTGGAGACGTCTG	11144	
Qy	9675	GGGGTTTGGGAGGGGGCGGGTTCGGGAGGGGTTCGGGTCGGGCTGTGTGGGGTGG	9734	
Db	11145	GBAAGCCTTGGAGCGCGCGGGGTTCGACCCGCT-----GTCCGCCCGCGGACGACG	11197	
Qy	9735	TGTGTCTCTTTCACCGGCGGGTGTACCGGTGTGCGGG---TGCGTGTCTGCTGTGCGG	9793	
Db	11198	TCGGCTTTCACCGGGATGCTCCACCAACACTACGTGACGCGGCTCGGAGTGCCTCG	11257	
Qy	9794	GGGCGCGCGGCTGAGCGGTGTGCGTTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	9853	
Db	11258	AAGACGTCACGGGCTACACGATGACCGCACCGCTTCGAGCGTGGCGTTCGCGCGGGTGG	11317	
Qy	9854	CGTGGTGCATCTTGTGAGTTCGGGCTTGTGATATGAGTTCGCTGCTGTCTCTGCG	9913	
Db	11318	CGTACGCTTTCGGCTTCGAGGGCCCGCGCTTCCCGTGGACACCGCGTGTTCGTCGCTG	11377	
Qy	9914	TTTTCGGCGGCGCGGGGTTCGCTGTATGCGGTGACGTGGGCTGAGGTGGGCTCTGTC	9973	
Db	11378	TGGTTCGGGATGACCTTGGCGCGCGACGGCGTTCGCGACAGGGGAGTGTCTCATGGCCCTGG	11437	
Qy	9974	CGGTGTGCGGAGGCGTGGCGCTTGCAACGAGACGTTGGGTGAGAGCGGTGGTGGGCTG	10033	
Db	11438	CCGCGCGCGACCGTGTATGGCCAGCCCGACGCTTCTCTCGAGTTCTCCCGCGCGCGG	11497	

QY 5670 CACCTGGCAAGGAACGACTCGCTGATTTCGACAAAGCCCGCATATCTCGACCGCG 5729  
DB 7335 CTACTGGGGACGGTCAGCGGATGACCGAGCACTTGGGCGACCGACCTTCGGCGCAA 7394  
QY 5730 CGGGTTTCGACCATGTCAACCGAGTTGGCCACGCGAGCGGTCAACGAGGCGATCGCGGA 5789  
DB 7395 CCAGCGGATCGGCATGTTCGGGCTTCCCGCCGACGAGGCGATGGCGCTCTGGACCGCG 7454  
QY 5790 CA---CCGNAACGGCGTATGTCTGATCGCCGACATCGACTGGAGCAAGATCGAACAC 5846  
DB 7455 CATCGCCACCGGTGACACGCTGCTCGCGCCAAAGTTTCGACGTTCGCGCGCTGCGGGCGAC 7514  
QY 5847 CTCCTCAGACACGACCTTGTGAGCGCGCCCGGGAAGGAGCGAGCTGTCCAGCGCC- 5905  
DB 7515 GCGGAAGCGCGGGCGCGCTGCGCGCTGTGTGGTGGCTTGGCCCGCTGCGCGCG 7574  
QY 5906 -----CCACTCCACCGCGGAGTTGCACAAACGCTGGGCCATCAGAGCTCGGCCGACCA 5960  
DB 7575 GCGCGCGGCAAGACCGGCTGCTGACCGAACGCTCGCGGGCTGGCGGAGACCGAGCA 7634  
QY 5961 ACGGGCCGATTCCTCGAGCTGTAAGAGACCATGTGGCGGAGTGCTCCGCGACCGGA 6020  
DB 7635 GCGCGCGGCTTCTCGACTGCTCGCGCGGACCGCGCGAGGTGCTCGGGCAGCGG 7694  
QY 6021 CCGGAAAGCATTCGCGCCCGACAGTCTGCTGCACTCGGCTTCGATTCACTCACGCG 6080  
DB 7695 CGCGNACTCCGTCATTACGAGACGACGTTCAAGNACGCGGCTTCGACTCGCTGACCG 7754  
QY 6081 CGTCGAGTTCCGAACCTGCTGATCAAGGCAACAGGACTCCGCTTCTGCTCTCGTGGT 6140  
DB 7755 GGTGAACTCGGACACCGCTCGCGCGCGGACCGGCTCACCTGTCTCCCGCGCATGAT 7814  
QY 6141 CTTGACACACCGACCCCTGCAAACTCGCGGTACACTGCGAGAACCACTCGGGGGAC 6200  
DB 7815 CTTGCACTACCGAAGCCCGCGCGCTCGCGACCACTGCGCGCAAGCTCTTCGATC 7874  
QY 6201 AGCAGCGGAGTGGCTCTTCAGCGGACCGCTTACCGCGGAGGCTTCTGTCAACGAGCC 6260  
DB 7875 GCGGGCAA-----CGGCGCGCGGATCGGCAACCGCGCGCGGAGGCC 7922  
QY 6261 GATCGCATCTGTGGCATGGCTGTCTGTTTCCCGCGGAGTGACTTCGGCGGAGCTT 6320  
DB 7923 GATCGCATCTGTGGCATGGCTGTCTGTTTCCCGGTGCGTGACAGCCCCGAGGACCT 7982  
QY 6321 CTGGGATCTGATCTCTCGAGCAGGACCGGATCGGCGGATTTCCCGACCGACCGGGCTG 5380  
DB 7983 GTGGCGGCTGGTGGCGGACCGGCGCGACCGCTTCCCGCGGCTTCCCGCGGCTG 8042  
QY 6381 GGACCTGGACACGCTCTACGACCCCGACCCGACACCCCGGACCTGTCTACACCGMAA 6440  
DB 8043 GGACACCGACCGGCTCTACACGAGACCCCGACACGAGGACGACGTAGCTCGGCA 8102  
QY 6441 CGGCGGATCTCTACGACGAGGCACTTCGAGCGCGGATTTCTTCGGCATCAGCCCCCG 6500  
DB 8103 CGGCGGCTTCTTCGACGACCGCGCGGTTTCGAGCGCGCTTCTTCGGCATCTCGCGAA 8162  
QY 6501 CGNAGCCTTCGCATGGAACCCCGACCAAGCTCTCTCGAAACCGCTTGGGAACCAT 6560  
DB 8163 CGAGGCGCTTCGCATGGAACCCCGACGAGCGGCTGCTGGAGACGCTCTTGGGAGCTGT 8222  
QY 6561 CGAACACCGCGGATCAACCCCGACACCTTCAACGAGCAACCCCGCGGAGTCTTACCGG 6620  
DB 8223 CGNCGGGCGCGNATCGACCCCGACACGCTGGCGGCGCAGGACATCGGCGTCTTCGCGG 8282  
QY 6621 CACCAACGAGCAAGGACTACGCACTTCGCGTGCACAAACGCGGGCGAGTCAACCGATGTTT 6680  
DB 8283 CGTCAACAGCACGACTACAGCATGCGGATGCAACCGCGCGCTTCTTCGGCATCTCGCGGCTT 8339  
QY 6681 CGCACTGACCGGAACCGCGGAGCGTCACTCTCGGCTGTAATCTGATACGCTTTGGTTT 6740  
DB 8340 CCGGCTCACCGGCGGTTTCGCGCAGCGTGTCTCTCGGCGCGCTTACCACTTCGGCGT 8399

QY 6741 TGAGGGTCTTCGGGTGTCGTTGGACACGGCTTGTCTCTCGTGTGTGTGCTTTGCACT 6800  
DB 8400 CGAAGGCCCGGCGCTCACGGTCGACACGGCTGCTGCTCTTCTGCTGTGCTGCGCTGCACAT 8459  
QY 6801 GGCCTGTACGCGTTGCGGTGAGTGTGCTGATGCGCGCTTGC CGGGGGTGTGACGCT 6860  
DB 8460 GCGGTCGAGCCCTGACGCGCGGAGTGTCTCATGGCGCTCGCGGGCGCGGTGATGCT 8519  
QY 6861 GATGTCGTCTCGGGTCCCTTCTGTGGAGTTTTCGCGGACAGCGGGTCTTGGCCGCGGACGG 6920  
DB 8520 GATGGGACCGTTCAGACGTTCTGTCGAGTTCTCGCGGACGCGGGCTTGGCCCCCGACGG 8579  
QY 6921 GCATTGAAGCGTTCTTCGCGCGCGGACCGGTCGCGGTGGGGTGAAGGTGTGGGAT 6980  
DB 8580 CCGCTGAAGGCGTTTCGCGACGCGCGGACCGGCTGCTCGAGGGCGTCTCGCGCT 8639  
QY 6981 GCTGCTGTGAGCGGCTTCTCCGACGCGCATTCGCAACGCTCACCTGCTCTCTGGCGGCTGT 7040  
DB 8640 GCTCTGTGTGAGCGGCTTCTCGAGGCTTCAGGCTGCGGGGACAGGCTCTCTCGCGCTGT 8699  
QY 7041 GCGTGGCAGTCCGCTCAACAGGACCGTTCGAGCAACGCTCTGACCGCGCCCAACGGGCC 7100  
DB 8700 CCGGGTTCGCGGTCAACTCCGACGCGGCTGCAACGCGTTGACGGCCCCGACGGCCCC 8759  
QY 7101 GTCCAGCAGCGTGTCTATCGCCAGGCGCTTCGCAACGCGGGCTTGTGCGGCGGTGATGT 7160  
DB 8760 GTCCAGCAGCGCTGTATTCGCAAGGACCTGGCGCGCGCGGACTGTCCACATCGGACGT 8819  
QY 7161 CGACGCGTGGAGGCCCAACGCGACCGGACCTTTTGGGCGACCGCATCGAGGCCAGGC 7220  
DB 8820 CGACGCGTGGAGCGACGCGACCGGACCGACCTTGGGCGACCGCATCGAGGCCAGGC 8879  
QY 7221 CCTCTCGGACCTTACGAGACAGGACCGTTCGCGGAGGCGGCGCTGTGGCTTGGCTCGGT 7280  
DB 8880 GCTGCTGGCACTTACGCGCAGAAC-----GGGAAACGCGCTGTGGCTCGGT 8933  
QY 7281 CAAGTCCAATGTCTGTCACACAGGCTGCGCGGGGTTCGCGGGGTGATCAAGATGT 7340  
DB 8934 GAAGTGAACTCTCGGCGACACGAGGCGGTGCGGGTGTTCGAGCGGTGATCAAGATGT 8993  
QY 7341 GATGGCGTGGGATGCTGTCTGCGCGGACGTTTCATGTGATGAGCGCTGCGCGCA 7400  
DB 8994 CATGGCATGCGCCACGCGCGCTTCTGCGCGGACGCTGCACTGCAACCGCGCTGCTCTA 9053  
QY 7401 TGTGACTGTCTCGCGGTGCGGTGCACTGCTGACGAGACGCTGCTTGGCGCGCGG 7460  
DB 9054 TGTGACTGTCTCGCGGTGCGGTGCACTGCTGACGAGGCAACGGGACTG---GTGAG 9110  
QY 7461 GGAGGGCGGCTACGCGGGGAGGAGTGTATCATTTGGCGTTCAGCGGCAACAGCGCCA 7520  
DB 9111 CAAAGGCGCACCGCGCGCGGGGCTGTCTGCTTTCGGCATCGCGGCGCACAGCGCA 9170  
QY 7521 GTCATCTCAAGNAGCACCGCGGAGCGTTCGCGGGGAGCACCCCGCGGCGAGGG 7580  
DB 9171 GTCGCTCTCAAGAGGTTGCGCACCGATCACACGCGCGAGCTGAGCGCGCGGAG--- 9228  
QY 7581 TGACGCGGCGAGCGAGCATGAGGCTGTCTGCGGAGTCTTGGGGTGTGGCGCTGCTGCT 7640  
DB 9229 -----TTCTGCTGCGGTGCTGCT 9248  
QY 7641 GTCGGCAAGTCGAGCGCGGCTTTCGCGCGCCAGGCGCCAGGCTTCGACGCCACCTCAC 7700  
DB 9249 CTCGCGCGGAGCGCGGGGCTTTCGCGGCGGACGCGGCGGCTTCGCGGCTTCTCGG 9308  
QY 7701 CGACACCGCGGCTTCGACCTTCGCGGATGTTCGATACCTTCGCGCCACCGCGCGGCT 7760  
DB 9309 CGACCGGACCGGCTTCGCGGCTTTCGCGGCTTCGACCTTCGCGGCTTCGCGGCGGCA 9368  
QY 7761 GTTCGACCAACCGCGGCTTCATCGCGCGGACCGGACAGCTTCTTCGCAAGCACTCCA 7820  
DB 9369 GCTGACCAACCGGGCGGCTTCTGCGGCTTCGACCGGCGGACAGCTTCTCGCGGACCTTGC 9428  
QY 7821 GCGACTCGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7880

Db 5136 CCGCGC-----GGATGCGTCGTCGCGCTGCGCGGAGCAGCTGCTTCGGG 5186  
Qy 3588 GTGGGCGGCGGCTTGTGGTGTGGCGGCTCAAGCGCCCGCGCTCCACCGCGCTTCGGG 3647  
Db 5187 GCTGGTGGAGGGGTGAGGTGCGCGCGCTCAAGCGCCCGCTGTCGGTGTGATCGCGG 5246  
Qy 3648 GATGCCGAGGGGTGGAGGAGTGTGCGCTACTGTGCGGACCGGGGTGCGGCGCG 3707  
Db 5247 GATGCCCATGCCCTCGACGCGACCTGGAATCTTGTCCGGGAGGATCCGGGTTCG 5306  
Qy 3708 GCGGATCCCGGTGCACTATGCTCGCACTGCCCGCATGTGAGCGCCCTGCGGAGAGTT 3767  
Db 5307 GCGGGTGGCGGTGGATACGCTCTCGCACACCGCGATGTGAGGACATCCGCGACACT 5366  
Qy 3768 GCTGAGCTGCTGGGGGACATCAGCCGCGAGCGCTCGGCGTGGCTTCTTCTCCACGCT 3827  
Db 5367 TGCCGAACTTGGCGGGATCAGTGCAGCGCGCGGTGTCGGCTTCTACTCCACGCT 5426  
Qy 3828 GGAGGCGACTGTGCTG-----GACACCAACACCTGGACGCGGCTACTGTGTACCGCAACT 3884  
Db 5427 CACGAGCGAGTGGGTGCGGACGCGGGGTGCTGGAGCGCGCTACTGTGTACCGGAACCT 5486  
Qy 3885 GCACAGCGCGTTCGTTTTCAGCGATGCTCGTCCAGCGCTTGGCGGATGAGGACACCGGCT 3944  
Db 5487 GCGCAACCAAGTCCGGTTCGAGCGCGCGCGACGCGCTGCTCGAGCAGGGGCAACAGCT 5546  
Qy 3945 CTTCGTGGAAGTCAGCCCGCACC-----CACCTCTGTCGCGGCATCGAAGACACCAACGA 4001  
Db 5547 GTTCGTGAGGTTCAGTGCACCGCGTACCGGTGACGCTCAGCCCTTGGAGGAGCTCACCGGGA 5606  
Qy 4002 AGACACCGCGGAAGACGTCAACCGGATCGGACGCTCGCGCGCGGCAACGACCG 4061  
Db 5607 CCGCATCGGACATTTGCGGCGTGAAGACGCTGCGCTGCGGCGTTCGCTTCATGG 5666  
Qy 4062 CCGTTCCTTACCGGCTGCGCCACCGCATACACCGGATCGGCAACCGCACTG 4121  
Db 5667 TGAGCTGTTCGTCGCGGATCGAGCTGAGCTGAGCGGCGATGTCGCGCGCGGCTG 5726  
Qy 4122 GCACACACATACACCCACACACACACACACACACACACACACACACACACAC 4181  
Db 5727 GGTGACTTGGCGACTTACGCGTTGAAACCGCGCACTACTGCTGAGCGCGCGGAGCC 5786  
Qy 4182 CACTTACCCCTTCCAAACACACACTACTGCTGAGAGCTC-AACGCGGGTTCGGGAT 4240  
Db 5787 CGCTTCGCGGAGACCGCTGCTGCGCACAGTGTGAGCACTCCCGGTTCGACCGACT 5846  
Qy 4241 CCGGTTCCGGTCCGGTCCGGTTCGGTTCGGTTCGGGCGGCGAGGACTGCGGCG 4300  
Db 5847 CACCGCGTGGCGAGTGTGCGCGCGGCGGAGCGCTGCGGCGTGGACGCGCTGCTGCC 5906  
Qy 4301 GSAGCGAGAGTGGAGTCCGGTTCTGGAGCGGTTGCGCGCAG----- 4347  
Db 5907 GACCGCGGCTGTCGAGGCGGCGCATCCGGTTCGCGGACCTTGGCGGCGACCCCGCTCGT 5966  
Qy 4348 ----GACCTGGAACCGTTCGCGACACACTTCGCGCTGCGCGCTCCGCGGCTGGACAC 4403  
Db 5967 CCGCGAACTGTGTCGACGCGCGGTGTGTCGCGCGGCGGCGGCGGAGGTCCA 6026  
Qy 4404 GGTGTGCGCGCACTCTCCGCTTGGCACCGGCACCAACAGCAACGAGCC----- 4452  
Db 6027 GCTGATGCTGCGCGAGCGCGGAGCAGCGGCGGCGCTCGAGTCTTTTCCCGGGA 6086  
Qy 4453 -CGCATCAACACTTGACTTACAGGAACCTGGAACCCCTCACTCCCTCCCAACCA 4511  
Db 6087 AGCGAGAGCGGTGGAACCGGCGACGCGCACTCGCTCCGCGCGCTGCGGT 6146  
Qy 4512 CCAACCCCAACAACTGGCTCATCGCCATCCCGAAACCCAGACCCACCAACCCCAACAT 4571  
Db 6147 GCCAGAACCGGCGGCGGAGAGCGCCACCGAGCTACCGTGGCGGCTTGGCGGAGCG 6206  
Qy 4572 CACCAACATCTCAACACTTCGACCAACCGGATCAACCCCATTCGCCCTCAACCTCAA 4631

Db 6207 GGACGCGTACGGGATTCACCCCGCGCTGCTGAGACGCGCGCTGCTGTCGGGCA 6266  
Qy 4632 CCACACCC-----ACACCAACCCCAACACCTCCACCAACACACCTCCACAC 4677  
Db 6267 CGACTGCTCCGCTCGGTGTGAGCGGGGTGCTCTGCTGGCTCCGGGGCCACGGCGT 6326  
Qy 4678 ACCGCAACAAAGCCCAAAACACACCAACCGGAGCATCACGGCC-----TGCT 4727  
Db 6327 GACCGTACGCGGAGCGGCGACCGGCTGCGCTGAGCGACCGCGCGGCGGAGCGCTCT 6386  
Qy 4728 CTCCCTCTCCGCTCGAGAGAAACACCCCAACCCCAACCAACCCCAACCAACCGGAC 4787  
Db 6387 GACCGTCAAACTCCGTCGCGGCGACCGCTTCTGTCGCGAGAGGAGCAACCGACGCT 6446  
Qy 4788 CTTCTCAACTCTACCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCTCTG 4847  
Db 6447 CTTTCGCTGACTGCGCGGAAATCCGCTGCCACCGCGGAAACCGCGGACTTCTCGCC 6506  
Qy 4848 GTACGCCACCAACACGCGCACCAACCAACCAACCAACCAACCAACCAACCAACCA 4907  
Db 6507 GTACGAAGCAGCTCGGCGGAGCGACCTCTCCGCGCTCCAGGCTCGGCTGCGAGACCC 6566  
Qy 4908 AGCCAAACCTGGGAGTTCGCGCGGACCAACCTCTCTGAAACACCCCAACCAACCGCGG 4967  
Db 6567 CGCGAAACCGGCTGCGCTGCTGTCGCGGAGCTGACACCGAAACCGCGCGGCGCGCAT 6626  
Qy 4968 AATCATGACCTCCCGACCCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5027  
Db 6627 CTGGGCTGCTGCGCTGCGCGAGTCCGAACACCGCGCGGATGCTGTCGGCGGACCT 6686  
Qy 5028 CACCAACCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 5076  
Db 6687 CGACGACCCCGCGCTGCTGCGCGGCTGCGCGGAGCGGCGAAACCGGAGTGGGTGCG 6746  
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Qy 5190 CACCGACCTCTACACCCCAACCAACCAACCAACCTCTCTCTCTCTCTCTCTCTCT 5249  
Db 6867 GCGCGGCACTCTGCTACCGCGGCGCGGCTCGGCACTTGTGCTGCTGCTGCTGCTG 6926  
Qy 5250 CCCCCACCCCGCGACACCACTCAACCCCACTCAACCAACCAACCAACCAACCA 5309  
Db 6927 TGAGGCTCCGAGCTGAGGAGAACTGACCGCACTG-----GGGGCATCGT 6974  
Qy 5310 CACCATCACACCTCGGACACCAACCAACCAACCAACCAACCAACCAACCAACCA 5369  
Db 6975 CGCATCGCGCTTGGCGAGCTGCGGAGCGCGGCGGCGAGCTCGAAGCGCTTCTTGGCG 7034  
Qy 5370 CCCCCCAACACCCCTCTACACCGCTCATCACCGCGGAGGATCTCTCGACGCGGAC 5429  
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Qy 5430 CTTACCAACTCTACCCCAACCAACTCAACAGTCTCTCGCGCGGCGGAGCGGCGG 5489  
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Qy 5490 CCACTCTCCCAACTCACCAACCAACCAACCCCTTCCCGCTTCTCTCTCTCTCTCT 5549  
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Qy 5610 CGAGCGCTCGCGGACCAACCGCGGACCAACCTCTCCCGCGGAGCGGAGCTGCGTGG 5669  
Db 7275 GGATGCTTGGCGCGGAGCGGAGCGGCTCGACCTCGCGCGGCTGCTGCTGCTGCTGCT 7334



QY 1368 CGGCGACCTCGACGAGGACACCGCGCCGTACCGGACTCACCCAGCGGCCACGAGGCAC 1427  
DB 3180 CGGGATACGCGAGGCGCTCGCGAGCGGT-----CGTCCG 3215  
QY 1428 GCGAGCGCGGACGACCCCGATCGCCATCATCGGCATGCGCATCCCGTTTCGCGGCGGAGT 1487  
DB 3216 GCGCGACCGCGGCGAGCGCATCGCGATCGTGGGATGGCTCGCCCTGCGCGGCTGGCGT 3275  
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DB 3618 CGCGCGGTGGCGCGGAGCTCGAAGGTTTCGTACACACCGGGTCTCGTTCGAGCGTGGC 3677  
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QY 1968 GTGCTCGGATCGCTGTGACCTGATCTGCGGTGCCAGTCTGCTCGGTCGGTCCGGTGA 2027  
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QY 2508 GGTGTGGTGGGTCTATCAAGATGTGATGGCTTCGGGAGGGGTGTTCGCGCGGAC 2567  
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DB 4507 -----GAGCGGTCGTCGCC 4523  
QY 2868 GGTGCGGTCGCGTTCTGTGCGCGGTTCGCTAGGTAGGTCTGAGGCTGGGTTGCGGCGCA 2927  
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QY 3228 CGGATGCGCGCTGCGAGGAGGCTCTGCGCGCGTGGTGGATGAGTCTGCTGCTGCTGCTG 3287  
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DB 5076 CGAGACCGCGGAGAGTGGTGGCGCTTCCGCGAGCCAGGCGCATCGCGCGGCGGAACTGCTCG 5135  
QY 3528 GGGCGCATGCTCAGTGGCGCTGCTGCTGCGCGAGGAGGTGGAGCAGCTCATTTGGTGA 3587

RESULT 10  
AAV21187  
ID AAV21187 standard; DNA; 53789 BP.  
XX  
AC AAV21187;  
XX  
DT 24-JUL-1998 (first entry)  
XX  
DE Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.  
XX  
KW Amycolatopsis mediterranei; rifamycin; synthesis; gene cluster;  
KW polyketide synthase; actinomycete; ansamycin; ds.  
XX  
OS Amycolatopsis mediterranei.  
XX  
FH Key Location/Qualifiers  
FT CDS 1825..15543  
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FT /label= ORF F  
FT /product= "polyketide synthase"  
XX  
PN WO9807868-A1.  
XX  
PD 26-FEB-1998.  
XX  
PF 18-AUG-1997; 97WO-EP04495.  
XX  
PR 20-AUG-1996; 96EP-0810551.  
XX  
PA (NOVS ) NOVARTIS AG.  
XX  
PI Engel N, Schupp T, Toupet C;  
XX  
DR WPI; 1998-169172/15.  
XX  
PT P-PSDB; AAW52845-W52850.  
XX  
PT Amycolatopsis mediterranei rifamycin synthesis gene cluster - used  
XX to produce rifamycin and rifamycin analogues  
PS Claim 4; Page 53-102; 205pp; English.  
XX  
CC The present sequence represents a Amycolatopsis mediterranei rifamycin  
CC synthesis gene cluster DNA fragment from the present invention. The  
CC DNA fragment comprises a DNA region involved directly or indirectly  
CC in the gene cluster responsible for rifamycin synthesis, including  
CC the adjacent DNA regions to the right and left which, by reason of  
CC their function in connection with rifamycin biosynthesis, qualify  
CC as constituents of this rifamycin gene cluster, and functional  
CC fragments, derivatives or constituents of these. The Amycolatopsis  
CC mediterranei rifamycin synthesis gene cluster DNA fragment can be used  
CC for producing rifamycin, rifamycin analogues or precursors. It can also  
CC be used for inactivating or modifying genes involved in ansamycin or

CC rifamycin biosynthesis. The DNA can be used for constructing mutant  
CC actinomycetes strains from which the natural rifamycin or ansamycin  
CC biosynthesis gene cluster has been partly or completely deleted. The  
CC DNA fragment can be used for assembling a library of polyketide  
CC synthases, which can be used for assembling a library of polyketides.  
CC A hybridisation probe of the invention can be used for identifying DNA  
CC fragments involved in the biosynthesis of ansamycins.  
XX  
SQ Sequence 53789 BP; 6707 A; 19183 C; 20504 G; 7395 T; 0 other;

Query Match 11.1%; Score 3399.8; DB 19; Length 53789;  
Best Local Similarity 49.6%; Pred. No. 0;  
Matches 15100; Conservative 0; Mismatches 12717; Indels 2610; Gaps 146;  
QY 474 CGTCTCCGTCGCGCCACGCGGATGAGCTCTCTGCCCGGAATCGCTTCGTCGACGAGGA 533  
DB 2304 CGCCCGCTGAGGGCTCGTGGGGTTGGCGTGCCTGGCGGTCTGACGTGCGGGTCTCGA 2363  
QY 534 CAACCCGCGCGGCTCGCCGTTCGACGCGTCAACCGGACCCCGGAGCACAGTCTGTTCCGG 593  
DB 2364 CCCCAGACACCGGGCTCGAGCTCCCGCGCGGAGGAGGCGAGGTCTGGTTCAGCGGGCC 2423  
QY 594 TGCCCGGAGCGCTCGCGGACCTGTGGCGACCTTACCGCGCGGAGGTGCGCACGGG 653  
DB 2424 GAACGTCTATGCTCGGCTTACCAACAGCCCGGAGCGACCCGCGCGGATGCGGGACGG 2483  
QY 654 CATGATCCGCTGGAGGTTCCCGCCACTCCCTCGATGTACGCCATCGAGGACGGGT 713  
DB 2484 CTGGTTCCGAGACCGGGGACCTGGCCCGCGGAGACGACGCCGGTTACTTACCATCTGGCG 2543  
QY 714 CGTCAGCGGCTGTGCCCCATCACCCACGCGCCCTCCCGCATCCCTTCCATCTCTCGGT 773  
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QY 831 GTCGAGCACGGTTCGGTTTCGAGCCGCGCGCGGTGCTTCTGACGAGGGGCGCAAGAC 890  
DB 2664 GCTCGGCGAGTGGCGTTCGCTTACGTCATCCCGGACCGACCGGTTTCGATCTTGGCGC 2723  
QY 891 GTTCGTGAGATGAGCCCGCACCCGCGTCTGACCATGCGGCTCCAGGAGCTCGCCCGGA 950  
DB 2724 GTTGATCGAGAAGTCCCGCAACAGCTGTCGCGCTACAAAGTTCGCGGACCGATCTCGA 2783  
QY 951 CCTGGGAGACACACCGGACCGCGACACCGTATATATGCGGACGCTGCGCGCGCGGCA 1010  
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DB 3024 CGGGCGTGGC-----TTCCGACCTTCGGCTTCAGCTCGCT 3059  
QY 1248 CATGGGTGTGAACTGGCAACCCCTCAGCAAGCGCACCGGCGCTGCGGTTTCCCGGTAC 1307  
DB 3060 GGCCATCGTGAGCTGGCAACCGGCTGACCGAGCACACCGGGCTCTGGCTGCCCGCCAG 3119  
QY 1308 GCTCATCTTGACACACACGCGCGCGGCTGCGCGCGCTTTCGACCGCGCGGCT 1367  
DB 3120 CGCGCTTCTTGACACACCGCGCGGCGGCTGCGCGCGCGCGCTGCGGCTGAGTCTCT 3179

25439 GTGAGGACGACACCGCTTCCGCGACCTGGGCTTCGACTCGCTGACCATCTCGGAATG 25498  
24601 AGCAGGAATCGCCAGGAACCGGACGACCTCCCGCTCCCTGCTTTCGACTAT 24660  
25499 CGCAACGCCCTCAACGCCGCCACCGGCTTGAGCTGCGCGCACCTGCTTACACCTG 25558  
24661 CCACCCCGCAGGAATGCTGCCATCTGCCACACAACTCGTGACCTAGACACGAA 24720  
25559 CCACCCCGCGGAGATGGGACTTCTGCTCGCGAACTCTCGGCACCTGCCCACC 25618  
24721 GAGGACGGGC-----ACTGTGAAATGCTTCCCGCAAG-----TGCGCCNT 24762  
25619 GACACCGCGCAGCGCTGCCAGCAGCGCTCCCGCAAGCTCTAGCTTCTGTTGAGCAG 25678  
24763 CGCGGTACCGTTCGAGAGCAACCGATCGCATCATCGGTATGCGATGCTGCCCGGC 24822  
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24823 GCGGTACGTTCTGCCGACGACCTGTGGGAATTGCTGCTTCCGGTAAGGACGCTATCGGC 24882  
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25123 ACCCCACCGGAGCTTTCGCGGATCAACGCTCAAGACACCGCGCGCATATCGCCAA 25182  
26021 TCACACCGCGGCTTCTGTCGCGACCAACGCGCAGGACTACCGACGCTGTTC----- 26075  
25183 AGCGGTGATGTGGAGACCATCAGGGCTACGCCCTGACCGGAGTTTCGGGAAGTGTGGCG 25242  
26076 -GCGCTCCGCTCGGACGCTGGCGGCTAGCTCGCCACCGCAACACCGCGGCTGATG 26134  
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14438 -CCACACCGCGCTCATACCGCAACACCGCGGAGCGGAGTCTCTCACCGCGCGCTAC 14496  
15536 GTGCAACCGGAGGCTGGCGACTAGCGCGCGTGGAGACCGCTGAGCAGCGCGGAGTTC 15595  
14497 TGGACCCCAAGCGCGCAACCGTCACTACGCGCACCAACCGGCGGCGCGCGCTGCTGCGGAC 14556  
15596 GCGGCGCTCACCGCGCAAGCTCGCGCGGCGCGCGCGCGCGCGCGCGCTGCTGCGCGAC 15655  
14557 CAGCGGTACCACTTACATGAACTCGGACCGGACACCGCTTACCAACCGCTTACCGAC 14616  
15656 CCGGAACTGGAATCTTCTGCTCTTCTGCGCTCATCGCGGCTGCTGCGGCGAGTGGCAAC 15715  
14617 GACAACTCCCAACACCGCGGACCGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 14676  
15716 CAGCGGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15775  
14677 CAAACCCACCTCTCAACCAACCTCGCG----- 14703  
15776 CCGGCGCTCGCGGACCTCGTTCGCTGGGCGCGTGGGCGGAGCGCGGATGGCGCGC 15835  
14704 ----- 14746  
15836 GACGATGCGGTTTCGAGACCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15895  
14747 ----- 14760  
15896 GCGATGACGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15955  
14761 ACCACACCGCTCGGACCTCCCGACCTTCCACCGCTTCCAAACCGGCTTCACTGCGCTCAA 14820

15956 GTGAGTGGCAGCGCTACGCAACCGCTGTTCACCTCGCGCGCGCGCGCGCGCGCTGATCGCC 16015  
14821 CCAACCGGCAAGCGAGGACCGCTCAACGAGCGGAGCGCGTGAAGCAACCGGACCGCA 14880  
16016 GCGTGGCGGAGGTTCGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16075  
14881 TCAACCGCGCTGCGGTGATGCTCTGCGGCGAAGTCTCCGAGGAGCGGAGACGAGAGCTG 14940  
16076 GCGTCCGAGGTGCTACCGCGGTTCGCGCGCTGGCGGAAACCGGAGCACTGGCGCTGCTG 16135  
14941 TTGCGCTGGTGGCGACCCATGCGCGCTGTGTGGCGCATGCGCACTCCGAAAGTATC 15000  
16136 ACCGACCTCGTCGCGACCGAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16195  
15001 GTTCGGAACAGGCGCTTCAAGAGCTGGTGTGATCTCTCGCGCGCAATTCAGCTTGT 15060  
16196 CCGGAGGCGCGCGCTTCGCGGAGCTCGGCTTCGACTCGCTGACCGCGGTGAGCTCGCG 16255  
15061 AATCGACTGTGCTGAGCTTGAACCTGCGGTTCGCGCGCGCGCGCGCGCGCTTCGATTCACCC 15120  
16256 AAGCGCTGGGCGCGCGGACCGGCTGTCTGCGCGCGGAGATCTCTCGCGCGGTGCTG- --AA 16372  
15121 ACTCCGATGGCGCTTTCGCGGTTCCTCGGCGCGCGGATGCTCGGAGCGGACACAGGACG 15180  
16316 ACACCGCTGGAACCTCGCGCGGAGTCTCTCGCGCGGAGTCTCTCGCGCGGTGCTG- --AA 16372  
15181 ACCACTGTGCGCGTAACTGCGGTTCGCGCGCGCGGATGCTCGGAGCGGACACAGGACG 15240  
16373 GTCGCGCGCGGTGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16432  
15241 GCGTGTGCGTACCGCGGTGATGACGCGGTTCGATGATCTCTGCGAGGTGCTGAGTGT 15300  
16433 GCGTGTGCGTTCGCGCGGCGGTGAGTCCCGGAAAGCTGTGAGGACCTGCTGCGCTTC 16492  
15301 GCGCATGACGCGATCGCGGATTCGCGAACCGTGGGTGGGACCTCGACACGCTGTAC 15360  
16493 GGCACCGAGCGGATCAGGAGTTCGCGTCAACCGCGGTGCGAGCGCGGACCTCTTC 16552  
15361 AACCGGACCGGACACACGAGTACACCGGAGCGGCGGATCTCTTTACGAC 15420  
16553 GACCGGACCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16612  
15421 GCAGCAATTCGATCCGAGTCTCTGCTATCAGTCCGCGTGGAGGCGCTGCGCGTGGAC 15480  
16613 GCGGAGGTTTGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16672  
15481 CCGCAGCAGCGGCTGCTGCGAAACAGCGTGGGAGGAGCATCGAACCGCTGATCAAC 15540  
16673 CCGCAGCAGCGGCTCTGCTGGAGACCACTGGGAGTCTTCGAGCGCGCGCGGATCGCG 16732  
15541 CCGCAGCAGCTCGTGGGACACCAACCGGCGTCTTCGCGCGGCTGAGCTTACGAGTAC 15600  
16733 CCGGAAACCGCTCGGATCCACCTGACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16792  
15601 GCGCGCGCTTCCACAGCTCCGCGAGGTTTCGAGGCGTATCTCGGCGCGGAGCGCA 15660  
16793 GCGCTGGGCG-----GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16843  
15661 GGCAGTATCGCGTGGGTGCTGCGCTAGCTCTCGCGCTGGAGGTTTCGCGCGCTTCA 15720  
16844 CCGAGTGTCTCCGCGCGGAGTGTGATGCTTCTGAGGAGCGCGCGCGCTTAC 16903  
15721 GTGACACTGCGTCTTTCGCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15780  
16904 GTGACACTGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16963  
15781 TCGGCGGAGTTCATGCGCGCTCGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 15840  
16964 AACGCGGAGAGCAACCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17023  
15841 TTGCTGAGTTCGCGCGGACGCGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15900

D	b	12656	CTGACGGCCGGTGA	CGTGATGTGTGGAGGCGCATGGTA	CGGGTACGACGCTCGGTGAT	12715
Q	y	12410	TGCGCGAAACCGGACCGGGGTT	-----	-----	12432
D	b	12716	CCGATCGAGGCGAGCGGCTGT	TTGGCGACGTATGGCGGGATCGTGAGCCTGAGCGGCGG	12775	
Q	y	12433	-----TTTCGTGGGGATCA	ATCTCGGAGGACTACACCAACCGGATACA	-----	12472
D	b	12776	TTGTTTGGGTT	CGGTGAAGT	CGAATCTGGGGCATACGACGGCTGCTCGCGGTGTGGCG	12835
Q	y	12473	-----	-----	-----	12472
D	b	12836	GGCGTTATCAAGATGGT	TTGGCGATGGCGCATATGGTGTGGTCCGCGGACGTTGCATGTG	12895	
Q	y	12473	-----	CACATCAGCCCTCAAAACGACGTCAGGGGTACTGCTCACTGGCAGC	12519	
D	b	12896	GATGCGCCTTCTTCG	ATGTGACTGGTCCGAGGGTGCGGTGGAGCTGCTCAGTGAACGAC	12955	
Q	y	12520	GGGGCAAGCATTTCTG	CTCAGCCGTAT	-----CTCTCACAACTTC	12558
D	b	12956	GGCGCTGCGCGAGACGGT	CGGGTGCGGCGGGCGGGTGTCTCTCTCCCTCGGCATCAGC	13015	
Q	y	12559	GGGCTCGAAGGCCCTCG	GATCACTATCGACACGGCGTGTCTCTCTCGCTCGTCCGCTG	12618	
D	b	13016	GGTACCAATGTG	ATGTCTATCTCGTTCGAGCAGGCGCCGGGCGCCAGCGCATCGCCCGGCC	13075	
Q	y	12619	CATCTGGCCTGCC	CAAGCGCTCCGGTTCG	-GTCAATGTCAACCATGGCGCTCGCAGAGCGGCGC	12677
D	b	13076	GGTGGCGGGCGG	CAAGCGGGTGCCTGTCCGTTGCTCTCTCGGGCGGTGGCCGAGT	13135	
Q	y	12678	CTCCGTATGGCACT	CTCCTCTTCAACGAGTTCTC	-----	12716
D	b	13136	GCCTCTGGGGCCAG	CGCCGCCCTGCTCGACACCTCCAGGCCGACCCGACCGCGAA	13195	
Q	y	12717	-----	TGCGCAGGGGGCCTGGCGGACAGAGCGCGGTGCAGCGGCTTTTGGCGGGCG	12768	
D	b	13196	CTCGTCGATGT	CGCACTGTCTTGGCGACACACCGGTCCTCGGCTTCGAGCAGCGGGCGGCC	13255	
Q	y	12769	GGCGACGGAGACGG	CTGCTCCGAGGTTGGGGATGCTGCTGCTGAGCGGCTCTCCGAC	12828	
D	b	13256	GTCTGGCGAGAG	CGCCACACAGTGA	TCGCCTCGTGGGGCGCTGGCCGCGCACCGC	13315
Q	y	12829	GCCCGCGCAACGG	TCAACGTTCTTGGCCGCTGCTCCGCGGACGCGCGCTCAACACGAGAC	12888	
D	b	13316	CCCGACCCCGCGT	CTCTGAGGGCGAGGCGCGCGGACCGCGCGCGCTGCTGTTC	13375	
Q	y	12889	GGCGAAGCAACGG	CGCTGACCGACCCACAGGTGCTTCAAGTCAAGGTCAATCGCCGAC	12948	
D	b	13376	ACCGGACAGGGC	ACGACGCGGCGGCGCATATGGGGCGTGAAC	CTCACGAGGTGCAGCGCGAG	13435
Q	y	12949	GCTTTGGCAACGC	ACACCTCTCCCTCGCGATGTCGATGGTGGAGGCC	-----	12999
D	b	13436	TTCCGCGCGCGT	TCACACGGGTGTGTGCGGTTTCGACCCGCTGTTGACCGGGCGGCTG	13495	
Q	y	13000	CACGGCACGGGAC	CAACCTTGGCGGACCGCGATCGAGGCTCAAGCCCTCGTTCGA	-AGCCTA	13058
D	b	13496	CGCGAGGTGT	GTTCGCGGAGGACGCGACGACAGGCGCGCACTGCTGGACGAGACCGGT	13555	
Q	y	13059	CGGTACGAGACCG	CCCCCAACGGCGCCCTCTTGGTTCGGAACCTCAAGTCCAAATCAG	CGG	13118
D	b	13556	TGACGACGCGGCT	CTGTTCCGCGTCGAGGTGGCGCTTCTCCGCTGCTGGAGAGTTGG	13615	
Q	y	13119	GCATCTC	-----	-----ATGGCGCTGCGGGTGTG	13143
D	b	13616	GGTGTCCGTCCG	ACTTCTGTGGCGGCCCATTCATCGGTGAGATCGCGCGGCGCACGCTC	13675	
Q	y	13144	GGCGGGTCA	TCAAGATGG	-----TGATGGCGCTCGGAAATGGTCTGCTG	13188
D	b	13676	CGCGGGTGT	GTGAGTGGAGGCGCTCGCTGCTGGTGGCGCGGCGGACGCTGATG	13735	
Q	y	13189	CCGCGGACGTT	GATGTGGATGAGCGCTGCCGCGATGTGGACTGTGTCGCGGGTGGGTG	13248	
D	b	13736	CAGCGCTGCG	ACCGGCGCGGATGTCGGGATCCAGGCGCCACCGAGGACGAGATCGG	13795	

QY	13299	CAGCTGTCACGGAGACCGTGTCCCTTGCGCCCGCGGGAGGGGGCGC-----	13299
Db	13796	GCGCACCTCGACGACACGCTGGCGATCGCCGCCGTCAACGGCCGCAGTCCGTGGTGATC	13855
QY	13295	-----TACGCGGGCAGGAGTGTCTTTCTGCGCGGCGCGCAAG	13313
Db	13956	TCCGCTGACGAGGAGCGCCCGAACAAGATCGCCGCCACGTTCCGCCGAACGCGGCGCAAG	13915
QY	13314	ATCATTTGGCGTTCAGCGGACCA-----AC	13338
Db	13916	ACCAAGCGGCTCGGGTGAGCCAATGCCCTTCACTCGCCCGATGGACCGGGATGCTGGAC	13975
QY	13339	GCCACAGTCATCTTCGACGAGACACCGCCCAACAATCCCGTCACACACACC CGCGAC	13398
Db	13976	GCTTTCGGATGCTCCGAGGGGCTGACTACCGGGGCGCGGCATCCGCTCGTCTCC	14035
QY	13399	GACGTCCGGAGAAATACGCCCGACGAGGATGCGGTAGTGGCGATGA-----	13448
Db	14036	GACCTCACCGCGCGCGCACGATGCGAGGTGTGACCGCGAGTACTGGTGCGG	14095
QY	13449	-----	13448
Db	14096	CACGTTCGAGAGCGCTGCGGTTTCGCGCACTCGCTGCGGACGTGCGGACGCCGGGGCC	14155
QY	13449	-----GGTGTCTCGCGCAAGTCCAGGGGTGTGCCGTGGCTGGTGTGTC	13490
Db	14156	ACCACCTTCTTGGAACTGGGCTCCGACGGCTGCTGACCCGATGCGCGGAGCACCCCTC	14215
QY	13491	GGCCAAAGTC-----GCAGCGGGCCCTGCGCGCCCGAGGCCAG	13527
Db	14216	GGTGACGACCAACGACGCGCAACTGGTGGCGATGTCTGCGCGCGCGCGCGAGGAAC TG	14275
QY	13528	GCCCTGACGCGCCACTCACCGACACACCGCGCTCGACCTCGCGACGTCGGGTACAC-	13586
Db	14276	GCGCGGCGACCGCCCTTGGCCGCTTCAGGTGGCGGCGTGGACGTGNACTGGCGGCG	14335
QY	13587	--CCTGCGCCACGCGCGCGCTGTTTGGACCA--	13618
Db	14336	TACCTCGCGGACCGCGCGCGCGACGCAACCGCACTTCCGCACTTCCAGCACGCG	14395
QY	13619	-----CGCGCACTTCATCGCGCGCGCGCGGACAC	13650
Db	14396	TACTACTGCGCGCACTGTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	14455
QY	13651	TTCTTCGAAGCACTCCAGCACTCGCGCGAGCGAACCCACCGCCCGCTCATCCAC- --	13707
Db	14456	CAGCACTGTGGCGCTGTGGAGCGCGCGACCGCCCGCACTCGCGACATCTCTCGG	14515
QY	13708	-----AGCAG	13712
Db	14516	CTGGCGCAACAGGACCTCACGCGGTGGACTCCCTGTCGCCGCCCTCACTCTGTGGCGG	14575
QY	13713	CGCCCCAGCGGACCGGGACCGGGAGCGCGCAGGAAGAAGACCGCAT-----	13759
Db	14576	CGCGCAACAGGAGAGCACTCTTGGACACCTCGCTGCTACCGCTGGAGTGGACACGA	14635
QY	13760	----TCATCTGTCGCGACAGGGACCCCAACGCGCGCGATGSCCAACCGCGCTTACCAC	13815
Db	14636	CTGACCAAGCGACCGCCCGGTCTCTGACGCGCACCTGGTGTGCTCGCGCGCC	14695
QY	13816	ACCCACCGGCTTTGCGCGCGGACCTCAACGACATCTGACCACTCTCGACCCCGACCTC	13875
Db	14696	ACCGCGGCGGACACGACGACCCCTCTCTGACGCGCTGGCGACGCCCTCGCGCTCGCAGCG	14755
QY	13876	GACCAACCCCTCTCTCCCTCTCTCACCGAGGACCCCAACCC-----	13918
Db	14756	GCGCGGTGCTGCTGCTGTTCTTGGACGACTCTTGGCGGACCGCGGGTGTCTCGCCGAA	14815
QY	13919	-----AGGACACCAACACTCTGAAGAGCGGCGCGCACTGTCTCAGCAGACCCGCTAC	13971
Db	14816	CGACTGGCGCGACCGCCAGCTGGACGCGCGGACCGCGGACCGAGGTGTCTCGCTGCTCGCGCTC	14875







CC sequence is a *Streptomyces noursei* nys2 DNA of nystatin PKS gene cluster.

Sequence 27541 BP; 3517 A; 10766 C; 9529 G; 3729 T; 0 other;  
XX SQ

Query Match 11.2%; Score 3443.4; DB 22; Length 27541;  
Best Local Similarity 52.3%; Pred. No. 0;  
Matches 11367; Conservative 0; Mismatches 8466; Indels 1914; Gaps 93;

Qy	6241	GAGGCTTTCTGTACCGAGCCGATCGCCCATCGTTGGCATGCGCTGTGTCTTCCCGCGCGGA	6300
Db	6422	GAGTCGGCGGCCCAAGAAACCGTGGCCATCATCGCATGACCTGTCTGTCTACCCCGCGCGC	6481
Qy	6301	GTGACCTCGGGAGCGACTTCTGGATCTGATCTCTCTCCGAGCAGACGATCGGCGGA	6360
Db	6482	GTCCGACGCCCGAAGACCTCTGGCGATGGTCAGGCCGGCAGCAGCGCTCACTCCCG	6541
Qy	6361	TTCCCAACCAACCGCGGTGGACCTTGGAACA CGCTCTTACGACCCGACCCCGACACCCC	6420
Db	6542	TTCCCAACCAACCGCGGTGGACCTTGAGGCGCTGCGCGCGCGCGACCGC-----	6595
Qy	6421	GGCACTGTACTACCCGAAACGGCGGATCTCTTACGACGAGGCCACTTCGACGCGAA	6480
Db	6596	-----TCCGGCGGATCTCTGACGACGACCCGACTTCGACGCGGAC	6637
Qy	6481	TTCTTTGGCATCAGCCCCCGGAGCCCTCGCCATGGAACCCCGACGAACTCTCTCTC	6540
Db	6638	TTCTTTGGCATCTCGCCGCGGAGCGGTGGCCATGGAACCCCGAACAGCGCTGTCTCTG	6697
Qy	6541	GAAAACCCCTGGGAAACCATCGAAACCGCGGATCAACCCCAACCCCTCCACGCGACC	6600
Db	6698	GAATCCGCTGGGAGGCTTCGAACGCGCGCCGATCGACCCGAGCTCGTAGGAGCAGC	6757
Qy	6601	CCCAACGGAGTCTTCAACGGGCAACAACGGAAGAGATACGCACTTCCGCTGCAACAACG	6660
Db	6758	CGCAACGGAGTCTTCACTCGCGCGGATGGCCCAAGACTACCGGGTCGCGCCCGCAGCGC	6817
Qy	6661	GGCAGTCAACCGATGTTTCGCACTACACGGAAACCGCGACGCTCTCCGCTCGT	6720
Db	6818	G-----CCGAGGCTTCCAACTCACCGGCAACACCGGACGCTGTCTCGGCGC	6868
Qy	6721	ATCTCTTACAGTTTGTGTTTGAAGGTCTCTCGCGTGTCTGTGGACAGCTTGTCTCTCG	6780
Db	6869	ATCTCTTACACTTTCGACAGTTCGGCCCGCCGCTCACCGTCGACACCGCTCTCTCTCC	6928
Qy	6781	TGTTGTGTGCTTTCATCTGTGCTGTGAGCGTTTGGTGCGGGTAGTCTCGATGCG	6840
Db	6929	TCCCTGTCTCGCTTCACTTCGCAACCGAGCGCTCGGCGCGGAGTGACCCCTCGCC	6988
Qy	6841	CTTTCGGGGGTGTAGCGTGTGTCTCTCGGCTGCTCTGTGGAGTTTTCGCGCGCAG	6900
Db	6989	CTCGCCGCGCGTCAACATCTGTTCGGGCCCGCGACCTTCTATCGMAATGGCGCCGAC	7048
Qy	6901	CGGGGTCTGCGCGGACGGGCAATTCAAGCGCTTCTCGCGCGCGCGGACGGGACCGGC	6960
Db	7049	GGCGGGCTCTCCGCGAGCGCGCTGCGCTCTCTTCGGGCAACCGCGAGCGCAACGGC	7108
Qy	6961	TGGGTGAGGGTGTGGGATGTCTGTGTGAGCGGCTCTTCGACGCGCCATCGCAACGTT	7020
Db	7109	TGGGCCGAAGCGTTCGCGATCTCTGTCTGTGAACGGCTGTTCGACGCGCTTCGCAACGGC	7168
Qy	7021	CACCGTCTCTGCGCGTGTGCTGGCAGTTCGCTCAACGAGACGCTGTGGAGCAACGTT	7080
Db	7169	CACGAGTCTCTGCGCTGTCTCGGGGCAACCGCTTCAACGAGACGGCGCTTCAACGCG	7228
Qy	7081	CTGACCGCGCCCAACGGGCGGTCCCAGACGCTGTATCCGCGCAGGCGCTTCGCCAACCGC	7140
Db	7229	CTGACCGCGCCCAACGGGCGCTCCCAGACGCTTCCCAGACGCTTATCCAGCAGGCGCT	7288
Qy	7141	GGCTGTCTGCGCGTGTGATGTGACGCGTGTGAGGCCCAACGGCACCGGCAACCTTTGGC	7200
Db	7289	CGACTCGCCCGCGGGACATCGACGTGTCTGAGGCGCAACGGCACCGGCAACCTTCGCG	7348
Qy	7201	GACCCGATCAGGCGCCAGGCGCTCTCTCGGACCTTACGGAACGAGCGGTTCGCGCGAGGG	7260

Db 25913 GCGAGCGAAGCGGTGTTGGTACGGGTGTTACGGGTGTTGGTGGGTGTTGGTGGCCGG 25972  
Qy  
Db 29281 CATCTGTGGAGCGACCGGCTACGGCATCTGTTCTGGCGGTGCGGCGGACCGGAC 29340  
Qy  
Db 25973 CATCTGGTGGGTGTTGGTGGGTGCGGCAATTTGTTGACAGTCTGTTCTGGTGGGT 26032  
Qy  
Db 29341 GCGAGGGTGCCTGGAGTTGCGGCGGAGTCTGGTGGGCTCGGCGGACGAGTGGAGTGC 29400  
Qy  
Db 26033 GCTGCGGGTGCCTGGGTTGCTGCGGAGTTGGAGTCTGTTGGGCGCGGGTGTGGTT 26092  
Qy  
Db 29401 GTCTGCTGCGACCGGCGGACCGGAGCAGCTGGCGGACCTCTGACAGCATCCCGAC 29460  
Qy  
Db 26093 GCGGCTGTGATGTGGTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26152  
Qy  
Db 29461 GATCGGCGCTGACCGGTGCTGACAGTGGCGGATCTGACAGCGGCGTATCAG 29520  
Qy  
Db 26153 TCGTATCGTGTCTGCGGTGCTGATGCGGTGCTGTTGATGACGCTGTTGGGT 26212  
Qy  
Db 29521 TCGCTGTCTGCGGAGCGCTCGGGGCGTCTCTCGGGCCAGGCGGAGCGCTGCTGCTT 29580  
Qy  
Db 26213 TCGTTGACCGCGGAGCGTGGCTGCGGTGTTGCGTCTGCGAAGTGGATGGTGGGAAC 26272  
Qy  
Db 29581 CTCGAGAGCTGACCGCGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 29640  
Qy  
Db 26273 CTCGATGAGCGAGCGTGTCTGATCTGAGCGGCTTGTGTTGCTGCTGCTGCTGCTG 26332  
Qy  
Db 29641 GCGGTGCTGCTGCTGCGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 29700  
Qy  
Db 26333 GGTGTGTTGCGGGGTGCGGTGAGGCAATGCGGCGGGAATGCGTGTGTTGACGGG 26392  
Qy  
Db 29701 CTGCTCTGCTGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 29760  
Qy  
Db 26393 TTGATGTTTCATCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26452  
Qy  
Db 29761 GAAGAGGCGACAGGATGAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 29820  
Qy  
Db 26453 GATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26512  
Qy  
Db 29821 GCGGGAATGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 29880  
Qy  
Db 26513 TCGGGTATGCGGTGTTGACGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26572  
Qy  
Db 29881 GACGCGAGCGGTTCCTGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 29940  
Qy  
Db 26573 ACGGGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26632  
Qy  
Db 29941 GGTTCGCGACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 30000  
Qy  
Db 26633 GATATGCGACCGCT-----CCTTCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26670  
Qy  
Db 30001 GCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30060  
Qy  
Db 26671 GCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 26728  
Qy  
Db 30061 CGTTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30120  
Qy  
Db 26729 CGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26788  
Qy  
Db 30121 CATGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 30180  
Qy  
Db 26789 AGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 26848  
Qy  
Db 30181 CCGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 30240  
Qy  
Db 26849 CCGGACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26908  
Qy  
Db 30241 ACGGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 30300  
Qy  
Db 26909 ACGGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 26968  
Qy  
Db 30301 GAGCACTTGGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 30343  
Qy  
Db 26969 GAGCACTTGGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 27011

## RESULT 9

AAD17185  
ID AAD17185 standard; DNA; 27541 BP.

AC AAD17185;

DT 29-NOV-2001 (first entry)

DE Streptomyces noursei ny82 DNA of nystatin PKS gene cluster.

KW Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster;  
KW antifungal; antibiotic; ny82; ds.

OS Streptomyces noursei.

FH Key Location/Qualifiers  
CDS complement (454..1191)

FT /\*tag= a

FT /product= "NysF protein"

FT /note= "CDS does not include start codon"

FT /\*tag= b

FT /product= "NysG protein"

FT /note= "CDS does not include start codon"

FT /\*tag= c

FT /product= "NysH protein"

FT /note= "CDS does not include start codon"

FT /\*tag= d

FT /product= "NysD3 protein"

FT /\*tag= e

FT /product= "NysI partial protein"

FT /note= "CDS does not include stop codon"

XX WO200159126-A2.

XX 16-AUG-2001.

XX 08-FEB-2001; 2001WO-GB00509.

XX 08-FEB-2000; 2000GB-0002840.

XX 10-APR-2000; 2000GB-0008786.

XX 14-APR-2000; 2000GB-0009387.

XX (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.

XX (SNTF) SINTEF STIPTTELSEN IND TEK FORSK.

XX (ALPH-) ALPHARMA AS.

XX (SINV-) SINVENT AS.

XX (DZIE/) DZIEGLEWSKA H.

XX (ZOTC/) ZOTCHEV S B.

XX (SEKU/) SEKUROVA O N.

XX (FJAE/) FJAERVIK E.

XX (BRAU/) BRAUTASET T.

XX (STRO/) STROM A R.

XX Zotchev SB, Sekurova ON, Fjaervik E, Brautaset T, Strom AR;  
PI Valla S, Ellingsen TE, Sletta H, Gulliksen O;  
XX WPI; 2001-557614/62.  
DR P-PSDB; AAE10138, AAE10139, AAE10140, AAE10141, AAE10142.  
XX New nystatin polyketide synthase polynucleotides and polypeptides,  
PT useful as antibiotics and antifungals -  
XX Claim 2; Page 151-166; 266pp; English.  
XX The present invention relates to the cloning and sequencing of the gene  
CC cluster encoding a modular type I polyketide synthase (PKS) enzyme  
CC involved in the biosynthesis of the macrolide antibiotic nystatin.  
CC The nystatin PKS is useful as antifungal antibiotics. The present



21884 TGCGCGCTGGTCAGCGACGGCGCCGACGCCACTGCGCCCGTTCCCCACCAACCGCGCGTGG 21943 Db  
24907 GACCTGGACACGCTCTACGACCCCGACCCCGACACCCCGGACAGCTGTCTACACCCGGAAC 24966 Qy  
21944 GACCTGGACAACTCTACGACCCCGACCCCGACCGCGCGCGGCGGACCCACGTCGCGGCC 22003 Db  
24967 GCGGATTCCTCTAGCGGCGACGGCCACTTTCGAGCGCCGAATCTTTCGGGATCAAGCCCGCC 25026 Qy  
22004 GCGCGCTTCCTGACGACGCGCGCTCTCTTCGAGCGCGACTTCTTCGGGATGAGCGCGCGC 22063 Db  
25027 GAAGCCTCGCCATGAGACCCCGACGAAACGACTCTCTCGAAGACCGCTTGGGAACCATC 25086 Qy  
22064 GAGGCGATGGCCACCGACTCCGAGCAGCGCTCTGCTCGAATCTCTCTGGGAAGCGTTC 22123 Db  
25087 GAAACGCGCGGATCAACCCCGACACCTCTCAAGCGACCCCGACCGGAGTCTTTCGCGGA 25146 Qy  
22124 GAAAGCGCGGATCGAACCCCGCTCACTGCGGACTTCGGGACACCGCGCTCTTCGCGGCG 22193 Db  
25147 ATCAAGCTCAAGACCAACCGCGGATATCCGCGAAGCGGTGATGTGGAGACCATCGAG 25206 Qy  
22184 GTCATGTACAACGACTACG-----GCACCACCTGACCGCGACGAGTACGAG 22231 Db  
25207 GCGTACGCTGACCGGACGTTGGGAAGTGTGGGTTCGCGCGGCTGCGCTACAGCTC 25266 Qy  
22232 GCGTTCGCGGCAACCGGACGCGCCCGAGCGTCCCTCCGCGCGGTCTCTACACCTC 22291 Db  
25267 GCGCTCGAAGGCGCGCGTGTGCGTGGATACGGGTGTTGCTGCTGTTGGTGGGTTG 25326 Qy  
22292 GCGCTGGAAGGCCGCGCTACGCTGGGACACCGCTGCTCTCTCTGTTGGTGGCTG 22351 Db  
25327 CATTTGGCGCGACGCGTTGCGTGGGTGAGTGTTCGATGCGCTTCCCGGGGTG 25386 Qy  
22352 CACTGGCGCGCAGCGTTGCGGCGGGGAGTCTGCTGGCGTTGGCGGTGGTGTG 22411 Db  
25387 ACGGTGATGCTCTCCGGTACGTTTGTGGAGTCTTCACTGACGCGGGTTCGCGCG 25446 Qy  
22412 ACGGTGATGACGCGGACGCTTGTGGAGTCTTCCGCGACGCGGGTCTGGCGCT 22471 Db  
25447 GACGCGCGTGAAGGCTATTTCGCGCGTGTGACGCTACCGGTCGCGCGAGGTTG 25506 Qy  
22472 GATGGTCTGTAAGGCTTTCGCGAGGCGCGGACGGGTGGCTGGTTCGAGGGGCTC 22531 Db  
25507 GGGATGCTGCTGGTGGAGCGGTCTCCGACGCGCGTTCGCAAGGTACCGTGTCTTGGCC 25566 Qy  
22532 GGCATGCTGCTCTGGAGCGGAGTCGAGCGGCTGCGCAACGGTCAACGAGATCTTGGCC 22591 Db  
25567 GTGGTGGTGGAGTGGCTCAACGAGGAGGTGCGAGCAACGGTCTGACCGCGGCCAAC 25626 Qy  
22592 GTGGTGGCGGCTTCGCGCGTCAACGAGGACGGTGGCTCCACCGGTCTGACCGCGCCAAC 22651 Db  
25627 GGGCCCTCCAGCAGCGTGTCTCCGTCAAGGCGCTGGCCCAATGCGGGACTGACCCCGGC 25686 Qy  
22652 GCGCGTCCAGCAGCGGTGATCTCGTCAAGGCGTTGGCCAGTGGCGGCTGTCCAGCGCC 22711 Db  
25687 GATGTCGACGCAAGTGGAGGCGCACCGCACCGGACCACTCTTGGGGAACCGGATCGAGGCC 25746 Qy  
22712 GACGTGGAACGCGTTGAGGCGCACGGCACCGGTACGACGCTCGGTGACCCGATCGAGGCC 22771 Db  
25747 CAGGCACTCTGGCGGCTTACGGAACAAACCGCGCCCAACCGCGGCTTGTGGTGGGA 25806 Qy  
22772 CAGGCGCTCTGGCCACCTACGCTGCGGACCGCGACCCCGAGAACCGCTGTGCTCGCG 22831 Db  
25807 TCCTCAAACTCAACATTCGGGACGCAAGGCGCGCGCGGCTGGCGGAGTCACTCAAG 25866 Qy  
22832 TCGATCAAGTCCAACTCGGTCAACCCAGGACGCGCGGTGTGCGCGGTGTCTCAAG 22891 Db  
25867 ATGGTATGCGCTGCGCAACCGGCTGTCTGCCACAGACCCCTCCAGTGGACGAGCCACC 25926 Qy  
22892 ATGGTATGCGGATGCGGACGCGCGTGTCTGCCGACACCTTGCACTGACGCGCGCTCC 22951 Db  
25927 CCCCAGGTGCACTGTGTCACAGGCGGAGTCAACTCTGACACAAACCGGTGCGCTGGGCC 25986 Qy  
22952 TCGCACGTGATTTGGAGCGTTCGCGCGCTCGAACTGCTCAACGAGCAGACCGCTTGGCGG 23011 Db

25987 GCGGACCCGCGCGCGCGCCACGCGCCGCGTGTCTATCTTGGGCTCAGCGCGACC 26046 Qy  
23012 G-----AGACCGGCGGCGCGTTCGCGCGGTGTCTCTCTCGGATCAGCGCGACC 23065 Db  
26047 AACGCCACATATCTCTCGAAGAGCACCCACTCCCCAGGACAGGATACCGACGACGAA 26106 Qy  
23066 AACGCCACGCTGTCATCGAGCAGTCCCGGAC-----CGCGTCCCGCCACG 23113 Db  
26107 CGCGTCGCAACGACGACGCGCTCGCCCATCCCTCTCTTCCGTCGCGGTGTGCGG 26166 Qy  
23114 CCGCGTCCGCGACCGGTTCGTGAGGAACCGCGCGCGTCCCTTGGGCTGTTCGCG 23173 Db  
26167 AGGTCTGAGGCGCGGTTCGCGCGCAGGCGTTCGCGCAGTACGTGTGACGCGCGC 26226 Qy  
23174 AAGACCCCGACGCGCTTCGCGACGAGCGCGCGCTCTCGCCACGTCGAGGCGCCAC 23233 Db  
26227 CCGGACATGTCACTGCGCGACATTTGGTTCGGGTCTGGCGCGGCGCGGCGGTACTGGA 26286 Qy  
23234 CCGGACGTGCGCGCGCTCGACATCAGTCTCTCTGATCGCCACCGCAGCGCTTCGAC 23293 Db  
26287 CACGCGCGGTCTCTGCGCGCGGACCGCGAGGAACCTGGCGAGGCACTGACAGCCCTG 26346 Qy  
23294 CACGCGCGGTCTCTGCGGACCGCGCGGCGGCGCTTGGCGCGCTTCAACCGCTTC 23353 Db  
26347 GCAGCGCGGAACCCCGACCCACATCACAGGCGCACACCGCGGCGGTGACCGCGCG 26406 Qy  
23354 GCGCGCGGAGACCGACCCCGCGCTCACCGGACCGTCCG-----CACCGCG 23404 Db  
26407 GCGGCTGCTGCTGCTTCCCGGACAGGCGCGGCGAGTGGCGGAGTGGGCTGACCTG 26466 Qy  
23405 GCGACGCGCTCTCTTCTCGCGCGGCGCTCCCAACGCGTGGCATGGCGCGCTCTC 23464 Db  
26467 CTCACCTCTCACCGGTCTCGCGAACACATCGACGATCGAGAAAGGCGCTCACCCCG 26526 Qy  
23465 TACGAGCGGTTCGCGCGCTTCGCGGAGCGCTTCGACACCGTCTCACCGCTTCAGCGG 23524 Db  
26527 TGGGTGCGCTGCTGCTGCGGACATCTGCAACCGCGCGCGGACCGGATGGCA 26586 Qy  
23525 GAACTCGGCGACCCCTTCGCGACATCATCTGGGCGAGGAGCGTCAACTCG---TCGAC 23581 Db  
26587 CAGCGGAGGTGTTCAGCGCGGTCTTTCAGCATATGCTCTCTCGCGCGCTGTGG 26646 Qy  
23582 CGGACGCGCTACACCAACCGCGCTTTCGCGCATCGAGTGGCACTCTTCCGCGCTCTG 23641 Db  
26647 CGCTCTACGCACTCGAACCGCGGTCTTCGCGCACTCCACGAGAGAAATCGCGCG 26706 Qy  
23642 GAAGCTTGGGCGATCACACCGGACTTCGTGGCGCGGCACTCTCATCGGAGATCGCGCC 23701 Db  
26707 GCGCACATCTGCGCGCACTCAGCCTGAAAGACCGCGCAAAACCGTTGCACTGGCGGAC 26766 Qy  
23702 GCACAGTTCGCGGCGTCTCTCTTCGCGAGCGCTTCGCGCTCTGTGGCGCGCGCC 23761 Db  
26767 GCGGCACTGGCGCGCGTACGAGGCGCGGCGGCGCATGCGCTCTACTGCCCTTGGCGCGCG 26826 Qy  
23762 GTGCTGATGCACTGCTGCGCGGAGGCGGCGGATGATCGCGTTCAGGCGCACGAGGAC 23821 Db  
26827 GACGTGACGAGCTCATTTTCGGAACGGTGGGAAGGCGAGTGTGGTGGGACGCTCAAC 26886 Qy  
23822 GAGGTCTGCGCGCTCTCACCGA-----CGAGCTCTCATCGCGCGCTTCAAC 23869 Db  
26887 GCGCGCCCACTCCACACCGCTCTCGCGGACACCAAGGCGGTGGATGAGGTGTGGCGGAC 26946 Qy  
23870 AGCCGCGCTCGTGTCTCTCGGCTACGAGAACGCGCCCTCGCGTTCGCGCGGAC 23929 Db  
26947 TGCACGACACCGCGCTACGCGGCGCAACCGCATCCCGTGTGATACGCTTCCACTGCCCG 27006 Qy  
23930 TTCGCGGACGAGGCGCGCGCACCGGCGGTGCGCGTTCAGCGCTTCCACTCGCGG 23989 Db  
27007 CAGGTCCAAACCTTCCAGGAGAACTCTGCACTGCTGGGAGACATCACCCCCGAGCGG 27066 Qy  
23990 CTGATGGCGCGGATGCTCGAGACTTTCGCGCGCTGCTCGAGAGGCTTCACTTCCCGCC 24049 Db



QY	22796	CGGTGAACGAGAACTCTCAGAGCCTCGCGAAACCTCTCGACATCGACGCTCTGTCTC	22855	22796	CGGTGAACGAGAACTCTCAGAGCCTCGCGAAACCTCTCGACATCGACGCTCTGTCTC	22855
DB	19776	AGGTATACGCGAAAGTGGCCCTGCGCAGCGCGGACACCGACCCCGCGCTTCGGAC	19835	19776	AGGTATACGCGAAAGTGGCCCTGCGCAGCGCGGACACCGACCCCGCGCTTCGGAC	19835
QY	22856	TGGACAGGTGGTCCCGCAGCTCTCGCCTGGCACCGCCACACACGACGACCAAGCCGGA	22915	22856	TGGACAGGTGGTCCCGCAGCTCTCGCCTGGCACCGCCACACACGACGACCAAGCCGGA	22915
DB	19836	TGCACCCGGCCCTCTCGACGCGCGCAACAACGCGCGCGCTTACGCGACCTTCGGCGCA	19895	19836	TGCACCCGGCCCTCTCGACGCGCGCAACAACGCGCGCGCTTACGCGACCTTCGGCGCA	19895
QY	22916	TCAACACCTTGACCTACACAGAAACCTTGAAACCCCTTCAACCTCCCGACACCAACAAC	22975	22916	TCAACACCTTGACCTACACAGAAACCTTGAAACCCCTTCAACCTCCCGACACCAACAAC	22975
DB	19896	TCAGCGCGCGGCTCGCTGCTTCCCTTGGAAGGCGTCTCGCTCGCGCGCGCGCGCA	19955	19896	TCAGCGCGCGGCTCGCTGCTTCCCTTGGAAGGCGTCTCGCTCGCGCGCGCGCGCA	19955
QY	22976	CCACACAACTTGCGCTCATCGCATCCCG-----GAAACCCAGACCAACCCCAACA	23029	22976	CCACACAACTTGCGCTCATCGCATCCCG-----GAAACCCAGACCAACCCCAACA	23029
DB	19956	CCACCGTCCGCGCGCGTCCCGCGCGCGCGGAGGACACCGTCAACATCGCGCTTACG	20015	19956	CCACCGTCCGCGCGCGTCCCGCGCGCGCGGAGGACACCGTCAACATCGCGCTTACG	20015
QY	23030	TCACCAATCTCTACCAAACTCCACACACGACGACATCCCCCATCCCTCACTGTCA	23089	23030	TCACCAATCTCTACCAAACTCCACACACGACGACATCCCCCATCCCTCACTGTCA	23089
DB	20016	ACGCGCGCGGACCGCTGTGTGTGTGACTTCCCTTGGTCTCCCGAGAGTCCCGCGG	20075	20016	ACGCGCGCGGACCGCTGTGTGTGTGACTTCCCTTGGTCTCCCGAGAGTCCCGCGG	20075
QY	23090	ACCAACCCACACCAACCCCAACAACCTCCACACACACCTTCCACACACCCGACAAAG	23149	23090	ACCAACCCACACCAACCCCAACAACCTTCCACACACACCTTCCACACACCCGACAAAG	23149
DB	20076	ACGCACCGGCGCGCGCACCGTCAACGCGACTCCCTTTCAGAGTGTGAGTGAACCC	20135	20076	ACGCACCGGCGCGCGCACCGTCAACGCGACTCCCTTTCAGAGTGTGAGTGAACCC	20135
QY	23150	CCCAAAACCAACAACGCGACCAATACCGGCTGTCTCTCTCTCGCTCGCCTCGACGAAA	23209	23150	CCCAAAACCAACAACGCGACCAATACCGGCTGTCTCTCTCTCGCTCGCCTCGACGAAA	23209
DB	20136	CGTTCAGGGCGCGCGCGCGCGACCGGCCACCGTGGCGTCTCTCGCGCGCGCGCGG	20195	20136	CGTTCAGGGCGCGCGCGCGCGACCGGCCACCGTGGCGTCTCTCGCGCGCGCGCGG	20195
QY	23210	CACCCACCCACACCCCAACAACCCACACACCGGACCTCTCTCAACCTTCAACCTCCCC	23269	23210	CACCCACCCACACCCCAACAACCCACACACCGGACCTCTCTCAACCTTCAACCTCCCC	23269
DB	20196	ACGCCCTTCGGCGACACCTTCGGCGCACCGGACATCCGACACCGCCCCCGGACCTGG	20255	20196	ACGCCCTTCGGCGACACCTTCGGCGCACCGGACATCCGACACCGCCCCCGGACCTGG	20255
QY	23270	AAACCCACACCAAAACCCCAACAACCCCTCTGTGTACGCGACCAACAACCGCACCA	23329	23270	AAACCCACACCAAAACCCCAACAACCCCTCTGTGTACGCGACCAACAACCGCACCA	23329
DB	20256	CGGCCCTCGCGACGCGCGAAGGGCGCGTCCCGACCTGTGTGTACACACCTTACACCA	20315	20256	CGGCCCTCGCGACGCGCGAAGGGCGCGTCCCGACCTGTGTGTACACACCTTACACCA	20315
QY	23330	CCACCCACCCCAACGACCC-----	23348	23330	CCACCCACCCCAACGACCC-----	23348
DB	20316	CCCGGCGCGCGCGTCCCGGACGCGCGCAACGCCACACCGCGCGCTCTCGCGCTCG	20375	20316	CCCGGCGCGCGCGTCCCGGACGCGCGCAACGCCACACCGCGCGCTCTCGCGCTCG	20375
QY	23349	-----	23348	23349	-----	23348
DB	20376	CCCAACAGTGGTTCGCGACGACGCTTTCGCGACCGCGCGCTGTCTGTACCCGCG	20435	20376	CCCAACAGTGGTTCGCGACGACGCTTTCGCGACCGCGCGCTGTCTGTACCCGCG	20435
QY	23349	-CTTCACACACCCACCCCAAGCCCAACCTTGGGGACTCGCCCGACACACCTCTCGAAC	23407	23349	-CTTCACACACCCACCCCAAGCCCAACCTTGGGGACTCGCCCGACACACCTCTCGAAC	23407
DB	20436	GGCCACGAGGACCGACCCGCGCGCGCGCGCGCGCGCTGTATCCGACCGGCC	20495	20436	GGCCACGAGGACCGACCCGCGCGCGCGCGCGCGCGCTGTATCCGACCGGCC	20495
QY	23408	ACCCACCCACACGCGCGGAATCATCGACTTCCCAACACCCCAACCCCAACACCTTC	23467	23408	ACCCACCCACACGCGCGGAATCATCGACTTCCCAACACCCCAACCCCAACACCTTC	23467
DB	20496	GCACCGAGAACCCCGCGGTTTGGCTCTCTCGACTTCGCTCGCCCGCGACACCGCGCGG	20555	20496	GCACCGAGAACCCCGCGGTTTGGCTCTCTCGACTTCGCTCGCCCGCGACACCGCGCGG	20555
QY	23468	ACCACCTCACCCAAACCTTACCCACCAACCCACCAACCAACCCCAACCTCGGCCATCCG	23527	23468	ACCACCTCACCCAAACCTTACCCACCAACCCACCAACCAACCCCAACCTCGGCCATCCG	23527
DB	20556	ACCCGAGACCTTGGCACCGCTTGGCGCGCAGCAGACGAGCCGACCTTCGCGTCC	20615	20556	ACCCGAGACCTTGGCACCGCTTGGCGCGCAGCAGACGAGCCGACCTTCGCGTCC	20615
QY	23528	CCGGCACCCACACCGCGGCTCACCCCAACACCTTCAACCCCAACCAACCAACCAACCA	23587	23528	CCGGCACCCACACCGCGGCTCACCCCAACACCTTCAACCCCAACCAACCAACCAACCA	23587
DB	20616	GGGGCACCGAGTGTGACGCGCGCGCTGGCGTGTCTCGCTGCGCACCAACCAACCA	20675	20616	GGGGCACCGAGTGTGACGCGCGCGCTGGCGTGTCTCGCTGCGCACCAACCAACCA	20675
QY	23588	CCGCCACCCCGGAAACACCTTATCAACGCGGGAACCGCGCGCTTGGCACCCAC	23647	23588	CCGCCACCCCGGAAACACCTTATCAACGCGGGAACCGCGCGCTTGGCACCCAC	23647
DB	20676	CTTGGAAACCCGAGCGCACCGTCTGTATACCGCGCGCACCGCGCGCTTGGCGGCTCC	20735	20676	CTTGGAAACCCGAGCGCACCGTCTGTATACCGCGCGCACCGCGCGCTTGGCGGCTCC	20735
QY	23648	TCACCCACCACTTACACCCCAACCAACCCCAACCTCTCTTCAACAGCGGAAACCG	23707	23648	TCACCCACCACTTACACCCCAACCAACCCCAACCTCTCTTCAACAGCGGAAACCG	23707
DB	20736	TCGCCCGCACCTTGGTGGCACCCACCGGCTCGCGACCTTGTGTGTGTGTGTGTGTGT	20795	20736	TCGCCCGCACCTTGGTGGCACCCACCGGCTCGCGACCTTGTGTGTGTGTGTGTGTGT	20795
QY	23708	GGCCCCACACCCCGCACCAACCTTCAACCAACCAACCTTCAACCAACCAACCAACCA	23767	23708	GGCCCCACACCCCGCACCAACCTTCAACCAACCAACCTTCAACCAACCAACCAACCA	23767
DB	20796	GCCCGCGCGG				



QY	19110	CATCCCCCAACACCCCTCTCAACCGTATCTCAACCGGAGGATCTCTGAC---GA	19166	16497	GCTGGCTGGCCACCGAGAACTCGGGAATCTGAGAGAGCTGGAGCCACCATGAGCA	16556	
Db	15417	CTCTCCCGCGACGACCGCTCACTCTCTTCTTCACTCCGCGCGGTGGCGGGA	15476	19990	-----	19989	
QY	19167	CGCCACCTTCAACAACTCAGCCCAACCACTCAACAGGTCTCTCGCGCCAAAGCCCA	19226	Db	16557	CGAACCCGACAAGTACGTCTGAGGACATCTCCGGTCTGCTGAAAGAGATCGAGCGGCTGC	16616
Db	15477	CGCCGGGAGCGGACCTGACCTTAGATCAGTCTGACGCGCTGCTGCGGCGCAAACTGAC	15536	QY	19990	-----	20032
QY	19227	CAGCGCCACCTCTCTCCACCAACTCAACCAACACACCCCTCAAGCCCTCTGCTCTTA	19286	Db	16617	CGCGGAGAAAGAACAGTCTGCTGGCGGCGGTGAGCCCGTCTGCGCATCG	16676
Db	15537	CGCGGCCACCACTGACGAGTGCACGCGCCCTCTGACCTGAGCGGTCTGCTCTT	15596	QY	20033	CTGTGCTTCTCCCGCGGAGTGCACCTCTGCGGAGACTTCTGGAATCTGATCTCTCCG	20092
QY	19287	CTCTCCCGCGCGCACCTCTGCGGCGCACCGGCGCAACCACTGAGCGCGCAACGCG	19346	Db	16677	GCTGCGCTTCTCCCGCGGCGTCACTCTCCCGAGGACTCTGCGAGCTGCTGCGGAG	16736
Db	15597	CTCTCCCGCGCGCGGTCTGCGGCGAGCGCGCGGCGGCGGCTACGCGCGCGCAAGC	15656	QY	20093	AGCAGGCGCATCGGCGGATTCCCAACCGGCTGGGACTGCGACACGCTCTACG	20152
QY	19347	CTACCTCGAGCGCTCTGCGCCACACCGCGCACACCACTCTCCCGGCGCACGATCGC	19406	Db	16737	GGCGGAGTCTATCGGCGCTTCTCCCGAGGACCGCGCTGGGACTCTGAGAAGTTGGCGG	16796
Db	15657	CTACCTCGAGCGCTCTGCGCGCACCGAGGTCTCTCGACCTGCGCGCGGTCTCGT	15716	QY	20153	ACCCGACCCCGACACACCCCGGACCTCTCTACACCCGAAACCGGGATTCTCTTACGACG	20212
QY	19407	CTGGGCGACCTGGCAAGGAAACGGACTGGCGACTGGTC---AAGTCAGCGAACATCTCGG	19463	Db	16797	CGCGGCGG-----AGGGCGGAGCTCTGCGGAGTCTGCGGCTTCTGTCAGGAG	16847
Db	15717	CTGGGCGACCTGGGCGAGGTGCGATGGCCACCGTCCCGAGGTCCAGGAGACTGCA	15776	QY	20213	CAGCCCACTTCGACCGCGAAATTTCTGGCAATPAGCCCGCGGAAAGCCCTCGCCATGAGC	20272
QY	19464	CGCGCGGAGATGTTGCGCATCCCGCGCGAGTTGGCGGTCAAGCTGTTGACGCGCGAT	19523	Db	16848	CGCGCGCTTCGACCCCGGCTTCTTGGCATCTCCCGCGGAAAGCGGTGCCATGAGC	16907
Db	15777	CGCGCAAGGGGTCCGCGCATGGAACCGGACCGGATCGCGCGCTCCAGCAGATGCT	15836	QY	20273	CCGAGCAACGACTCTCTCGAAACCGCTGGGAAACCATCGAACAACCGCGGATCAAC	20332
QY	19524	CGCGAGCGGCGCGAGTCTCTCTGTCGCGCATATCGACTGGAGAAATGGGACCGGT	19583	Db	16908	CGCAGCAGCGCATCTCTGAGATCACTCTGGGAAAGCCCTGGAAACCGCGCGGATCGAC	16967
Db	15837	GGAGCAGCAGCACACACCTCGCGGTGACCTCTATGACTGGAGGGGTTCGCAACGAG	15896	QY	20333	CCCACACCTCCAGCGCACCCCGGAGTCTTACCGGACCAACAGGAGGAGGCTCGGCTCAC	20392
QY	19584	TCTCTCTCC-----AGCAAGTCTGCTGGTCTGAGGACTTCTCCCGGACACAGGGA	19635	Db	16968	GTCACACCTCGCGGCTACCCCGACCGCGTCTTCTGCGGACCAACCGGCGAGACTAG	17027
Db	15897	CTTACCGGCGACCGGACCGGCTGTTGAGCAGGTGCGCGGAGCGGTCCGCGCGGT	15956	QY	20393	CGGCACATCTCGGTGAGCGCGGAGCGGTACCGAGGAGTCTGCTGACCGGGGAGCGCA	20452
QY	19636	A-----CTGAGGAGCGCGAGTACCGTTGAGCAGACGAGAGACACAACTCTCG	19685	Db	17028	CGAGGTCATCAAGGCGTCCGCGGAGGAGTCTGAGGTCTACTCGACACACCGGCGACGCG	17087
Db	15957	GACCGCGACCGGCGCACACCGCGGCGGACGAGTGGACTCCGCGACCCCGCGCTCG	16016	QY	20453	CCAGATGCTCTCGGCGGAGTCTCTACATCTCTGGTGGAGAGGCTCGGCTCACCC	20512
QY	19686	GCAATCTCTCATGGTCTGCTGAGTTCGAGCAGAGAGAGTCTGCTCAGCTCTGCTCG	19745	Db	17088	CCAGGTCATCTCGCGCGGCTCTCTACACCTCTGCGCGGAGGCGCGCGCTCACCG	17147
Db	16017	CGCGCACCTGGAGAGTCTGCTCGCGCGGAGCGCGCGCGGCTGCTGAGGCGGTCTCG	16076	QY	20513	TCGACACAGCTGCTCTCTGCTCTGCTGCGCTCTGACCTCTGCGCTGCGAGTCTCAGGT	20572
QY	19746	CATCACTCGCGGAGTCTCGCGCGGAGCTCCGAGGCGCATCCCGCGCGGTCTGCT	19805	Db	17148	TCGACACGCTCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	17207
Db	16077	CGCGAGGCTCGCGACCTCTCGGCGACGACACCCCGGAGGCTCTGCTCTGCTCTGCT	16136	QY	20573	CCGCTGAATGCAATGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT	20632
QY	19806	GTTCAGGAGTCTGAGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT	19865	Db	17208	CGCGGAGTCTCTCATGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	17267
Db	16137	CTTCGCGAGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT	16196	QY	20633	TCACGAAATTCGCGCGGCGGAGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT	20692
QY	19866	ACAGAGGAGTGGTCTGCGGAGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	19925	Db	17268	TCGTCGCTTTCACCGCGCAGAGCGGCTGCGCGCGGCGGCTGCGAGGCTCTCTCGG	17327
Db	16197	CGCCCTCGGCTCTGCGGCGGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT	16256	QY	20693	CGCGGCTGAGGTCAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT	20752
QY	19926	CGCCCAATTTCTGCTCTCGGAGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	19973	Db	17328	ACCGGCGGAGGACCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT	17387
Db	16257	CGCGGCGACCTTGGCGGCTGCTCTTCTGCGACCGCGCTTCTGCGGAGGAGCGCGGCG	16316	QY	20753	CCGACCGCGCGGCGGAGTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	20812
QY	19974	-----AACTCCGCTTCCGCGA-----	19989	Db	17388	CCGACCGCGGCGGCGGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	17447
Db	16317	CCCGGAGACCGCGGCGGCTCTGCGGAGGCGCTGCGGAGGCTCTGCGGAGGCTCTG	16376	QY	20813	AGGACGCTGAGCAACGCTCTGACCGCGCGGCGGCTCTGCGGCGGCTCTGCGGCGG	20872
QY	19980	-----	19989	Db	17448	AGGACGCGGCTCTCAACCGGCTGACCGCTCTCAACCGGCGGCTCTGCGGCGGCTCT	17507
Db	16377	GGCAAGCGGCGCTCTCTGACATGCTGCTGAAACTCTCGGAGGAGGAGCGGAGCGG	16436	QY	20873	GCCAGGCGCTCTGCGCAACGCGGAGTCTGACCGCGCGGCGGCTCTGCGGCGGCTCT	20932
QY	19990	-----	19989	Db	17508	GGCGGCGCTTGGACAGCGGCGGCTCTTACCGCGCGGCGGCTCTGCGGCGGCTCT	17567
Db	16437	CCCGCGCGCGGAGGCGGCGGCTCTGGAATCTCTGAGACATGAGCGCGGAGCGCT	16496	QY	20933	GCAACCGGCGGAGGCGGCGGCTCTGAGGCGGCGGCGGCTCTGCGGCGGCTCTGCGG	20992
QY	19990	-----	19989				

Db 13284 GGGAG-----CGGTCTTGGTCTTCCCGCGCAGGAGATCCAGTGGTG 13325  
Qy 16962 CGGATGGCCACCGGCTCTACCAACCCACCCCGTCTTCGCGCGGCACTCAAGACAT 17021  
Db 13326 GGGAAATGGCGCGGAATCTCTGCGACATTCGAGGTGTTCGCAACCGGATCGATGACTG 13385  
Qy 17022 CTGACACCACTCGAACCCCACTCGACCAACCCCTCTCTCCCTCTCTCAACCCAGGACCC 17081  
Db 13386 CGGAGGGCCCTCGCCCGCTAGCTGCTGCTGCTGCAACGAGTCT----- 13433  
Qy 17082 CAACACCCAGGACACCAACACCTTGAAGAGGGCGGCGACTGTCTCAAGAGACCCCGTA 17141  
Db 13434 -----GGCGGGGAGGGGAGCCCGCCCTGTCTGGAGCGGTGGACGT 13475  
Qy 17142 CGCCAGCCCGCCCTCTTCGCTTCCAGTTCAGGTTCAGCTCCACCGCTCTCAACGAGGGTA 17201  
Db 13476 GGTCCAGCCCGGCTGTTCGCGCATGATGTTGGGCTGTTCGGGCTCTTGGCGCT---CCCA 13532  
Qy 17202 CCACATACCCCCCACTACTAGCGCGGACACTCTCCCTCGGCGAAATCAACCGCGCCACCT 17261  
Db 13533 CGGCGTCTCGCGGCGGCTGGTGGCCACTCTCGCAGGGCGAGATCGCGCGGCTGGGT 13592  
Qy 17262 CGCGGATCTCTACCTCTACCGAGCGCACACCTCTATACCCGAACCGGC---ACCT 17318  
Db 13593 CGCGGAGCCCTCAGCTGGCGAGCGCGCGCTGGTGGGCTGTGCGAGCCAGGCACT 13652  
Qy 17319 CATCANAACTATGCCCCCGGCGACCATGACACACCTCTCAGACCCACCCACCATCAC 17378  
Db 13653 GCGGCACTGTCCGAGCGGGCGGATGATGTGGTCTTCGCGCCCGGTAGAGGGGTGAC 13712  
Qy 17379 CCACACCTCTACCGCCCGGAAACGACTCTGCGCATCGCGGCATCAACACCCCACTC 17438  
Db 13713 CGCACTCTCGCCCGGCTGGAGAGGCGCTGTCTGCTCGCGCGGTCAACGGCCCTCGTC 13772  
Qy 17439 CCGTGTATAGCGGACACCCCGCACCGTTCACACATCATACACCTCTTGGCAACACA 17498  
Db 13773 CGTGTGTCTCTCGCGGACACCGAGCGCTCGACGCTCTGACGCTCTGCGAGGAAACA 13832  
Qy 17499 AGGCATCAAAACCAAAACCTCTCCACCAAAAGGCTTTCACCTCCCGCCACACCAACCC 17558  
Db 13833 GGGCGTGGGGCCCGAAGGTGTCTGTGGAATACGCTCTGCGACGGCGGCGAGCTCGAGGC 13892  
Qy 17559 CATCTCTAACCAACTCCACGACACACCAAAACCTCTACCTACCAACCCCAACCCCAACCC 17618  
Db 13893 CGTCCGCGAGAACTCGCCCGGTCTCTCGCGCGGTGACCGCGCGCGCCCGAGGTGCG 13952  
Qy 17619 CTTATACCGGCAACACCCCAACCGACCAACTCTCTCAACCCCACTACTGAGCCCAACA 17678  
Db 13953 GTTCTACTCGAGGGTCAACCGGAGCGCGGTGGACGACGCGCTTTCGAGCGGCTACTG 14012  
Qy 17679 AGCCGCAACACCGTCACTAGCCACACCAACCAACCTCTCAACCAACCGGCTGAC 17738  
Db 14013 GTACACCAACTCTCGCGAGACGTTCGCTATGAGAGGCGACCGCGGCTCTCGCGCG 14072  
Qy 17739 CACCTATCTGAACCTCGGACCGGACCAACCTCTACCAACCTCTCAACCAACCAACCTCC 17798  
Db 14073 CGGACACCGGCTTCTCATCGAGGTCAAGCGCGACCGGTGCTCGCGCGCGGATCCAGGA 14132  
Qy 17799 GAACACCCCAACCAACCTCTCACTCTGACCCACCGGCGGACGACCGGCGGCGGCGGCG 17858  
Db 14133 GACGAGGAGGCGGTAGCGGAGGCGCACCGCGGGTTCGCGGTGGTCTCGGCTCGCTCGG 14192  
Qy 17859 CTTACCAACTCTGCGCAAAACCAACCAACCTCTGGGACCGCCCACTACACCAACCAACA 17918  
Db 14193 CGCGACGAGGGCGGCGCGGGGCTTCTTGAAGTGTCTGCGGAGGCGGCGACCAACCGG 14252  
Qy 17919 CAACCAACCCCAACCAACCTCTGACCTCTCCCACTCTCCCACTCTTCAACCAACGAGA 17978  
Db 14253 CGCCCGGTGAGTGGACCAACCACTTCCCGCGGTCTGCGCTTACGAGCGGTGAGCTGCG 14312  
Qy 17979 CTACTGGCTGGAAGACACAGCGGGGTGCGGATTCGGGTTCGGGTTCGGGG 18038  
Db 14313 GACCTACCCCTTCCAAACGACAG-----GACTTCTGGCGGAGCGCGGCG 14357

Qy 18039 GGCAGGACTGTCGGGGGAGCGCAGAGGTGGAGTTCGGGTCTTGGAGCGCGTGGCCG 18098  
Db 14358 CGCAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14417  
Qy 18099 CAGGACCTTGGAAACGGTTCGCGACGAGCTTCGCGGTGCGCGCGCGCGCGCGCGCG 18149  
Db 14418 CAGGACCTTGGCGCGCTCGCGACGCGCTTCGCGGTGCGCGCGCGCGCGCGCGCGCG 14477  
Qy 18150 CTTGGACCGGTGTCGCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCT 18209  
Db 14478 GCTCGGACCGGTGTCGCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCG 14537  
Qy 18210 CATCAACACCTTGAACCTTACCGAGAAACCTTGGAAACCTTCAACCTTCCCAACCA 18269  
Db 14538 GATCGAGCACTCGCTTACCGCTTCCAGTGAACCGGTGCGCGAGCGCGCGCGCGCG 14597  
Qy 18270 ACCCACAAACCTTGGCTCATTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCT 18329  
Db 14598 CACCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14648  
Qy 18330 CAACATCTTCAACCACTTCCACCAACCGCTTCGCGCTTCGCGCTTCGCGCTTCGCG 18389  
Db 14649 CTGGGTTCGCGCGGTGCTGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCG 14708  
Qy 18390 CACCCACCAACCCCAACCACTTCAACCAACCGCTTCGCGCTTCGCGCTTCGCGCT 18449  
Db 14709 CACCGACCGCGGTGCGCTGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCG 14759  
Qy 18450 CGGACCATTCACCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18509  
Db 14760 CGAGGAGTTTCAACCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14819  
Qy 18510 CCCCCACACCCACCGCGCTTCTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCA 18569  
Db 14820 CGGTCTGGTACCGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 14879  
Qy 18570 CCACCCACCAACCCCTCTGTTAGCGCCACCAACCGCGCTTCGCGCTTCGCGCTTCGCG 18629  
Db 14880 CGGCTGACCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14939  
Qy 18630 CCGCTTACACACCCACCGCGCTTCTGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCT 18689  
Db 14940 CGGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14999  
Qy 18690 ACACCCACCAACCGCGCTTCTGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCT 18749  
Db 15000 ACACCCGACCGCTGGGGCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15059  
Qy 18750 CCACCACTTCAACCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCA 18809  
Db 15060 GCGCGCTTCAACCGCTTCTGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCG 15119  
Qy 18810 CACCGCACCAACCGCGCTTCTGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 18869  
Db 15120 CACCGCGGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15179  
Qy 18870 CACCCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 18929  
Db 15180 CGGTGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15239  
Qy 18930 CTTACCACTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCT 18989  
Db 15240 GGTGCGCGCTTGGATGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15296  
Qy 18990 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19049  
Db 15297 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15356  
Qy 19050 CTTACCATCACCTTGGAGACCGAGCAACCGAGCAACCTTCAACCTTCAACCTTCAACCT 19109  
Db 15357 GGTACCTTCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15416





Db	9021	GGGAGTCAAGGCAATTGTCGTGTCGTGGCGGGGGGGGAGTATGTCGTGCGCT	9080
Qy	12603	CTCGCTCGTGGCCCTGCATCTGGCTGCCAGCGCTCCGGTCGGTGAATGACACCATGGC	12662
Db	9081	GTTCGTGACATGTCGAAACCGGCTGGTCAGTTGAGTTCGAGGGGGGGTGGTGGCGCG	9140
Qy	12663	GCTCGAGGCGGCGCTCGTCAATGGCCACTCCCTTCGTCTTCCACAGTTCCTCTCGCCA	12722
Db	9141	CGTCAAGGCGCGCTCGTGTGTCGCGCGGAGCGCGAGCGCTGGAACGCGCTGCA	9200
Qy	12723	GGGGGCTGGCGGAGAGCGCGGTCGMAAGCGTTTCGGCGGGGGGGAGCGGACCGG	12782
Db	9201	CGCGGGCTGACCGCGAGCATCGGGCGCGCGGATCGGGTGGACTACGCTCGCA	9260
Qy	12783	CTGGTCCGAGGCTGGGGATSC-----TGCTGTGGAGCGGCTCTCCGACCGCGCG	12836
Db	9261	CTCGACCAAGTTCGAGGACCTGCAGAGGAATGCTGAGGTGCTGGCGAGCTGGCGCC	9320
Qy	12837	CAACGGTCAACGTGCTCTGGCGCTCGTCGCGGAGCGCGCTCAACAGGAGCGGCAAG	12896
Db	9321	GGGACGTCGAGGTCGCTTCTTCGACCGTGCAGCGGACTGGCTGGACACCGCGCG	9380
Qy	12897	CAA-----CGGCTGACCGACCAACCGTGTTCACAGTCAAGTCAATCCGCCAGGC	12950
Db	9381	GATGACGCGGCTACTGTTCCGAAACCTGCGCGGACCGGGTGCGGTTCGCGGAGCGGT	9440
Qy	12951	TTTGGC---AACGCACACTCTCCCTGCCGATGTCGATGCGTGGAGGCCACGGCAC	13007
Db	9441	GGCGACCTGTCGGCGGAGATACCGCGCTTCGTCGAGGTCAAGTTCGCAACCGGTGCT	9500
Qy	13008	GGGGACCACTCTGGGCGACCCGATCGAGGCTCAAGCCCTCGTCGAAGCCTACGGTCAGGA	13067
Db	9501	GACGATGGGCTTGTGACCTGATCGAGGAGCGGGGTCAAGCGCTCGCGACCGGCAC	9560
Qy	13068	CGGCCCCAAGCGCGCGCCCTCTGGCTCGGAACCTCAAGTCCAAATCGAGTGGGCACTCAT	13127
Db	9561	CCTGGCGCTGACCAAGGTGGCGGGCGCTTCTGCTGTGCGCGCGCGAGGTCTGCT	9620
Qy	13128	GGCGCTGGGGTGGGGGGGTCAACAAGTGTGATGGCGCTGCGGAATGGTCTGCT	13187
Db	9621	GGCGGTGTGAGCTGGACTGGCGGGGGCGTTTGAGGGGACCGGTGCGGCGCGGGTGA	9680
Qy	13188	GGCGGAGCTTGTCATGTGGATGAGCCGTGCGCGCATGTGAGTGTGTCGGGGTGGCT	13247
Db	9681	CTGCGCCACTACGCTTCCAGCGGAGCGGTACTGGAACACCGCACCGCGCGGACCG	9740
Qy	13248	GAGCTGCTGAGGAGAGCGTGGCTGGCGCGGGAGGGGGGTGACGGGGGGAGG	13307
Db	9741	CACCGGGCGAGCGCGCGCGATGGACCGCGAATTTCTGGGCGCGCTGCAACAGGCGGACGT	9800
Qy	13308	AGTGTCACTATTCGGGTCAGCGGACCAACCGCCACGCTCATCTCGAGGAGCAACCGC	13367
Db	9801	CTCGGGCTGACCGCGCGCTCGGACACGAGGACTCGTGGCGCGCATCTCGCGCGG	9860
Qy	13368	CCACAACATCCGCTCAGACACACCGCGGACGCTCCCGGGAGATCAGCGCGGACGA	13427
Db	9861	CCTCACTCTGGCGCGGCGCGCTCCAGCGACCACTCTGACTCTCTGGCGGTACCG	9920
Qy	13428	GAGTCCGCTAGTGGCGATGAGGCTGCTGCGGAGTCAAGGGGTGTCGGCTGGCTGT	13487
Db	9921	CGTCACTGGAGCGCCCTCGCGCAGGTGCGCGCGCACCTTACCGGACCTGGCTGT	9980
Qy	13488	GTGCGCAAGTCGACGCGGCTGCGCGCCAGCGCCAGGCGCTGACGCCCACTCAC	13547
Db	9981	GGTCAACCAAGGATCGAGACACCACTGTGGCAGGGGGTGGAGAGCTACGGCGC	10040
Qy	13548	CGACCAACCGGCTCGACTCTGGCGAGCTCGGGTACACCTCGGCCACCGCGGCGCT	13607
Db	10041	CGAGTGGCGCGCTGCTCTGAGAGAGGTGACCGACCGCGCGCTCTGGGGAGG	10100
Qy	13608	GTTGACACCGGGCACCTCATTCGCGCGGACCGGACGCTTCTGCAAGACTCA	13667
Db	10101	GCTGG-----CGGGCGGAGGACGTGACCGGACATGCTCTCGCTCTCGCGCGCGCA	10154
Qy	13668	GGCACTCGCGGAGCGAAACCCACCGCGCTCATCCAGAGAGCGCCCGAGCGGGAC	13727
Db	10155	GGACGAGCGCGACGCGCACCCCGGCTCACCCGGGACTCGCGTCACTCGCTCTCCCTCGT	10214
Qy	13728	CGGACCGGGAGGCGCGAGAAAGACGCAATCATCTGTCTCGGACAGGGACCCCAACG	13787
Db	10215	CCAGGCTCTGGCGAGCGCGAGGCGAGCGCGCTGTGGTTCTGACCCCGCGGCGCTT	10274
Qy	13788	CCCGGATGGCCCAACCGGCTTACCAACACCCCGCTTTCGCGCGCGCACTCAACGA	13847
Db	10275	CGCCACCGGCGCTCGACCCCGTCAACCGGCGCTTCGAGAGCAGATTCGGGGGTGCG	10334
Qy	13848	CATCTGACACCACTCGACCCCACTCGACACCCCTCTCTCCCTCTCTCAACCCAGGA	13907
Db	10335	CTGACCAACCGGCTGGAGACCCCGAGCGCTGGGGGGGACCGTGGACCTCGCGGACAC	10394
Qy	13908	CCCCAAACCCAGAGACACCACTCTCGAAGAGCGGCGGCACTGTCTCAGAGACCGG	13967
Db	10395	CCTGACCGCGGCGCGCCAGCGCTCGCGCGCGC-GCTGTCCGGGCGCTTCGCGCGCG	10453
Qy	13968	CTAGCGCGCGCGCTCTTTCGCTTCAGGTCGCTTCACCGCTCTCTCAACCGAGCG	14027
Db	10454	--AGGACGAGCTCGCGCTCGCGCGCGGGTACTGGCGCGCGCATCTGTGCTGCGCG	10511
Qy	14028	CTACCAATCAACCCCACTACTAGCGCGGACACTCTCTCGCGGAAATCAACCGCGGCGCA	14087
Db	10512	ACACCGCGCGGACGACCGGCAAGGACTCTGGCGCGCGCGGACCACTCTGATCAACCG	10571
Qy	14088	CCTCGCGGATCTCAACCTTCAACCGGACCACTCACTCACTCACTCACTCACTCACT	14147
Db	10572	CGGCTCGCGGACCTCGCGCGGAGCTCGCGCGCTGGCTGGCGGAAACCGCGCGGAGCA	10631
Qy	14148	CATGCAACCATGCGCGCGGACCACTCACTCACTCACTCACTCACTCACTCACTCACT	14207
Db	10632	CGTG-----GTGCTGTCAGCGCGGCGGTGCGAGCGCGCGCGGAGC	10673
Qy	14208	CCACCACTCAACCGCGCGGAAACGACTCGCATCGCGCGCTCAACACCGCGCGGCTC	14267
Db	10674	GCGCGACTCATCGGGAGGAGCGAGTGGGCA---CGGAGTGAACGCTCGCGCGCTG	10730
Qy	14268	CCTGTCTATAGCGGACCGCGGACCGGTCGCTCAACATCACTCACTCTTCTGCAACACA	14327
Db	10731	CGACATCAACCGCGGAGCGGTCGCGCGCTGCTGGCGGACCTCAACCGCGGCGGCG	10790
Qy	14328	AGGATCAAAACCAACCTTCCCGGACCAACCGCTTCACTTCCCGCGCGGACCAACCG	14387
Db	10791	CACCTGCGGACCTGCTATCCAGCGCGCGCGCATCGAGCTGTCGCGCTCGCGGACAC	10850
Qy	14388	CATCTCAACCAACTCCACAGGACACCAACCGCTTCACTTACCAACCGCGCGGACCGC	14447
Db	10851	CACGTGGGAGTTCGCGGAGTCTGTCAGCGGCAAGGTCAACCGGCGGACGATCTCGA	10910
Qy	14448	CCTCATACCGCGCAACCGCGGACCACTCTTCAACCGCGGACCTTCTGAGACCAACA	14507
Db	10911	CGAATGCTGACGAGCGGAACTGGAGACTTGTCTGTACTCTCTCAACCGCGGAT	10970
Qy	14508	AGCGGCAACCTCGACTAGGCAACCAACCGGACCGCTTCCACCAACCGGCGTCA	14567
Db	10971	GTGGGAGCGCGGTCAGCGCGCTAGTTCGCGGCAACCGCTTCTGTCTCGCGCTCGC	11030
Qy	14568	CACCTACATCGAACTCGGAGCGGCAACCACTTCAACCGCTTCAACCGGCAACCTCGC	14627
Db	11031	CGAGCGCGCGCGCGGAGTTCGCGGACCACTCTCACTTCACTTGGGCGAGTGGCGCA	11090
Qy	14628	CAACACCGGACCGGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT	14687
Db	11091	CGACCGGCAACCGGAGTGGCGGACCGGATCGCGGCGGAGGCTCTGGAGTACT	11150
Qy	14688	CCTCAACCACTCGCAAAACCAACCACTTGGGACCGCGGCGGCGGCGGCGGCGGCG	14747
Db	11151	CGACCGGAGTGGCGCTCACCGGCTCCAGCACTGCTTGGAGCGAGACCGGCTCAT	11210

10434 GCGTGTGCTGGCGCAGCCTGAAACGACTTGAGTCAATCCGGTGATGTTTCCAGCCAGCG 10493  
Db |||||  
6864 CAGACTGCTCGAC-ATCATGATGAAGAGTTTCAAAACCAACATAGAGAAATTTGTTCTTC 6922  
Qy |||||  
10494 GTCCGGTGACACACGAGCCGGGTCGACGTCCTGCCAGCGCTCCGGTGGGTGCC 10553  
Db |||||  
6923 GTTCGGACCCGATGACGAGGACGGACCGATGAGAAACCCAGCAGCCAGCCAGCCAGCC 6982  
Qy |||||  
10554 TGCTCGCGCGTGGTGTGATGATTCGGGTTCGGAGGTGTTGCCGTGTTGTCGGGTGGGTC 10613  
Db |||||  
6983 AGCAGAGAAATCGTGCAGTAICTCCGGCGGGTCACTTCAGATCTTCGCGCTGCCGCC 7042  
Qy |||||  
10614 GGTG--TTGGTGACGGGTGGACGGGTGCTGGGTGCGCGGTGCGCGGATCTGGCT 10671  
Db |||||  
7043 GCGCATTTGGCAACTGGAATCAAGAACAAAGAGCCCATGCCATCGTCGGAATGGGCT 7102  
Qy |||||  
10672 GGTGTGTGGG-----TGCGGATCTGCTGTTGGTGAGCGGGGTGGTCCGAT 10722  
Db |||||  
7103 GCGGACTTCCCGCGCGCGTCAATTCGCGGAATCCCTGTGGACCTGTGGTGGTTCGGCG 7162  
Qy |||||  
10723 GCTCCGGGTGCGAGGGTCTCGGGCGGAGCTGGCGCGTTCGGGCGGAGGTGCGGATT 10782  
Db |||||  
7163 GCGAGCCATTTCCGGATTCCCGCTGACCGCGGTGGACCTGGAACCTCACCGAA 7222  
Qy |||||  
10783 GTTGGTGTGATGTGGGGAGCGCGGGAGTGGTCGGCTCTCGAGGGTGTTCCTGCC 10842  
Db |||||  
7223 ACGCGACGGCAGCAGCCACCCAGAAAGCGGATTCCTCTACGACGCGCGGAATTGG 7282  
Qy |||||  
10843 GGGTGTCCGTGACGGGTGCTGTGATGCGGGTGTGTGCTGGACGATGCGAGATCGCC 10902  
Db |||||  
7283 ACGCGCCTTCTTCGGCATCTCGCGCGCGAGGCGACTGCTATGAGACCCCGAGCAGCGC 7342  
Qy |||||  
10903 TCTCTCACGCCGAGCGGTGGGACGGTGTTCGGCGCAAGTGGATGCGCTCTTTTG 10962  
Db |||||  
7343 TCTCTCGAAGTCG-CTGGAGGGCTGGAGCGCGCGGATCGCCCCACAGCCCTG 7401  
Qy |||||  
10963 CTGATGAGCTGACCGGGGTATGAGCTGTGCGGTTGCTGCTGTTCTCTCGCGCGCG 11022  
Db |||||  
7402 CGCGCAGCGGTTCGGCGTGTCTGCGCTCTTACCACTGGGGCGCGCCCTCGSCCGAC 7461  
Qy |||||  
11023 GGGATCTTGGGTGCGCGGGGAGGGCAACTACGCGCGGCGCAATGCGCTCTGAGCGG 11082  
Db |||||  
7462 GCGCCACCGCAACTGCACGGCCACCCCTGACCGGACCGCGCAGCGGTGTGTCG-G 7520  
Qy |||||  
11083 TTGGCGTACCGCGCGCGCGCGGTCTGCGCGGGGTGTCGCTGGCGTGGGGGTGG 11142  
Db |||||  
7521 CGCCTGGCTACACCTCGGCTCGAAGGCCCGCGCTCACCGTCGACACCGCCTGCTC 7580  
Qy |||||  
11143 GAAGAGCCAGCGGATGACCGGGCACTTGGCGGCAACCGACCGGCGCATCATCGT 11202  
Db |||||  
7581 CTCTCTCCCTGCTGCGCTGCACCTGGCGGCCAGTCCCTGCGCGTCCGGCAATCTCGCT 7640  
Qy |||||  
11203 TCCGCTCTGCATC-CCATGTGACCCCGGACGCACTGGCGCTCTTCGATGGCGCCTGGC 11261  
Db |||||  
7641 GCGCTGATGCGCGCGTCAAGATCTCACGAGCCGTCCGCTCTTCGTCGAGTTCAAGCGC 7700  
Qy |||||  
11262 TCTGACCGCGCG--TCTGCTGCGCGCGACCTGCTGCTCCGCGCGCGCTTCGCGCC 11320  
Db |||||  
7701 CAAGGCGCGCTGGCACCGAGCGCGCTGCAAGCGGTCTCCGAGCGCGCGAGCGCAC 7760  
Qy |||||  
11321 TGCT-----GCAGGACTCTTGCCTCCCGCACCGCGCGCGCACCAACCGCACCA 11368  
Db |||||  
7761 CGTTGGSCCGAGGCGTCTGCTGCTCGCGAGCGGTCTCCGAGCGCGAGCGAA 7820  
Qy |||||  
11369 CACTACCGGTGGTGGACAAACCGCGCCAGCTGACCGCGGTGCGCGCGCGAGAC 11428  
Db |||||  
7821 GCGCATCCGCTCTGCTGCGCGGTGCTGCGCGGTCTCCGCGTCAACAGGACGCGCGCTCAA 7880  
Qy |||||  
11429 ACRAACACACACACACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11486  
Db |||||  
7881 GCGCTGACCGCGCCCAAGCGCCCTCCAGAAACGGGTCTATCCAGAGCGGTGCTGCGCG 7940  
Qy |||||  
11487 GGGCACACACACCGCGACCATCTCCCGCGACCGCGCGTTCGCGGACTCTCGGTTTCA 11546

7941 GACCGGCTGACCCCGCGCATCGACGCGCTCGAGCGCACCGCACCGCACCGGCT 8000  
Qy |||||  
11547 CTCCTCACCAGCGCTGCAACTACGCAACGCGGTCTTCGCGCACCAAGGACTCGGCTCCC 11606  
Db |||||  
8001 CGCGACCCCATCGAGGCGCAGCCCTGCTGCGACCTACGCGCAGGACACACCCCCGA 8060  
Qy |||||  
11607 CACCACTCGCTTCGACACCCCAACCCCAACCCCTCACCCACCTCACACACA 11666  
Db |||||  
8061 CACCGCTGTGGCTCGCTCCCTGAACTCAACATCGGGACACCCAGCGCGCGCGG 8120  
Qy |||||  
11667 ACTCAGCACAAACCGGCAACGCTGTTCGCCCCGTGTGGCGGAGCTGCAAACTCGA 11726  
Db |||||  
8121 CGTCCCGGTGTCATCAAGATGCTCATGGCGTTCGCCACCGCACCTGCGCGCACCT 8180  
Qy |||||  
11727 ATCCGCTCTTCGCGCTTCGCAAAACCGACAGCGCGAGCAAGAGTCACTCGGCT 11786  
Db |||||  
8181 GCACCCGACGCGCTCTCTCGCATGCTGCTGCTGCGCGGATCGGTACGCTGCTGAC 8240  
Qy |||||  
11787 GAAGTCACTGTTGAGTGGAAACGCGCACCCAGCATCCGACAGCGGAAAGCTGATGA 11846  
Db |||||  
8241 CGAGGCGCAGAGTGGCGGAGACCGGACGCTCCGCGCGGGCGCGGTGCTCTGTTGG 8300  
Qy |||||  
11847 CGACGAGAGTTCATACCGCAACAGAGGCTGA--GATTTTCAAATTCATTGACAAACGAC 11904  
Db |||||  
8301 CATCAGCGGCACCAACGCGCACGCTGCTGGAACAGGACACCCACCCCGCGGACACGCG 8360  
Qy |||||  
11905 CTCGCGCTCTCTGNAACCGGAGGCTGCACTCCGCCCCGTATCCGCTGGGCGCTGCTAGG 11964  
Db |||||  
8361 GAGCGCGGACGACGCGCGCCACCGAACCGGCGCGCGCGCGCGCTGCTGCTG 8420  
Qy |||||  
11965 ACGTGAAT---GCAATTGGCGAATGAAGCAAGCTCTCTGGAATACCTCAAGCGGTCA 12020  
Db |||||  
8421 GATGCTCTCCGACACTCCCGCGAGCGCTCGCGACCAAGCGCGCGCTGCGCGCGCAG 8480  
Qy |||||  
12021 TCGGACCTGACCGCACTCGCCGCTGCTGTAAGAGTGTGCGAGCGTGA---GAGG 12076  
Db |||||  
8481 GGTGAGACCGACCCCGCTCCGCCCCAGGACATCGGCGACACCTTCACACCGCGCG 8540  
Qy |||||  
12077 AGCGATCGCAATTTGGGGATGGGTGCTGTACCAAGCGGGGCGAGTCAACCAAGC 12136  
Db |||||  
8541 CGCCTGTGTAACGACGCGCGCTGCTGCTGCGCCCCCGACCGCGCGCACTCTCGCGCG 8600  
Qy |||||  
12137 GACT---GTGGCATCTGTCAGTCCACACGAGCTATCGGGGAGTTCGCGACCA 12191  
Db |||||  
8601 TACCCAGAGTTGGCGCGCGCGCTCGCGAACGCGCTGTCGAGGCGCTTCGCGGAGT 8660  
Qy |||||  
12192 CCGTGATGGAACCTGAGCAGCTCTACGACCCGAGACCCGACCGCTCAGGAACAGTTA 12251  
Db |||||  
8661 CGAGGTCGAGCGGTTCGTTGTTCCCGGTCAGGTTTCGAGTGGGTGGGATGGGCGC 8720  
Qy |||||  
12252 CACGCGAGCGGAGGTTTCTCTATGAGCG-----GGGACTTCGAGCGCGCTT 12302  
Db |||||  
8721 CCAACTCTCCTGATGAGTGGCGGTTCGCGGAGCGGATTCGCGAGTGTGCGGCGCACT 8780  
Qy |||||  
12303 CTTGAGTTGTCACCGGTGAGGCGCTGGCAATGAGCCCGCAGCAGCGCTGCTGCTCGA 12362  
Db |||||  
8781 CGCGAGTTACCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8840  
Qy |||||  
12363 AACCACTTGGGAACGTTTCGAACAGGCGGAAATCGACCCGAGGTCCTATCGCGGAAGCG 12422  
Db |||||  
8841 GTTGAGCGGTCGATGTTGGTGCAGCGCGCTGCTTCGCGGTGATGTTGTTGCTGCTG 8900  
Qy |||||  
12423 GACCGGGTTTTGTTGGGATCAATTCGGAGGACTACACCAACCGGATACACATFAGCC 12482  
Db |||||  
8901 GTTGTGGGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8960  
Qy |||||  
12483 CTCAAAACGAGTTCAGGCTTACCTGCTCACTGGCAGCGCGCAAGCATTTGCTGCTGCTG 12542  
Db |||||  
8961 CGTTCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9020  
Qy |||||  
12543 TATCTCTACAACTTCGCGGCTCGAAGGCGCTTCGATCACTATCGACACCGCGTGTCTC 12602



CC The present invention relates to the cloning and sequencing of the gene  
CC cluster encoding a modular type I polyketide synthase (PKS) enzyme  
CC involved in the biosynthesis of the macrolide antibiotic nystatin.  
CC The nystatin PKS is useful as antifungal antibiotics. The present  
CC sequence is a *Streptomyces noursei* nysI DNA of nystatin PKS gene cluster.  
XX  
XX  
SQ Sequence 65140 BP; 8270 A; 25171 C; 22273 G; 9426 T; 0 other;

Query Match	12.3%;	Score 3788.2;	DB 22;	Length 65140;
Best Local Similarity	51.4%;			
Matches 12852;	Conservative	0;	No. 0;	
Indels 1733;	Gaps	0;	Mismatches	10418;

Qy	6256	GAGCGGATCGCCATCGTTGGCGATGGCCCTGTCTGTTTCCCGCGCGAGTGACCTCGCGCGAC	6315
Db	2827	GACCCGGTGTGGTCTGTCGGAATGGCCTTGCGCTTATCCGGTGTGGTCTGCCGCCGAG	2886
Qy	6316	GACTTCTGGGATCTGATCTCTCCGAGCAGACGGATCGGCGGATTCCTCCACCGACCGC	6375
Db	2887	GACCTGTGGGAACCTGGTCCGACCGGCCGACGCGAACCGCTTCTCCGGACGACCGC	2946
Qy	6376	GGCTGGGACCTGGACACGCTCTACGACCCCGACCCGACACCCCGGCACCTGCTACACC	6435
Db	2947	GGCTGGGACCTGGCGGCACT-----GGCCGGCGAGGACCCGCGCGAGCGCGACC	2997
Qy	6436	CGAAACCGCGCGATTCTCTTACGACGCGAGGCCACTTCGACGCGCAATTTCTCGGCATCAGC	6495
Db	2998	CGGAGGCGGATTCTCTCACCGGCGCGCGCACTTCGACGCGCCTTCTTCGGCATGTGCG	3057
Qy	6496	CCCCGCGAAGCCCTTGCCATGGACCCCCAGCAACGACTCTCTCTCGAAACCGCCTCTGGAA	6555
Db	3058	CCCCGCGAGGCCGTCTCCACGACCCCGCAACAGCGCCTCTGCTCTGAGAACCGCCTCTGGAA	3117
Qy	6556	ACCATCGAAACACGCGGCGATCAACCCCCACACCTCTCACGAGCACCCCCACCGAGTCTTC	6615
Db	3118	GCCCTGAGCGCGCGGGCATCGAACCGCATCTCCTGTGCGGCGACGCGACCGGGGTCTTC	3177
Qy	6616	ACCGGCACCAACGAGACGAGTACGCACTTCGCGTGCACAAACGCGGCGCACTCAACCGAT	6675
Db	3178	GTCCGCGCCAGCGGCCAGGACTACGCGCGCGCTCACCCACAGCCTCTGCGCGACGACCTGGAC	3237
Qy	6676	GGTTTTCGACTGACCGGAAACCGCGCGGACAGGTCACTCTCCGCTGCTATCTCGTACACGTTT	6735
Db	3238	GGACACGCGCTTACCGCGCCTGGCCCCCGGGGTGCGCTCTCCGCTGCGCTTGGCGTAGCTCCTG	3297
Qy	6736	GGTTTTCAGGGTCTCTGGGTGTCTGGTGTGACACAGCGCTTGTTCCTCTGCTGTGGTGGCTTTG	6795
Db	3298	GGCCTCGAAGGCCCCCGCGCTCACGCTCGACACACAGTCTCTCTCTGCTGTGTCTCCGCGCTG	3357
Qy	6796	CATCTGGCCTGTCAAGCGGTTTTCGCTGCGGGTGAGTGCTCGATGGCGCTTGCCGGGGGTGTG	6855
Db	3358	CAGTGGCGGTCTCGCGCCTTGGCGCGGGGGAGTGACACCGCCCTGGCGCGCGCGCTC	3417
Qy	6856	ACGCTGATGTCTCTCGGGTGCTTCTGTGTGAGTTTTCGCGGCGACGCGGGGTCTGGCGCGCG	6915
Db	3418	ACGCTGATGTCCACCCCGCGCGCTTCTGTCTGGCCACACCCCGACAGGGCGGCTCTCGCGCC	3477
Qy	6916	GACGGGATTCGAAGGCTTCTCGCGCGCGCGGACCGGACCGGCTCGGGGTGAGGGGTG	6975
Db	3478	GACGGCCGTGCAAGCGCTTCTCCGACGCGCCACGGCACCGCTCTGGGCGGAGGGGCTC	3537
Qy	6976	GGGATGCTGTGTGTGAGCGGCTCTCCGACGCGCCATCGCAACGCTCAACCTGTCTCTGGCC	7035
Db	3538	GGCATCGTCTGTCTGGAGCACTGTCCACCGCCCGCGCGCGCGCAACCCGCTCTCTGCC	3597
Qy	7036	GTGTGTGTGTGCGAGTGTGGTCAACGAGGACGGTGTGAGCAACCGTCTGACCGCGGCCAAC	7095
Db	3598	GTGTGTGTGTGCGGCTCTGGCGCGTCAACGAGGAGGGCGCTCTCCACGCGCTTCAACGACCCAGC	3657
Qy	7096	GGGCGCTCCAGCAGCGTGTATCTCCGCGAGGCGCTCTCGCAACGCGCTGTCTGGCGGCT	7155
Db	3658	GGTCCCCGCCAGGAACCGGTATCCGCGCGCGCTCTCGCCGAGCGCCCGACTCTGCCCGCCG	3717
Qy	7156	GATGTACGCGGCTGTGAGGCGCCACGGCACCGGCACCACTTTTGGGCGGACCGCATCGAGGCC	7215

[illegible]







Db 34967 CGGAAGCGCTGTGGAGATGTTCCACCGGACCGACGAGTGTATCTCCGGATTCCCGGACG 35026  
Qy 24896 ACCGGGCTGGACCTGGACACGCTCTAGACCCCGACCCGACACCCCGGACCTGCT 24955  
Db 35027 ACCGGGCTGGACCTGGAGGCGCTGCGCAACAGCGGACCGACCCCGGACACCGACG 35086  
Qy 24956 ACACCCGAAACCGGCGATTCCTCTACGGCGGAGGCGACCTTCGACGCCGAATTCCTCGGCA 25015  
Db 35087 TCAGCAGGCGCGCGGATTCCTGGAATGATCGCCGACTTCGACCCCGGCTTCTTCGGGA 35146  
Qy 25016 TCAGCCCGCGGAACCTTCGCAATGGAACCCCGACCAACGACTCTCTCTCGAAGACCGCT 25075  
Db 35147 TCTACCGCGGAGCGGTCACTATGGAACCGCAACAGCGGCTCTGCTGACCAACCGCT 35206  
Qy 25076 GGGAAACCATCGAACAACCGCGGCGATCAACCCCGACACCTCAACGGACACCCCGGAG 25135  
Db 35207 GGGAGGCGGTGAGCGGCGCGGATCGACGACCAACGCTGCGCGCCACCGGACCGGCG 35266  
Qy 25136 TCTTCGCGGAATCAACGCTCAAGACCGCGGCGATATCGCCAAAGCGGTGATG 25195  
Db 35267 CGTTTCATCGGACCAACGGCCAGGACTAGCCCTACTGCTGCTCGCTCCCTGGAGACG 35326  
Qy 25196 AGACATCGAGGGCTAGCCCTCGACCGGAGTTCCGGGAAGTGTGGCGTCGCGCGGGTGG 25255  
Db 35327 CCACC-----GGCGAGCTCGGCAACCGGCAACCGGCGCGGCGCTCGGTCGCTCT 35380  
Qy 25256 CTTACACGCTCGGCTCGNAGGCGCGGCGGTGCTGGTGATGACGCGGTGCTGCTGCT 25315  
Db 35381 CTTACACCTCGGCTCGAAGGCGCGGCTCACCGTGCACACCGCTGCTCTCGTCTGCG 35440  
Qy 25316 TGGTGGCGTGTGATTTGGGCGGCGGAGCGGTTCGCTGCGGTGAGTGTGCGGCTTG 25375  
Db 35441 TGGTGGCGTGTGATTTGGGCGGCGGAGCGGTTCGCTGCGGTGAGTGTGCGGCTTG 35500  
Qy 25376 CCGGGGTGTGACGCTGTGCTCTCGGGTACGTTTGTGGAGTTCACGTACAGCGG 25435  
Db 35501 CGCGCGGCTCAACGTATGAGGCAACACCGGCTGCTGCTGCTGAGTTCAGCGCGCAGGCG 35560  
Qy 25436 GTCTGGCGCGACCGGCGGTTCAGGCGCTATTCGGCGCTGCTGACGCTACGCGTGG 25495  
Db 35561 GCGTGGCGCGGACCGCGCTGCAAGGCGTTTCGCGGACCGCGCGACCGGCTGCTGCT 35620  
Qy 25496 CCGAGGCTGTGGGATGCTGCTGTGGAGCGGCTCTCGACCGCGCTGCTGCAACGCTAC 25555  
Db 35621 CCGAGGCGCGGCTGCTGCTGTGGAACGCTCTCGACCGCGCGGCGGCAACGCGGCG 35680  
Qy 25556 GTGCTCTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 25615  
Db 35681 CGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 35740  
Qy 25616 CCGCGCGCAACCGGCGCTTCAGGACGCTGCTATCGGTGAGCGCTGCGGCAATGCGGAC 25675  
Db 35741 CCGCGCGCAACCGGCGCTTCAGGACGCTGCTATCGGTGAGCGCTGCGGCAATGCGGAC 35800  
Qy 25676 TGACCGCGCGGATGCTGACGAGTGGAGGCGCACCGGACCGGACCTCTGGGGGAC 25735  
Db 35801 TGGCCACCGCGGATGCTGACGAGTGGAGGCGCACCGGACCGGACCTCTGGGGGAC 35860  
Qy 25736 CGATCGAGCGCGGACCTCTGCGGCTTACGGACCAACCGGCGCGGCGCGGCGCGGCG 25795  
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Qy 25796 TGTGCTGGGATCCCTCAATCCAGATCGGCGGCGGACGCGGCGGCGGCGGCGGCGG 25855  
Db 35915 TGTGCTGGGCTCGATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 35974  
Qy 25856 GAGTCAATCAAGTGGTGGGCTTGGCGCAACGGGCTGCTGCGACAGCGCTTCCAGTGG 25915  
Db 35975 GGTGATCAAGTATGATGAGGATGCGGCAACGGGCTTCTCGGCGGACCTTGGAGCTG 36034  
Qy 25916 ACAGCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 25975

36035 ACCGGCGCTCCACCCAGTGTGAGTGGACACCGGCGAGCTGGAATCTCTCACCAGCGCC 36094  
25976 TGGCTGGCGCGCGGACCCCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26035  
36095 ACCGCTGGCGCG-----AGACTGGCAGGCGCGCGCGGCGGCGGCGGCGGCGGCGG 36148  
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36149 TCAGCGGCGACCAACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36208  
26096 CCGAGGAGGAAACCGGCTGCGGCAACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26155  
36209 CTGACGAGCACTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36268  
26156 CGGTGTGGGCGGAGTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26215  
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26216 TGGCAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26275  
36329 ACCGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36379  
26276 CCGTACTGGAACACCG-----CGCGCTGCTCTGGCGCGGCGGCGGCGGCGGCGGCGG 26332  
36380 CCGCGCTGGAACACCGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36439  
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26393 GCGGTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26452  
36500 GACGACCGCTGCGCGG-----CCCTCTTCTCGGCGGCGGCGGCGGCGGCGGCGGCGG 36553  
26453 TGGGCGTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 26512  
36554 TGGGCGGCGGAACTCCAGCGCGGCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36613  
26513 AAGCGCTCACCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26572  
36614 ACCTGCTGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36670  
26573 ACCCGCATGCGAAACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26632  
36671 ACAGCGCGCTCAACGAGACCGGCTTCAACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36730  
26633 TGGCGCGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26692  
36731 TCTACCGCTGATCGAATCTCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36790  
26693 GAGAAATCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26752  
36791 GCGAGATCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36850  
26753 TTGCACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26812  
36851 TGGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36910  
26813 CCCTGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26872  
36911 AGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 36958  
26873 TGGCAGCGCTCAACCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26932  
36959 TGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 37018  
26933 AGGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26992  
37019 CCGTGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 37078  
26993 CCTCCACTGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 27052  
37079 CCTTCACTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 37138

[illegible]

QY	24040	CAGTGGCATACTCGGGGCAACGATACCTGGACGGCTCGCGACGCATCTGTCAGACA	24059
DB	33917	CGGGCAACTACGCGCGCTCGCAACGCGCTCTGGACGCGCTCGCGCAACAGCGCGGGTG	33976
QY	24100	CATGGACTTCCTCGGGGCATCGATCGCTGGGGCCCTTGGGCCGGAAGAGGGGATGTCGGCC	24159
DB	33977	CTCGGCTGCGCGCCACCTCGGTCTCTTGGGGTGCTTGGGAGCGGGGCGGATATGGCCGAC	34036
QY	24160	GGTGATGCGGCTCATGTTTACCTTGGAAAAAGCGGGCATTTCTGCGATGGAGCCACGCATG	24219
DB	34037	GCCGACGGCGGACGAGGCGCGCCCGCGCGCGCGGTGCGCGGCATGGACCCGACACCTC	34096
QY	24220	GGCTTCGGCGCATTCATCGTGGCGGGGCGACGGGCCGAATTCACACTGATCATCGGG	24279
DB	34097	GCCGTGGAAAGCCCTGCTGCGCCTGGTCGCGA---GAAAGAGCCGACGCGGTGTGTGCC	34153
QY	24280	GACATCGACTGGGAGCGCTTCGTCGCCGCTTACCGCTCGACGCGCACAGCCCGCTCATC	24339
DB	34154	GAGGTGGCCCTTGACACCGGTTTCGGCGGCGCCTTCGGCGGACGCGACCCAGCGCCTGTGTG	34213
QY	24340	GAGGACATTCGAGAGTTTCGGCAAGCGGCTCAGGAGCTGGAAGCAGCTGCTGCTGCACGGCA	24399
DB	34214	CGGGAGTTCCCGGCTACCGAGGGCG-----TCGCGCGCC	34250
QY	24400	AAGACGACACAGCTCAGCGGATTCGACGTCCTCTCGTGAGGGAATGGGCCGACTGACG	24459
DB	34251	AGGCGGAGCAGCCCGGACGCGGGCG---GGCTGGCCCGGACTGGCGCGCTGCGG	34306
QY	24460	TCCTCAAGACGAACGAGTGTGCTCGGCGCTGATTCGGACAGGCATCTGCACCGTTCTC	24519
DB	34307	CCGCGCCGCGCTTGACACCGGTTGGACCTGTGTGCGACCGCCGCGCGCGAGGTGCTC	34366
QY	24520	GGCCTTCGTAATCCGGAAGGCATCGAGGACCAACGAGCCTTCGCGGACCTCGGCTTCGAC	24579
DB	34367	GGCTACCCGACACCGAAGCGGTGCGCGCGGAACGGTCTCTTCGCGACCTGGGTGTGCAC	34426
QY	24580	TCGCTGACGTCGGCTCAGTTCAGCAAGAACTCGCAAGAAACCGGACTGCCACTCCCC	24639
DB	34427	TCGCTCGGCGCGTCGAGCTGCGCAACCAACTGAGCGCGGCCACCGSCCTGAACCTGCGG	34486
QY	24640	CGTCTCTGGTCTTCGACTATCCACCCCGCAGGAATGTCTGCCCA-----	24686
DB	34487	GCGACGCTGGTGTTCGACCAACCGACCCCGCTGTCTTGGGGAGCACATCTCGGCGGG	34546
QY	24687	-----	24686
DB	34547	CTCTCCCGGACGAGCCCGCGGGTCCGACGACGAGACGAGATCGGGCCCTGCTGGCC	34606
QY	24687	-----	24696
DB	34607	TCCGTCCCGCTCGACCAACTCGCGGAGATCGGGGTCTTCGGAGCCCTGTCTCAGCTCGCC	34666
QY	24697	CAACTGTGCGACTTGAAGCAAGAGGACGCGGCACTGTGCAATGCTCTCCCGCAAGTG	24756
DB	34667	GGACCGCGCGCGCGCGCGGACGCGGAGTCCCTGCACTCGATGACAGTG	34726
QY	24757	GCCCATCGCGGTACCGTTCGAGG-----	24778
DB	34727	GCAGACCTGGTTCGGGCGCGCTCAACGCGCCAGTCCGACTGTAGCGCGATGATGATGAGC	34786
QY	24779	-----	24778
DB	34787	AGACGATGAACGCGCCCGAGAACCCCGAGACCCCGGAGAACACGTTAGTCGCCGACTCC	34846
QY	24779	-----	24778
DB	34847	GCGCGCGGTCAAGGAGACCGACCGGCTCCGGCGGAGAACCGGATGTCTGGTCGCGCGG	34906
QY	24779	---ACGAACCGATCGCCATCATCGTATGGCATGTGCTTCCCGCGGGGTAGGTTCTG	24835
DB	34907	CCAAGGAACCGATCCCGTGGTCGCGATGGCTGTGCGCTTCCCGCGCGCGTACGATCCC	34966
QY	24836	CCGACGACCTGTGGGAATTGCTTCGCTTCGGGTAAAGACGCTATCGGCGCTCTTCCCGACCG	24895



18617 CCCACCCCAACGACCCCTTCAACACCCACCCAAAGCCCAAACTGGGGACTCGCCGCA 18676  
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18677 CCACCTCTCGAAACACCCACCCACCGACCGCGGGAATCATAGACTTCCCAACACCCCA 18736  
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19313 CTTTCTCTTCTGCGCTTCAATCGCGCGGCTTGGGGGCTGCGCGCGCGCGCGCGGAG 29372  
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19742 TCCGATCCATCTCGCGCAGTGTCTGGGCGGAGCACTCCGAGGCCATCCGCGCGGTC 19801  
19787 TCACGGAAGGCGCGACCGCTCTCGGCCACGCGGACACGACCTGTCTGAACCCGACC 29846  
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19847 TGCCCTTTCGGGACCTGGGCTTCGACTCGTGACCGCGGTGACCTGGCAACCACTCA 29906  
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19922 AGTCCGCCAATTTCTGCTCTCGAGATCGGCGAGTTCAGGCCGACAACTCACTCGCG 19981  
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30199 -CGCGCGGCGGACCGGCGCGGATGCGACCGCGCGGAGGATTCCTTACGAGCGCA 30257  
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30258 CCGACTTCGACCCCGGCTGTTCGGCATCTCGCGCGGAGGCGCTGTGATGAGCCCG 30317  
20276 AGCAAGACTCTCTCGAAACCGCTTGGGAAAACATCGAAACAGCGCGGCACTCAACCC 20335  
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30378 CGACGCTGCGGCGGAGGCGGACCGCGGCTTCTGTCGCGGCGGCTTCCGCGG----- 30432  
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30543 ACACGCGCTGCTCTCTGCTGCTGCTGCGCTTACCTTGGCGCGGAGGCGCGCTTGGCG 30602  
20576 GTGAATGCACTGGCGCTTGGCGCGGCGGCGGAGTTCATGACCAACCGCGGATCACTTCA 20635  
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30663 TCGAGTTTCAGCGCGCAGGCGCGCTGTCGCGGAGGCGCGCTGCGCGCGCTTCTCCGAG 30722  
20696 CCGCTGAGGTTACCGGCTGGGTTGAGGTTGGGGATGCTCTGTTGAGGAGGCGCTTCCG 20755  
30723 ACGCAACGCGGACCGGCTGGTTCGGAAGGCGTGGGATGCTCTGCTGTCGAAACGCTTCC 30782  
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Db 26880 ---GGACGGGAGCGCGCGCGCGGTCTCCGCGCTTCAGCGGCACCAAGC 26936  
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Db 26937 CCCAGTCTATCTCAGAGAGAGCCCGGAAACCGAAGCCCGCCCGCGCGCGGAGC 26996  
Qy 16538 AGCCCCGGGAGAGACGCGCGGAGAGATGTTCCGGGGAGCGCGCGGAGACGCGCG 16597  
Db 26997 CGCGCGGAGGACAGCGCCACCGTCTGTC-----CCTGGGTGCTCTCG 27041  
Qy 16598 GTACCGGGGAGAGCGACTGGTCTCTGTCGCGGAGTTCAGGGGTGTGGCGGTGGTGG 16657  
Db 27042 GACGAGCGCGGAGCG----- 27058  
Qy 16658 TGTCCGCAAGTCGAGCGCGCGCTGCGCGCCAGCGCCAGCGCTTCAGCGCCACCTCA 16717  
Db 27059 -----CTCAGGCGCAGCTGACCGGTCTACCGCGGCACCG 27095  
Qy 16718 CGGACACCGCGCTCGACCTCGCGAGCTCGGGTACACCTCGCCCAAGCGCGCGCG 16777  
Db 27096 CGGCCACCGCGCGCTCGCGGGGAGCTCGCGGTCTGCTGGCCACCGACCGACGC 27155  
Qy 16778 TGTTGACACCGCGCACCTCATCGCGCGGACCGGACACCTTCTCTGCAAGCACTCC 16837  
Db 27156 TCTTCCCGACCGCGGTCTGCTCGCGGC----- 27187  
Qy 16838 AGGCACTGCGCGAGCGGAACCCACCGCGCGGTATTCAGAGAGAGCGCGCCAGCGGGA 16897  
Db 27188 ---CCGACCGGGTGGCGAGGCGCGCGCGCGCGCGCGCGCA----- 27230  
Qy 16898 CGGGACCGGGAGCGCGAGAGAGACCGCATTCATCTGCTCCGAGACGGGACCCCAAC 16957  
Db 27231 -----CCCCGGCGGACCGCGTCTGTTCTCGAGAGGGCGCGCAGC- 27275  
Qy 16958 GCGCGGCAATGCGCCACGCGCTTACACACCCACCCCGTCTTCGCGCGCACTCAACG 17017  
Db 27276 AGCGCTGATGGCCACGACCTGTACAGCGCTTCCCGGTCTAGCGCGACGCACTGGACA 27335  
Qy 17018 ACATGACACCACTCGACCGCCACCTCGACACCCCTCTCCCTCTCTCACCAGG 17077  
Db 27336 CGTCTCTCGCCCGATTCGACACCGTGTGAGAGTCCCGTGGCGCGCGCTGTTGCGCG 27395  
Qy 17078 ACCCAACACCGAGACACCAACCCCTCGAAGAGCGCGCGCTTCGACAGACACCC 17137  
Db 27396 CGCGGGACCCCGCA-----GGCGGCTCTCTGACAGACCG 27434  
Qy 17138 CGTACGCGGAGCGCGCTCTTGGCTTCAGGTGCGCCCTCCACCGCTCTCTCAGCGAGC 17197  
Db 27435 GCTTACACGAGCGCGCTGTTCCGCGTTCAGGTGCGCACTGTTCCGGCTCG---CCGAGT 27491  
Qy 17198 GCTACACATACCCCGCACTACTAGCGGAGACATCTCCCTCGCGGAATCAGCGCGCC 17257  
Db 27492 CTTGGCGGTGAGCGCGGACTTGTGCGCGGCACTTCCATCGCGGAGATCGCGCGCGC 27551  
Qy 17258 ACTGCGCGGCACTCTCACCTCACGAGCGCACACCTCTCATCACCAAGCGCGCACCC 17317  
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Qy 17375 TCACCAACACCTACCGCGCCAGCAAAAGACCTCGCGATCGCGGCACTCAACACCCCA 17434  
Db 27672 TCGCGCGGTGCTTACCG-----ACGGCGTGCACCTCGCGCGGTCAAGCGGCGCC 27722  
Qy 17435 CTTCCCTGTCATCAGCGGACCCCGACAGCGTCCAAACACATCACACCTCTGCGCAAC 17494  
Db 27723 GCTCGGTGCTGTCGGGGGCGCGAGGAGCGCCCTCGCGGGTTCGCGAGCGGCTCGCG 27782  
Qy 17495 AACAGGCAATCAAAACCAAAACCTCCCAACCAAAACGCTTTCACACTCCCGCCACACCA 17554

Db 27783 CCAGCGCGCGCGCAGCCCGCGGTGACGGTACGCCACGCGCTTCCACTCGCGCGTATGG 27842  
Qy 17555 ACCCATCTCTCAACCAACTCCACAGACACCCAAACCCCTACCTACACCCACCCACACA 17614  
Db 27843 ACCGATGCTTACCGATTTCGCCGGGTTCGGAGGGCTTACCTACACAGCGCGGCA 27902  
Qy 17615 CCCCCTCTCATCACCGCCCAACACCCACCC-----CGACCAACTCTCTACCCCCCACT 17665  
Db 27903 TCCCCTCTCTCAACCTCTCTCGCGCGCGCGCGCGGCGGAACTGCGCACCCCGACT 27962  
Qy 17666 ACTGGACCCAAAGCGCGGAAACCGTTCGACTAGGACCAACACCCCAACCTCTCCACC 17725  
Db 27963 ACTGGGTGCGGACAGTTCGCGAGACCGTTCGCGGTTCGCGGAGCGGTGCGCGCTGACG 28022  
Qy 17726 AACACGGGTTCACCACTTACATCGAACTTCGAGACCGGACCAACCTTACCACTCTCACCC 17785  
Db 28023 AGCGCGGCGCGCGGACCTTCGTGAGATTCGCGCCGAGCGGGGTGCTTACCGCGCTTACCC 28082  
Qy 17786 ACCAACAACCTCCCAACACCCCAACCACTTCACTCACTCACTCACTCACTCACTCACT 17845  
Db 28083 AGCAGACCTTCGACACCGTTCGAGCGCGCGCGCGCGCTGCTGCTGCGCTTCAGCGCC 28142  
Qy 17846 CCAAAACCACTCTCTTACCAACCTTCGCAAAACCAACCACTTCGAGACACCCCA----- 17900  
Db 28143 GCGACCGCGCGCGGACCTTCGCGCTTCTGGAGGCGCTTCGCGGAGCGGTGCGCGCTGACG 28202  
Qy 17901 ---CCACTACACCAACCAACCAACCAACCAACCAACCACTTCGACCTTCGCGCA 17956  
Db 28203 CGGCGCGCTCTGCGCGCGCTTCTGAGGCGACCGGCGGCGACCGGACCGATTCGCGCA 28262  
Qy 17957 CTTACCTCTTCAACACCACTTACTGCTTCGAAAGCACACAGCGGGTTCGCGATCCG 18016  
Db 28263 CTTAGCGCTTCCAGCGGGAGCGGTACTTGGCGCGAA----- 28297  
Qy 18017 GTTCGGGTTCGGTTTCGGGCGGGAGGAGCTGCGGGGCGGACGGCAGAGGTGAGTGC 18076  
Db 28298 ----- 28297  
Qy 18077 GGTTCGGGACGCGGTGCGCGCGCAGGACCTGGAAACGGTTCGCGACACGCTCGCGTGC 18136  
Db 28298 -----CTCGCGGAC 28307  
Qy 18137 CCCCCTCGCGCGCTGACACGGTGTGTCGCGCACTCTCGCGCTTCGCGACCGCGCAAC 18196  
Db 28308 CGTTCGCGCACCGCGCGGAGCGCGCGG----- 28337  
Qy 18197 AGCAACAGCGCGATCAACACCTTCGAGACCTTACAGGAAACCTTGAACCTTCACTCC 18256  
Db 28338 -----CCTGGCGCTTACACGAGACCTTGGCGCGCGCTTCGCGCGC 28376  
Qy 18257 CCACACCAACCAACCAACCAACCTTGGCTCATCGCCATCCCGAAACCCAGACCCAC 18316  
Db 28377 CCGAGCGCGCGCGCGCGCGCGCGCGCTTGGTCTCTGTCGCGCGGGAACCGCGACA 28436  
Qy 18317 ACCCGCACTACCAACATCTTCACCACTTCACACACCGGATCACCCCATCCCTCC 18376  
Db 28437 CGCGTGTGAGCGCGCTTCGCGAGCGCTCGGCGCGACACCTTCACGCGCGAAGCG 28496  
Qy 18377 TCACCTCTCAACCAACCAACCAACCAACCTTCAACCAACCGGACCAAGAGCC 18436  
Db 28497 AGCGCTTGGCGGAGCAGTTGAGCGCGC----- 28524  
Qy 18437 AAAACCAACCAACCGGACCCATTCACCGCGCTCTCTCTCTCTCTCTCTCTCTCTCT 18496  
Db 28525 -----CGGCGACACACCTTCGCGCGCTTCGCTCTCTCTCTCTCTCTCTCTCTCT 28577  
Qy 18497 CCAACCCCAACCAACCAACCAACCAACCTTCTCACTCACTCTCTCTCTCTCTCTCT 18556  
Db 28578 GGTCTCGCGGAGCGCGCTTGGCGCGCGCGCTCTCTCGCACCTTCGAGGAGCGCGG 28637  
Qy 18557 CCAACCAACCAACCAACCAACCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18616  
Db 28638 TGCA-----CGGCGCGCTTGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 28676

QY	14303	ACATCAACACCTCTGTCGAACAAACAAGGCAATCAAAACCAAAACCCCTCCCAACCAACGACG	14362
DB	24741	TGGCCGGGCTCTCGCCGAATGTCGGAGACAGACCCCGCTGTCGCGGTGTTTCCACACGG	24800
QY	14363	CCTTCCACTCCCCCAACCAACCCCATCTCAACAACTCCACAGCAGCACACCCAAACCC	14422
DB	24801	CCGCGCTGTGTGAGGACCAAGTGTGTGACGCGCTCAACCGGAGAACTTTCGCGCGGTGC	24860
QY	14423	TCACCTACCAACCCCAACACCCCTCATCACCGCCCAACACCCACCCGACCAACCTCC	14482
DB	24861	TGCGCGCAAGACCGTTCGCGGCCAACACCTGCACGAGCTGACCGCGAGACTTGAGACTCG	24920
QY	14483	TCACCCCCCACTGTGAGACCAACAGCCCGGAAACACCGTGCATACGCCACCAACACCC	14542
DB	24921	CCGCTTTGTCTGTCTTCCTCCACGCGCGGCGTCTCGCGCGCGCGGACAGGGCAACT	24980
QY	14543	AAACCCCTCCACCAACACGGGCTCACCACTACATCGAACTCCGACCCCGACACACCCCTCA	14602
DB	24981	ACGCGGGGCAACGCCCACTGTGACGCCCTTCGCGAAACACCGCGCTCCACAGCGCTGA	25040
QY	14603	CCACCTTCACCCACGACAACTCTCCCAACACCCCAACCAACCACTCACTTCAACCAACC	14662
DB	25041	CCGGCTGTCCGTGCGCTGGGGCCGTGGGCGGGCTCCGGCATGCTCGCGAGCGCGCG	25100
QY	14663	CCACACACACCCCAACACCTCTCACCAACTCTGCCAAACACCAACCACTGAGCTGGC	14722
DB	25101	AACTCACCGACCGGCTACGGCGGGCGGCTTCGAAACCGTCCGCCCCGAAACCGGCCGTGC	25160
QY	14723	ACCCCAACCACTACACCCACACCAACCAACCCCAACCAACCAACCACTTCGACCTCC	14782
DB	25161	GGCGCTGTCTGGGGCCATCGAAGACGACGA---CACACACGTTCGGCTTCGCCGACATCG	25217
QY	14783	CCACCTACCCCTTCCACACCACTACTTGGGTCAACCAACCCCGCAAGCGAGCGACCC	14842
DB	25218	ACTGGAGCGCTTCCAGCGCGCTTCGCCCGGTCCGCCGTGCGCGTTCGTTCGCGGACC	25277
QY	14843	CGTCACCGAGGAGG-----CCGTGAGAAACCAACCAACCACTCAACCCCGCTGCGTG	14896
DB	25278	TCGCCGAGACCGCGCGGGCACCCCGCACCGCCACCGCGCCCAACCGCTTCGGCTGGCGC	25337
QY	14897	ATGTCTCTGTGGGCAAGTCTTCGACGAGCGAGACGAGAGCTGTTGGCTTGGTGGCA	14956
DB	25338	AGCAACTGCGCGAACTGCGGAGACAGCGGCCGCGAGCGGTCTCTGACATGTGTCGTA	25397
QY	14957	CCATGCGGCGCTGTGTGGCCATGCCACTCCGGAAGTGAATGTTCCGAACAGGCGCT	15016
DB	25398	CCCAAGTCGCGCGCTCTCGGCCACACCGCAACCGCGCACCGCTCCAGGACACACGCT	25457
QY	15017	TCAAAGACTGGGTTTGATTTCTTCGCGCGCAATTCAGCTTGTGAATCGACTGTGCTG	15076
DB	25458	TCCGACCACTGGGCTTCGACTCGCTGACCATCTGTGAATCTGGCAACGCCCTCAACGCGC	25517
QY	15077	ACGTTGACCTTCGCGCTTCGCGGCACACGCTGATCTTGATTAACCCCACTCCGATGGCGTTT	15136
DB	25518	CCACCGGCTGAGCTTCGCGGCCACCCCTGGTCTACGACTGCCACCCGCGGAGATGG	25577
QY	15137	GCGAGTTCTTCGCGGCGGATGTCGG-----ACGCGACA	15172
DB	25578	CGGACTTCTGCTCGCGCAACTCTCGGACCGCTGCCACCGACACCGCGCGACCGTGC	25637
QY	15173	CAGGCAACCACTGCTTCGCGCTTACTGCGGT-----CCCGCGGACG	15217
DB	25638	CCAGACGGGCTCCCCCAAGCTCTAGCTTCGTTCGAGCAGGCGGTACCCCTTTCGACG	25697
QY	15218	AGCCGATTCGCATCTGTCGCATGGCTTCGTGTACCCCGGTGATGTACGAGCGTTCGATG	15277
DB	25698	ACCGATGCGCGTCATCGGCATCGCTGCGCTTCCCGCGGCGTCAACACCCCGGAGG	25757
QY	15278	ATCTCTGGCAGTGTGTCAGTGTGGCCATGAACCGATTCGGCGGATTCGCCGACGACCGTG	15337
DB	25758	AGTCTGTGCACTCTTCGACAGGCGCGGACCGGATCAGCGCTTCCCGACGACCGCG	25817

Qy	15338	GGTGGAGACTCGACACGCTGTATCAACCCCGGACCCCGGACCA	CCACCGAAGACAGCTACACCC	15339
Db	25818	GCTGGACCTCGCGCGCTGGGCGC-----CGGCGCTCCGACACC		25859
Qy	15398	GGAGCGCGATTCCTTTACGACGACGAGCAATTCGATCCCGACTTC	TTCCGTGATCAGTC	15457
Db	25860	TGAGGGCGGCTCTTCGACCGGGCTCGCCGACTTCGAGCCCGGTTCT	TCGGCATCTCGC	25919
Qy	15458	CGGCTGAGGCACCTGGCGGATGAGACCCCGACAGCGGCTGCTGT	GTGAAACAGCGTGGGAGA	15517
Db	25920	CCCGAGGGCGCTGGCCATGGAACCCACAGCGGCTGCTGTGAGACCA	CTCGTGGAGG	25979
Qy	15518	GCATCGAACACGCTCGATCAACCCCGACAGCCTCGTGGAACAACA	ACACCGCGCTCTTCG	15577
Db	25980	CGCTGAGCGGGCGGATCGACCCCGACACGCTCGGGGCTCCACCA	CCGCGGCTCTTCG	26039
Qy	15578	CCGGGCTGACCTACACGACTACGCGCGGCTTTCCACAGCTCCGG	CAGGTTCTGAGG	15637
Db	26040	TCGGCACCAACAGCCAGGACTACCGAGCGCTGTTCGCGCGCTTC	CGCCTCGGACGTTGGCGG	26099
Qy	15638	GGTATCTCGGGCACGAAGCGCAGGCAGTATCGCTCGGGTCGTCTG	CGCTACGCTCTTCG	15697
Db	26100	GCTACGTCGCCACCGGCAACACCGCCAGCGTGAATCTCGGCGC	CGCTCTTACGGCGCTCG	26159
Qy	15698	GCTTGAAGGTCCGGCCCTCACATGTGACACTGCTGTCTTCTGCT	TCCTGTCGCTCTTCG	15757
Db	26160	GCCTGAAGCCCGGCGCTCACATCGACACCGCCTGCTCTCTCGCT	CGCTGCGCCCTTCG	26219
Qy	15758	ACCTGGCCTGTACGGGCTTCGGTCCGGCGAGTGTTCATGGCCCT	TCGGGGTGGCGTCA	15817
Db	26220	ACTTGGCCGGCGGGCGCTTCGCGCGGCGAGTGGCGACTCGTGT	GTGGCGGCGGCTCT	26279
Qy	15818	CGCTGATGTCAACCCCGGCGGTTCTGTGGAGTGTTCGCGGAGG	CGGCGGCTTGGCGGCTG	15877
Db	26280	CGGTATGGCAGCCCGACTCTTCTGTGAGTTCTCCACGAGGCGC	CTTGGCACCCG	26339
Qy	15878	ACGGGCGGTCAAGCGTTCTTCGGACGCGGCTGACGGCACCGG	CTGGGGTGGGGTGTCTG	15937
Db	26340	ACGGCGCTGCAAGGGTTCTCCGACGCGCGACGGCACCGCTGTG	TCGGAAGCGCTCG	26399
Qy	15938	GAATGCTGTGTGGAGCGGCTGTGGACCGCGCGGCGCTCGGTCA	CCGAAATCTCTCGGG	15997
Db	26400	GCATCTCGTCTTGAACGCCCTCTCGCGCGCGCGCAACGGCC	ACACAGGTCTCTCGGCC	26459
Qy	15998	TGTTGCTGGCAGTGGGCTCAATCAGGACGGTTCGAGCAACGGG	CTGACGGCGCCCAACG	16057
Db	26460	TGATCCGGGCAACCGCGTCAACAGGACGGCGCTCCAA	CGGCTGACCGCGGCCAACG	26519
Qy	16058	GGCGCTCCAGGAGGTTGATCCGCTTGGCCCAACCGGACCTGAC	CCCGCCCGCGG	16117
Db	26520	GCCTCTCCAGCAGCGGCTCATCGCCAGGCACCTCGCCGACCG	CGCGCTGCGCGCGCGG	26579
Qy	16118	ACGTGATGGGTGAGGCCCAACGGACACGCGCACACTTTTGGGGA	ACCCGATTCAGGCCCC	16177
Db	26580	ACATCAGCCGATTCAGGGCGCACGGCACCGGCACACCTCTGGG	GACCCGATCAGGCGCC	26639
Qy	16178	AGGCGCTCTCGCCACTTACGACAGGACCGCCCGGCAAGAAC	CGGCTGTGGCTGGGCT	16237
Db	26640	GCGCCCTGATCACCGCTTACGGCCCGGACCCGGACCGCCGAA	ACGGCCGCTGTCTGTGGGCA	26699
Qy	16238	CGATGAAGTCGAACATCGGCCACCGCAGGCTTGGCGAGTGTGG	CGGGGTCTATCAAGA	16297
Db	26700	CCGTCAAGTCCAACATCGGGCACACCGAGCCGCGCGGTCGCG	CGCGGTCTCATCAAGA	26759
Qy	16298	TGTTGATGGCGCTGCGGAATGTTCTGTCCCGCGGACGTTTGCAT	GTGTGAAGCCGTCTCGC	16357
Db	26760	TGCTGATGGCGATGGGCCACGGCACCTCTGCCAGGACGCTCAG	CTGTGGGACACCCGCTCCA	26819
Qy	16358	CGCATGTGACCTGCTCCGGGGGCGGTGCAAGCTGCTGACGGAG	CGGTCGCCCTTGGGCCG	16417
Db	26820	GCCACGTCGACTGGAGCGCGCGCACCGTTCGCGCTCTCGACGA	CGCGCGGCGCTTGGGCAAC	26879
Qy	16418	GCGGGAGGGCGGCTTGGCGGGGAGAGGTGTCTATCGTTCCGG	CGCTCAGCGGCAACCAACG	16477

Db 22536 ACACCTGACCGCGCGCTGCGCGCTTGTCCGACGCGCGCGCCGACCCCGCGCTGTGTC 22595  
Qy 12179 AGTTCGACCGACCGTGTGATGGAACCTGAGGACGCTTACGACCGGACCCCGACCGCT 12238  
Db 22596 AGGGACCGCGGACCGCGCGCGCTTCTTCTTACCGGACGAGGACGCGCC 22655  
Qy 12239 CAGGAACAGTTACACGCGGACGAGGAGGTTTCTATGACGCGGCGACTTCGACGCGC 12298  
Db 22656 CCGGATGGCGCGGACCTTACAGGACCGCTACCGGTGTTCCGACCGGCTGAGACGAG 22715  
Qy 12299 CGTTCCTGAGTTGACCGGTGAGGCGCTGGCAATGACCCGACGAGCGCCCTGCTGC 12358  
Db 22716 TGCTGGCGCGCTGACAGGACCGGACCGCGCGCTGCGAGGTGCTTTCGCGCGCGC 22775  
Qy 12359 TCGAACCACCTTGGGAAAGTTTC---GACAGGGGGAATCGACCGGAGTCCATGCGCG 12415  
Db 22776 CCGATCTCGCGAGCGCGCTTCTGGAACCGGACCGGCTACGCCAGCGCGCGCTTTCG 22835  
Qy 12416 GAAGCGGACCGGGGTTTTCGTGGGATCAATCCGGAGACTACACACCGGATACACAC 12475  
Db 22836 CCGTCGAGGTGCGGTGTTCCGCTGCTGACGTCTTGGGCTGACCCCGGACTTACTTG 22895  
Qy 12476 ATACGCGCTCAACGAGTCTGAGGCTACTCTCTCACTGGCAGCGGCAAGCATTTGCGT 12535  
Db 22896 CCGGCACTCTCGTCGCGAACTCGCGCGCGCACTGTCGCGCGCTGCTGCTGCGAGC 22955  
Qy 12536 CAGGCGGTATCTCTACAACTTCGGGCTGAAGGCGCTGCGATCACTATGACACCGGT 12595  
Db 22956 AGCGCTGCACTGTGTGCGCGCGCGCGGCTCATGAGGCGCTGCGCGAGGCGCGC 23015  
Qy 12596 GTTCTCTCTGCTGCTGCGCGCTGCACTTGGCGCTGCAAGCGCTCGGCTCGGTGAATGCA 12655  
Db 23016 CGATGTCGCTGAGGCGCGGAGGACGAGTCTGCGCGCTCTGAGGCGCTCACCG 23075  
Qy 12656 CCAATGCGCTCGACGCGCGCGCTCGTCAATGGCACTCCCTTCTGCTTTCACGAGTTCT 12715  
Db 23076 ACCGGGTGCTGCGCGCGCTCAACGCGCGCGGTCCGTGCTGCTGCGCGCGCTCGAG 23135  
Qy 12716 CTCGCCAGCGCGCTGCGCGC-----AGACGCGCGGTGCAAGGCGTTTCGCGCGCGC 12770  
Db 23136 AGGAGTGTCTCTCTCGCGCGACCTTTCGCGCGCGACGCGCGCGCGACCAAGCGCGCTC 23195  
Qy 12771 GGACGGGACCGGCTGCTCGAGGCTGTTGGGATGCTGCTGTGGAGCGGCTCTCCGACGC 12830  
Db 23196 GGGTGAACATGCTCTCACTGCGCGCTGATGAGCGCATGCTGACGACTTTCGCGCGC 23255  
Qy 12831 CCGCGCAACGCTACCGGTCTTGGCGCTGCTGCGCGGACGCGCGTCAACGAGGACG 12890  
Db 23256 TCGCGCGCGGCTGACCTACCAACCGCGCGACGATCCGTTCTGTCGAACTGTCAGCGCG 23315  
Qy 12891 CGCAAGCAGCGCTGACCGCAACCGGCTGTTCA-----CAAGTCA 12934  
Db 23316 GCTTGGCCACCGGACAGGCTCGGACCGCGCGGACTACTGCGTGGGACGCTCGCGCGC 23375  
Qy 12935 AGGTATTCGCGAGGCTTTGGGCAACGACACTCTTCCCTGCGGATGTCGATGCGGTGG 12994  
Db 23376 CGGTGCGCTTCGCGAGGCGCATGCTGCTGCGCACCGAGGCGGACTTCCACCTTCC 23435  
Qy 12995 AGGCCACGCGGACGCGGACCACTTGGGCGACCCGATGAGGCTCAAGCCCTCTGTCGAG 13054  
Db 23436 TGGAGCTCGCGCGGACGCGGTGCTCAGCGCGATGCGCGGAGAGCGCTTACCGACCGCT 23495  
Qy 13055 CTTAGGTCAGGACCGCCCAAGCGCGCGCGCTCTGCGTTCGGAACCGCTCAAGTCCMACA 13114  
Db 23496 CCGCAGCGCACTGTCTGCGGACCTTCTGCGGCGGACCGCGCGGAGGACTGCGCTTGTCA 23555  
Qy 13115 TCGGCACTTCATGCGCGCTGCGGCTGCGGCGGTGATCAAGATGATGGCGCTGC 13174  
Db 23556 CCGCGTTCGCGCGGCGGACGCGGCGCGCGCTGACCTGAGGCGGCTACTTTCGCGC 23615  
Qy 13175 GGAATGCTGCTGCGCGGACGTTGATGTGATGAGCGCTGCGCGCATGTGGAATGCT 13234

Db 23616 ACCACGCGCGCGCGGACCAACGCTGCGCGACTACGCGTTCACACGCGAGCGTACTGGC 23675  
Qy 13235 CCGCGGTGCGGTGCTGCTGCTGACGAGAGGCTGCGCTGCGCGCGGCGGAGGCGCGC 13294  
Db 23676 CCGACACACCGCGCGCGACGAGCGCCACAC---GCCCGGATCCGCGCTCGACCGCGAGT 23732  
Qy 13295 TACGCGGCGGAGGAGTGTCTCATTTGCGCGTTCAGCGACCAACGCGCCACGTCATCTCG 13354  
Db 23733 TCTGCGCGCGCTGAGCGGACGACGCTGCGCGCGCTCGCGCGCTCTGCTGACCTGACG 23792  
Qy 13355 AGGAAGACCGCGCGCAACATCCGCTACAGACACCGCGGAGAGCTCCCGGAGAT 13414  
Db 23793 ACGCACCGTACCGCGATGCTCCCGCGCTACACCGCTGCGCGCGCGCGCGCGAGC 23852  
Qy 13415 CAGCGCGGACGAGATGCGGCTAGTGGCGATGAGGCTGTGCGCGGAGTCCAGGGGTGT 13474  
Db 23853 AGACCGAATGGAC-----TCTGCGGTACCGGCTTACCTTGGAAAGCGCGCGCGG 23904  
Qy 13475 GGCGTGTGCTGTGCGCGCAAGTTCGAGCGCGCGCTTGCAGCGCGCGGCGTCCAGGCCCTGC 13534  
Db 23905 CGCCACCGCACCGCGCGCTACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 23963  
Qy 13535 ACGCCCACTACCGACACCGCGCGCTCGACCTGCGGAGCTGCGGTACACCTCTCGCC 13594  
Db 23964 AGGACCGTACGAGGACGCGGACCGCGCGCTTGGGACGCGGCTGAGACCGCGCTGGCA 24023  
Qy 13595 ACGCGCGCGCGTGTTCGACCAACCGCGCGCGCTTATCGCGCGCGGACCGGACACTTCC 13654  
Db 24024 CCACACGCTCGGCTGACGCTACACACCGGCGCGCTGCGCGCGCGGCTGCGCGATCA 24083  
Qy 13655 TGCAGCACTCAGGCACTTCGCGCGAGCGGAAACCCACCGCGCGCTCATCCAGCAGCAG 13714  
Db 24084 CCGAAGCGCGCGCGGACCGAGGCGCTTACGCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 24143  
Qy 13715 CCCAGCGGGAACCGGAGACCGGAGGCGCGGAGGAAAGCGCATTCATCTGCTCCGAC 13774  
Db 24144 CCGCGAGCGCGCGCACCGCGGTGCGCGCGCGCGCTCACCTCACCAACCGCGCTCC 24203  
Qy 13775 AGGCAACCAACGCGCGGATGCGCGCGCGCT---ACCACACCGCGCGCTTTCG 13831  
Db 24204 AGGCGCTCGGCGACCGCGGATCGACGCGCGCTGTGGAAGCTCACCGCGGCGCGTGG 24263  
Qy 13832 CCGCGCACTCAACGACATCTGCAACCGCGCGCGCGCGCGCGCGCTCGACACCGCGCTTCC 13891  
Db 24264 CCGTGGCGCGCGGACAGGTACCGCGCGCGGACAGCGCGCTTGGGCGCTTGGGCGC 24323  
Qy 13892 CCCTCTCACCGGACCGGACCGGAGGACCGGAGGACCGCGCGCTCGAGAGGCGCGGAC 13951  
Db 24324 GCGCGTGGCGTGGAACTGCGCGCGGTTGCGGCGGCGCGCTCGACCTGCGCGCGCGC 24383  
Qy 13952 TGCTCCAGCAGACCGGTACCGCGCGCGCGCTTTCGCG-----CTTCCAGGTGCG 14002  
Db 24384 TGGAGCGGACGCGCGCGCGGTGCGCGCGGTGCTGCGGCTACCGAGCGCGGAGCG 24443  
Qy 14003 CCCTCCACCGCTCTTACCGGACCGGTACACATACCGCGCGCGCGCTTACGCGCGGAGACT 14062  
Db 24444 GCGTGGCGCTGCGCGCGCTTCTCTCTCGCGCGCTGCGCGCGCGCGCGCGCGCGCGC 24503  
Qy 14063 CCCTCGGGAATACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 14122  
Db 24504 CCGACCGCGCGCGCGCGCGCTTCGACCGCGCGCGCGCGCGCGCTGATACCGCGCGCGC 24563  
Qy 14123 CCCTCATCACCAAGCGGCGCGCGCTTATGAAACCATGCGCGCGCGCGCGCGCGCGCGC 14182  
Db 24564 CCGGCGGATC---GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 24620  
Qy 14183 TCCACACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 14242  
Db 24621 TGCTGCTCACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 24680  
Qy 14243 TCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 14302  
Db 24681 TGGAGGAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 24740

QY 10128 GGTGTTGG-----GTGTGTTGAGGGTGGCTGGGGCTGGAGCGGTTTTGCGGTTTCGG 10181  
Db 20377 GCTCGCGGAGCACCGCGCGGCAACGGAATGCGCCGCTGTGCTGTCTGTGGGCACTCG 20436  
QY 10182 GCTGTGTGTGTGACCCGGGGTGGTGGTGGCC-----GGCCGGAGGAGCGGCCGGT 10235  
Db 20437 GGCAGGACGACCTAACTGGCGCGGTGATCCACAGATGATCCCGGCGAGCGGCTGGA 20496  
QY 10236 GATGTGTGGGTGCGTGTGGGGCTGTGGTGTGGTGTGGGGCTGGAGCTGAGATCCGGA 10295  
Db 20497 GTTCATGAGCCGCACTGCGCTGTAGCGGCTGTGAGCGGGCTGTGAGCAACAGAGAA 20556  
QY 10296 CCGGTTTGTCTCTCGACTTGACACCGACACCGGACCGGACTCGACACCGGTGCTGG 10355  
Db 20557 CGTGTCTCGGTCGCGGAGTGTGACTGTGGAGACCTACACCCGCTGTACACCTCGCGCG 20616  
QY 10356 TGTGTGTGGGGTGGATGTGTGGGGTGTGG-----GGGGGGGGGGGGGGGGGGGG 10387  
Db 20617 ACCCACCCGCTCTTCGACGAGGTGCGGAGGTTCGCGGCTCACCGCGCGCGCGAGCA 20676  
QY 10388 -----CGCGGTGGGTGGTGTGAGCGCGAGTTGGGGTGGCGTGGGGAGC 10435  
Db 20677 GAGCGCGGAGCGTTCGCGAGGCGAGTTGCGCGCGGCTGTGCGGCGCTGTTCGACGC 20736  
QY 10436 GGTGTGTGGCCGACGCTCTGAACGACTTGTGATCTCCGGTGTATGTTCCAGCCGACGCT 10495  
Db 20737 CGAGCAGCAGCGACCTCTCTGAGACCGTCCGACCGAGGCGGCTCGTCTCGGCT 20796  
QY 10496 CCGGTGACACAGAGCCCGGGTTCGACGTGCTGCGCGCTGCGAGCGCTCGGTGGCGTGG 10555  
Db 20797 GTCTCCCGCGAGGACCTCACGACCGAGCGGCTTCCGCGAGCTCGGCTTCGACTCGCT 20856  
QY 10556 CTCGCGGTGTGATGATCGGTTCGAGGTGTTGCC-----GTGGTGTGGGTGG 10610  
Db 20857 GACCGCGTTCGCGCTGCGCAACCGGCTCGCTTCGCTCACCGGCTGACGCTGCTCCCTCGAC 20916  
QY 10611 GTCTGTGTGTGACGGGTGGACGGGTGTGTGGGTGGGGTGGGGCGGCACTTGCG 10670  
Db 20917 GATGTTTCGACTACCCCAACCGCGCGCTGCGCGCTATCTGACGGGAGCTGGC 20976  
QY 10671 TGGTG-TGTGTGGGTGGGATCTGTGTTGGTGGAGCGGCTGGTTCGGGATGTCG- 10728  
Db 20977 GCGCGCCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 21036  
QY 10729 GGTGCGGAGGTCTCGGCGGAGCTGGCGGCTTGGGGCGGAGTGGGATGTTGG 10788  
Db 21037 CGACCCGATCGGATCTGTCGCGATGAGTGTGCGCTACCCCGCGGGGTGCGCTCCGCGA 21096  
QY 10789 TGTGATGTGGGGAGCGCGGAGGTGTGTCGCGCTGTGGAGGTTGTTCTTCCCGGGTGT 10848  
Db 21097 GACCTGTGGGATCGCCTTGACGAGTTCGACGAGTTCGCGATCTCCGCTTCCCGCGGACG 21156  
QY 10849 CGCTGACGGTGTGTCGATCGCGCTGTGTGTGTCGATGTCGACGATCGCTCTCTC 10908  
Db 21157 GCGCTGGGACGCGAGGGGCTCTACGACCCGAGCCGACCGCGCGCGCGCGCGCGCTCTC 21216  
QY 10909 AGCCCGAGCGCTG-----GGCACGTGTTCGGGCGGAGTGGATGCGGCTCT 10958  
Db 21217 CGTCAGGGCGGATCTCTGCGGAGTGTGCGGAGTTCGACCGCGGCTTCTTGGGATCTC 21276  
QY 10959 TTTGTGATGAGTGTGACCGGGGTATGGAGTGTGCGGTTGTGCTGTCTCTCTCGGC 11018  
Db 21277 GCGCGCGAGGCGCTGTGATGAGCCCGACGAGCGGCTCTGTGTGGAGACGCTTGGGA 21336  
QY 11019 CG-----CGGGATCTCGGGTTCGCGCGGCGAGGCAATACGCGCGGCAATGCGCTC 11074  
Db 21337 GCGCTTCGAGCAGCGCGGATCGACCCGCTCGGCGAGCGGCGGAGCGCGGACCTT 21396  
QY 11075 TGGACGCTGCGTACCGCGCGCGCGGGGTCTCGCGGGGTG-----GGGGGG 1121  
Db 21397 GTCGCGCGCGCTACCGAGGACTACGCTTCGCGGTGTCCTCAACACGAGGGGCTCGAAG 21456

QY 11122 -----TCTGTGGCTGGGGCTGTGGGAAGAGCGGAGCGGATGACCG 11165  
Db 21457 CCACATGATACCGGCACTCTCAGTGTGTGTTCGCGCGGGTGTCTACTCTTCGG 21516  
QY 11166 GCACCTGGCGGACCGACCGGGGATCATCTGTTCCGTTCTGATCCCATGTCGAC 11225  
Db 21517 TTTCAGGGGCGCGCGTCACTGTCGACACGCGCTGCTCTCTCTGTTGTCGATGA 21576  
QY 11226 CCGGACGACACTGGGCTCTTCGATGCGGCGCTGTGACCGCGCGGCTCTGTCGTC 11285  
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QY 11286 GCGGACCTGTGCTCGCGCGCGCTGCGCGCTGTGTCAGGACCTCTCTCGCGGAC 11345  
Db 21637 CATCATGTCCACCGCGATGCTGTTGTCGCTTTCAGCGCGGAGCGGCTCTCGCGAGGA 21696  
QY 11346 CCGCGCGCGCA-----CACCGGACACCACTACCGGTGTGGGCAACCG 11393  
Db 21697 CGCGCGCTGCAAGGCTGTACGCGGACCGCGCGGATGACCTTCGCGAGGGGTCTCG 21756  
QY 11394 CGCCGAGCTGCAAGCGCGCTG-----GCGGCGGACACACGACGACGACGAC 11447  
Db 21757 CTTGCTGTCTGTGAGCGGCTGTGCGACCGCGCGGCAACGCGGCTCTCGCGT 21816  
QY 11448 CTTCTCGCTGTGCTCGCTCTCCCATCATCGCCACCGCTCTGCGGCGGACACCGCGGAC 11507  
Db 21817 GATCGCGCTCGCGCTCAACAGGACCGGCGCTTCAACGCGCTGACGCGACCAACCG 21876  
QY 11508 CATCCCCCGGACCGCGGTTTCGCG-----GACTTGGCTTTCGACTCTCTACCGCGTGA 11564  
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QY 11565 ACTACGAAACCGGCTCTCCGCGACCGCGGCTCGCGCTCCCGACCGCTCGCTCGA 11624  
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QY 11625 CCACCCCAACCCCGGCTCTCACCGCTCTCACACCACTCTCACAGCGGCTCTCGGCGG 11677  
Db 21997 GCGCTGTCTGCGACCTACGCGGAGGACCGCGCGCGCGCGGCGGCTGTCTCGGCTC 22056  
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QY 11733 CTTCTCGCGCTCGACAAACCGGACCGCGGCGGAGGTCACCTTCGCGCTGAGTGC 11792  
Db 22117 GTCGCGCGCTCTCAGGAAGGCTGTGTCGCGGCTCTGTCGACATTCGACCGGCTCTCAC 22176  
QY 11793 ACTCATGTTGAGT-----GGAAGCGACCCCGGAGCTCTCGAATTCGGA 11827  
Db 22177 CCAGTGTGCTGCTCTCGGCGGCTATCGGCTGTCTACCGGACCGCGCTGCGGCGG 22236  
QY 11828 CAGCGGAAGGCTGTGATGACGACGAGAGTTCAATCGGCAACGAGGCTGAGATTTCA 11887  
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QY 11888 AATTTCATTGACAACTGCGCTGTCTTGAACCGGACCGCTGCGCTCTCGCGCGGATC 11947  
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QY 11948 CGCTGGGCGCTGTAGGAGCTGAATGCAATTTGGGGAATGAGGAGGCTCTCTGGAATACC 12007  
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QY 12008 TCAAGCGGCTCATGCGGACCTGACCGCACTCGCGCTGCTGTGACGAGTGTGCGA-- 12065  
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QY 12066 -----GGGTGAGGAGGCGGATCGGATTTGTGGGATGCGTGTGTTACCGAGGCGG 12120  
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QY 12121 GCGACGTCAACCGCGGCTGTGCGATCTCTCAAGTCCGAGCGGAGCGCTATCGGG--G 12178

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8820 CCACCTCTCAACCACTCG----- 8839 Qy  
18937 CTTCTGTGTGCGCGCGCGAGGTCTTGTGCGCGGTGTGGAGTGTGGAGTGTGGGCGGT 18996 Db  
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9298 GTGAGTGTGATGCGCGGGTGGAGTGTGTTGTGTTGGGGTGTGCG----- 9345 Qy  
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Qy 5388 CACCACTGATCAGACCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5447  
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Qy 5448 CACCACTTCAACCAACCTTCTTCCGCGCAACCGCGCGCGCGCGCGCGCGCGCGCG 5507  
Db 15586 CGCGAGTTCCGCGCGCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15645  
Qy 5508 CACCAACACACCGCGCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5567  
Db 15646 GCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15705  
Qy 5568 CGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5627  
Db 15706 CAGTGGCAACCGAGCGGCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15765  
Qy 5628 CCGCGCACACCCACCACTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5687  
Db 15766 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15825  
Qy 5688 ACTCGCTGATTCGGAACAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5747  
Db 15826 CATGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15885  
Qy 5748 ACCGAGTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5807  
Db 15886 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15945  
Qy 5808 GGTATCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5861  
Db 15946 CTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16005  
Qy 5862 CTT-----GGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5903  
Db 16006 CTTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16065



Db 28327 ATCCGCGGACGGCAGCCTCCGCGGCGGACAGCACCCACCGCTTCTCACC GCC 28386  
Qy 14698 CTCGCCAAACACACACACCTGGCAGCCACCCACCACTACACCCACACACACCAACCC 14757  
Db 28387 CTCGCCCAACACACACACCTGGCAGCCACCCACCACTGGCAGCCACCACTACACCC 28446  
Qy 14758 CACACCCACAC-----CCACCTCGACCTCCCCACCACTACCCCTTCCAAACAC 14802  
Db 28447 CAAACCCACCCACCCACCAACACCACTCGACCTGGCCACCACTACCCCTTCCAAACAC 28506  
Qy 14803 CACCACTACTGGCTCAACACACCCCGGCAAGCGAGCGACCCGTCACCGAGCG 14854  
Db 28507 CAGCACTACTGGCTCAACACACCCACCAACCAAGCAACCGACCTCAACCAACCG 28558

## RESULT 7

AAD17186  
ID AAD17186 standard; DNA; 125401 BP.

AC AAD17186;

XX 29-NOV-2001 (first entry)

XX Streptomyces noursei nystatin PKS gene cluster DNA.

XX Polyketide synthase; PKS; macrolide; nystatin; PKS gene cluster;  
KW antifungal; antibiotic; ds.

XX Streptomyces noursei.

Key Location/Qualifiers  
CDS 6337..34771  
FT /tag= a  
FT /product= "NysI complete protein"  
FT 34792..51099  
FT /tag= b  
FT /product= "NysJ protein"  
FT 51155..57355  
FT /tag= c  
FT /product= "NysK protein"  
FT 57503..58687  
FT /tag= d  
FT /product= "NysL protein"  
FT complement (58786..58980)  
FT /tag= e  
FT /product= "NysM protein"  
FT /note= "CDS does not include start codon"  
FT complement (59045..60241)  
FT /tag= f  
FT /product= "NysN protein"  
FT /note= "CDS does not include start codon"  
FT complement (60238..61296)  
FT /tag= g  
FT /product= "NysB2 complete protein"  
FT 120628..121308  
FT /tag= h  
FT /product= "NysR4 (long) protein"

PN WO200159126-A2.

XX 16-AUG-2001.

XX 08-FEB-2001; 2001WO-GB00509.

XX 08-FEB-2000; 2000GB-0002840.

PR 10-APR-2000; 2000GB-0008786.

PR 14-APR-2000; 2000GB-0009387.

XX (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.

PA (SNTP) SINTEF STIFTELSEN IND TEK FORSK.

PA (ALPH-) ALPHARMA AS.

PA (SINV-) SINVENT AS.

PA (DZIE/) DZIEGLEWSKA H.

PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAERVIK E.  
PA (BRAU/) BRAUTASET T.  
XX (STRO/) STROM A R.  
PI Zotchev SB, Sekurova ON, Fjaervik E, Brautaset T, Strom AR;  
PI Valla S, Ellingsen TE, Sletta H, Gulliksen O;  
XX WPI; 2001-557614/62.  
DR P-PSDB; AAE10143, AAE10144, AAE10145, AAE10146, AAE10147, AAE10148,  
DR AAE10149, AAE10150.  
XX New nystatin polyketide synthase polynucleotides and polypeptides,  
PT useful as antibiotics and antifungals -  
XX Claim 1; Page 188-254; 266pp; English.  
XX The present invention relates to the cloning and sequencing of the gene  
CC cluster encoding a modular type I polyketide synthase (PKS) enzyme  
CC involved in the biosynthesis of the macrolide antibiotic nystatin.  
CC The nystatin PKS is useful as antifungal antibiotics. The present  
CC sequence is a Streptomyces noursei nystatin PKS gene cluster DNA.  
XX  
SQ Sequence 125401 BP; 15664 A; 49692 C; 42871 G; 17174 T; 0 other;  
Query Match 14.2%; Score 4347.6; DB 22; Length 125401;  
Best Local Similarity 51.4%; Pred. No. 0;  
Matches 15336; Conservative 0; Mismatches 12354; Indels 2136; Gaps 144;  
Qy 915 GGTGCTGACCATGGGCTCTCAGGAGCTCGCCCCGAGCTGGCGGACACACCCGACCGC 974  
Db 11269 GCGCAGGGCTGGCCCTCTTCGACGCTGCGTGGCGGACCGACCGACCTGGTTCC 11328  
Qy 975 CGACACCGTGATCATGGGACGCTGCGCGCGGCGAGGACCCCTGAGACCACTTCTTGAC 1034  
Db 11329 GGTCCGCTGGACCT---CCCGTCTCCGCGCACGGGGTGAAGTGGCGCGCTGCTGAG 11385  
Qy 1035 GTCTCTCGCCCACTACGGGGGCGATGTGAGACGTCCGCGGACACCGCTCTCGGCACG 1094  
Db 11386 GTCGTTGATCCGCTCGGGGCGCGGAGCGCGCTCGCGGCTCCGCGACCGGGGAA 11445  
Qy 1095 CCTGACCGCGCTGTCCCCACGACGACGACGCTGCTCTCTGGACCTGGTGCAGCCCA 1154  
Db 11446 CCTCGCCAGCGCTGCGCGCGCTGGAGGACGCGCGGACGAGATGCTCTGGACCT 11505  
Qy 1155 CACATGCGGTGCTGAACGACGACGGAACGAGGACACCGCGTCGAGTCCGCGCCATC 1214  
Db 11506 CGTCCGCGTCAGGTGCGCCCTCGTCTCGGCGACGCGGCTGGCGACGTCGACGCGG 11565  
Qy 1215 GCGAGTTTCGCCACCTCGGCTTCGACTCGCTCGATCGGCTCGAATCGCGCAACCGCCT 1274  
Db 11566 CCGTGCCTTCGCGACCTCGGCTTCGACTCGCTGACCGCGCTCGAATCGCGCAACCGCCT 11625  
Qy 1275 CAGCAAGCCACAGGCGCTTCGCGTTGCGCGTGCACGCTCATCTTCGACCAACACCGCGCGC 1334  
Db 11626 CAACACCGTCACCGCGCTGCGCTGCGCGCACCTGCTCTTCGACTACCGACCGTCCG 11665  
Qy 1335 CGCGGTCCCGCGCGCTTCGAGACCGCGGCGCTCGGCCACCTCGACGAGGACACCGCGCC 1394  
Db 11686 GCACCTCGCCACGTACGTCCTGGACGAGTTGTTGGGACCGGATGCGGAGGTGGGACCGT 11745  
Qy 1395 CGTACCGGACTCACCCAGCGGCGGACCGGAGGACCGGCGGACCGGACCGGATCGCCAT 1454  
Db 11746 GCAGCGGCGCGCGG-----TTGCGGTGGCGGACGATCGATCGTCT 11787  
Qy 1455 CATCGGATGCGATGCGCTTTCCGCGGCGGAGTCCGCTCCCGAGGACCTGTGTGGAGCT 1514  
Db 11788 CGTGGCATGCGCTCCCGCTACCCCGGTGGCGTCAGCTCCCGGAGGACCTGTGTGGCGCT 11847  
Qy 1515 GCGCGCTTCGGGCGGAGACGCGCATCGGCGCGCTTCCCGACCGACCGCGGATGGCCACCGA 1574  
Db 11848 GCTACCGAAGGCAACCGAGCGCGTCTCGGGCTTCCGAGCAACCGCTGTGTGGAGCTGGA 11907

Qy	12505	CTGCTCACTGCGACGGCGCAAGCATTTGGCTCAGCGCGTATCTCTTACAACTTCGGGCTC	12564
Db	26236	ATCGCAACGCGACGCGAGGCAGCGTTCGACCGCGCGGTGGCCCTACAGCTTTGGCCCTT	26295
Qy	12565	GAAGGCCTGCGATCACTATTCGACACCGCGTGTTCCTCTCGCTCGTGGCCCTGATCTG	12624
Db	26296	GAGGGTCGGCGCGTGAACCGTCGATACGGCGTGTTCGTCTGGTGGCGGTGTGATTTGG	26355
Qy	12625	GCCTGCCAAGCGCTCCGGTCCGGTGAAATGCACCATGGCGCTGCGAGCGCGCCCTCCGTC	12684
Db	26356	CGCGCGCAGGGGTTGCGTGGCGGTGAGTGTTCGATGGCGCTTGC CGGGGTGTGACGGTG	26415
Qy	12685	ATGBCCACTCCCTTTGCTTTTAAACGAGTCTCTCTCGCCAGCGGGCTCGCCGACACGCG	12744
Db	26416	ATGTGCTCTCGGGTACGTTTGTGAGTCTCTACGCTACGGGGTCTGGCGCGACGCG	26475
Qy	12745	CGGTGCAAGGCGTTTTCGGCGCGCGCGGACCGGACCGGCTGCTCGAGGGTGTGGGGATG	12804
Db	26476	CGGTGCAAGGCGTTATTCGGCGCGGCTGTGACGCTACCGGGTCTGGCGCGAGGGTGTGGGGATG	26535
Qy	12805	CTGCTGGTGGAGCGGCTCTCCGACGCGCGCGCAACGGTCAACGCTGCTCTGGCCGCTCGTC	12864
Db	26536	CTGCTGGTGGAGCGGCTCTCCGACGCGCGCTCGACGCTCAACGCTGCTCTGGCCGCTGGTG	26595
Qy	12865	CGCGCAGCGCGCTCAACAGGACGGCGCAACCGGCTCAACCGCACCCAAACGGTCTGT	12924
Db	26596	CGTGGCAGTGGCGTCAACAGGACGGTTCGAGCAACGGTCTGACCGCGCCCAACGGGCCC	26655
Qy	12925	TCAACAAGTCAAGTCACTCCGCGAGGCTTTTGGCCAAACGACACTCTCCCTGCGCATGTC	12984
Db	26656	TCCAGCAGCGTGTCACTCGTCAAGGCCCTGGCCAAATGCGGGACTGACCCCGCGCATGTC	26715
Qy	12985	GATCGGTGGAGGCCACGCGACCGGGACACACCTGGGCGACCCCATCGAGGCTCAAGCC	13044
Db	26716	GACGCACTGAGGGCAGCGCACCGGACCACTCTGGGGGACCCCATCGAGGCCCAGGCA	26775
Qy	13045	CTCGTCSAAGCTTACGCTCAGGACCGCCCGCCAAACGGCGCGCCCTCTGGCTCGGAACCTC	13104
Db	26776	CTCTGGCCGCTACGGACAACACCGCCCGCCACCGCCCTTGTGGCTGGGATCCCTC	26835
Qy	13105	AAGTCCAACATCGGCNACTCATGGCCGTGCGGGTGTGGGCGGGGTATCAAGATGGTG	13164
Db	26836	AAATCCAACATCGGGCACGACAGGGCGCGCGGGCGTGGGCGGAGTCAATCAAGATGGTG	26895
Qy	13165	ATGGCGCTCGGAATGGTCTGCTGCTCGCGGACGTTGCACTGCGATGAGCCGTGCGCGCAT	13224
Db	26896	ATGGCCCTGCGCAACGGGCTGTCTCCACAGACCTCTCACTGGACGAGCCACCCCGCAG	26955
Qy	13225	GTGCACTGTGCCGCGGTGCGTGCAGCTGCTCAACGAGACGGTGCCCTGCGCCGGCG--	13282
Db	26956	GTGCACTGTGTCCACAGCGCAGTACAACCTCTTGACACACCGTGTGCTGGCCCGCGAC	27015
Qy	13283	GGGAGGGGCGGCTACGGCGGGCAGAGTGTATCATTTTCGGCGTCAAGGGCACCAAGCC	13341
Db	27016	CCGCGCGCGCGGCACGCCACGCGCGCGTGTATCATTTTCGGCGTCAAGGGCACCAAGCC	27075
Qy	13342	CACGTCACTCTCAGGAAGCACCGCCCAACATCCCTCAGACACACCGCGCGAGCAC	13401
Db	27076	CATGTGATTTTGAGAGGGCGCTG-----CGCGCGCGGGCGGT	27114
Qy	13402	GTCCCGGGAGAATCAGCCCGCAGCAGGATGCGGTTAGTGGCGATGAGGCTGTCTCCCGGC	13461
Db	27115	GCTGCGGTGTGGGTGTCTGGTGGTGTCTCCGAATCCAGCCCTTCGCTGGCTGAGTCT	27174
Qy	13462	AGTCCAGGGGTGTGGCGGTGGTGTGTCTGGCCAAAGTCGAGCGCGCCCTCGCGCCCGAG	13521
Db	27175	GAGCCGCTGCCGTGCGGTGCGGTGTCTGGCGAGGTCTGAGGGCGGGTGTGGGGCGGAG	27234
Qy	13522	GCCAGGCCCTGCACGCCACCTCAACGACACACCGCGCTCGACCTCGCGAGCTCGGG	13581
Db	27235	GCAACGCGTTGCGCGAGTACGTGGCAGCCCGCCCGACATGTCACTTCGCCGATCGGT	27294
Qy	13582	TACACCTCTGCCCAACCGCGCGCGTGTTCGACCAACCGCGGCACACCTCATCGCGCCGAC	13641

Db	27295	GC	GGGTCTTG	CGCCGCGCGCGCGCGCGTACTGGAACACCGCGCGGTATCTTGCGCGCGGAC	27354
QY	13642	CG	CGACACCTT	CTGCTGAAGCACTCCAGGCACCTCGCGCAGCGCAACCCACCCCGCGCTC	13701
Db	27355	CG	CGAGAACT	TGCGCGCAGGCACCTGACAGCCCTTGACCGCGCAACCCACCCCAATC	27414
QY	13702	AT	CCACAGCAG	CGCCCGCGGACCGGACCGGGAGCGCGCAGGAAACACGCGCATTC	13761
Db	27415	AC	CACAGGC	ACACCCCGGCGAGCTGACCGCGCGCGG-----TCGCTCTC	27459
QY	13762	AT	TGCTTCG	GACAGGCGACCCCAAGCGCCCGGATGCGCCACGCGCTTACCAACCCAC	13821
Db	27460	GT	CTTCCCG	GACAGGCGCGCAGTGGCGCGGATGGCCCTGACCTCTCTCACCCTCTCA	27519
QY	13822	CG	CGTCTTG	CGCGCGCACTCAACGACATCTGCACCACTCTGCACCCCGCCTCGACAC	13881
Db	27520	CC	CGTGTTC	CGCGGAAACACATCGACGATGCGAAGAGCCCTCACCCCCCTGGTGCCCTGG	27579
QY	13882	CC	CTCTCTC	CCCCCTCTCACCCAGGACCCCAACACCCAGGACACCAACCTCGAAGAA	13941
Db	27580	TC	CTGACCG	ACATCTGCACCGCGACCCCGAC-----	27612
QY	13942	GG	CGCGCA	CTGCTCCAGCAGACCCCGTAGCCCGCGCCCGCTTTTGGCTTCCAGGTC	14001
Db	27613	--	GACCCGC	ATGGAACCGCAGCTGGTCCAGCCCCGTCTTTCAGCATCATGGTC	27669
QY	14002	GC	CTTCCAG	CGCTCTCTCACCGACGCTACCAATCACCCCGCCTACTAGCGCGGACAC	14061
Db	27670	TC	CTCT---	CGCGCCCTGTGGCGCTCTTACGGCATCGAACCGCAGCGGTCTCGGCCAC	27726
QY	14062	TC	CTCGCGA	AAATACACCGCGCCCACTTCGCGCGATCTCACTCTCACTCGACGCGCAC	14121
Db	27727	TC	CGAGGAG	AAATCGCGCGCCACATCTGCGGCGCATCTAGCTTGAAGACCGCGCC	27786
QY	14122	AC	CTCATCA	CCCAACCGCCCACTCTATGCAAAACCATGCC---CGCCGCAACCATGACC	14178
Db	27787	AA	AACGGT	TGCACTGCGCAGCGCACTGGCGCGCTGACGAGCGCGCGCGCATGGTC	27846
QY	14179	AC	CTTCCAC	ACACACCCCGCCACCATCCGACCACTTACCGGCC---ACGAAACGAC	14235
Db	27847	TC	ACTGCCC	CTGCGCGCCGAGCAGTGCAGCAGCTATTTCGAACGGTGGGAAGGCGAG	27906
QY	14236	CT	CGCATCG	CGCGCATCAACACCCCACTCTCCTCGTATCAGCGCACCCCGCACAC	14295
Db	27907	TT	GTGGTGG	AGCCTTCAACCGCCCGCCACTCAACCGCTCTCAACCGCTCTCGCGCGAC	27966
QY	14296	GT	CCAACA	CATCACCACCTCTTGCCAAACAAAGGCATCAAAACCAAAACCTTCCCGAC	14355
Db	27967	GT	AGAAGAA	CTCTCACCCACTGTGCGCACCGCGCTAGCGGCGCAACCGCATCCCCGTC	28026
QY	14356	AA	CAAGCCT	TCCATCTCCCGCCACCAACCGCATCTCAACCACTTCAACGACACAC	14415
Db	28027	GA	CTAGCCT	CCACTGCGCCCGCCCGCTCAACCGCTCAACCGCTCTCAGACGAACTCTCTG	28086
QY	14416	CA	AACCTCA	CTTACACCCACCCACACCCCTCTATCAGCGCAACACCCCAACCGCA-	14474
Db	28087	GG	AGATCA	CCCCCGCGCTCCACCTGCGTTCTTTCTCAACCGTGTGAGGCACTGT	28146
QY	14475	-----	CCAACT	CTCTCAACCCCGCCACTACTGGACCCCAACGCGCGCGCAACCGCTC	14523
Db	28147	GT	CTGTA	CAACACCTTGACGCGCGCTACTGGTACCGCAACCTTCCACCGCGCTC	28206
QY	14524	GA	CTAGGCA	CACACCAACCCCTTCAACCAACGCGGTTCACGCTTACATCTGAATC	14583
Db	28207	CG	CTTCA	CGCCATCCAGACCTTGACCGGACGCGACACCGCGCCCTTTCATCGAAATC	28266
QY	14584	GG	ACCCGA	CAACACCTTCAACCCCTTCAACCGCAACCTTCCCGCAACCCCGC---ACC	14640
Db	28267	AG	TCCCCA	CCCCCTGTTCGCCGCTTGAAGACCAACCGGAAACCAACCGGAAC	28326
QY	14641	AC	CACTCT	CACCTTCAACCGCCCAACCAACCCCGCCCAACCCCGC---TCCTTCAACCA	14697







Db	20122	ACCCTCTCGCCCTGTGTCCTCCACATCGCCACCGTCTCTCGGCCACACACCCCGAC	20181
Qy	6028	GCATCGCGCCGACAGTCGTTCCGTGCACTCGCTTCGATTCATCTACCGCCGTCGAG	6087
Db	20182	ACCATCCCCCGACCGCGGTCGCGACCTTCGGCTTCGACTCCCTCACCGCCGTCGAA	20241
Qy	6088	TTCCGAAACTCTGTCATCAAGGCAACAGAGCTCCGCTTCCTGTCGTGTCCTTCGAC	6147
Db	20242	CTACGCAACCGGCTCTCCCGACACCGGACTCCGCTCCCCACACACCTCGCCCTTCGAC	20301
Qy	6148	GACCCGACCCCTCCMAACTCCCGCTGACCTGCGAGAACCACTCGGGGGACACAGAGG	6207
Db	20302	CACCCCAACCCCAACCCCTCACCCACCACTCCACACAACTTCCTGGGCTCGACAGC	20361
Qy	6208	GAGTCGGCTCTTCAGCGCAGCGTTACCGCGGAGGCTTCGTGTC---ACGAGCCGATC	6264
Db	20362	ACTGCTCATCCAGCTCCCGTGTGCGGTGTGCTGCGAGACGAGACGAGCCGCTC	20421
Qy	6265	GCCATCGTTGGATGGCTGTGTTTCCCGCGGAGTGACCTCGCGGACGACTTCTGG	6324
Db	20422	CGGATCATTTGGATGGCGTCCGCTATCCCGGAGCGTCACTCAGCGAGGAGCTGTGG	20481
Qy	6325	GATCTGATCTCTCGAGCAGACGCGATCGCGGATTCGCCACGACCGCGGCTGGAC	6384
Db	20482	GAACTGCTCGCATCGGGGAGGACAGGTCGGCGAGTTTCCGACGACCGTGGGTGGAC	20541
Qy	6385	CTGGACAGCTCTACGACCCCGACCCCGACACCGCGGACCTGTACACCCGAAACGCG	6444
Db	20542	CTGGAGACACTGTTGATCCGGACCGGTCGGCGGGGACCTCGTACHACCCGCTGTGG	20601
Qy	6445	GGATTCCTCTACGACGCGAGCCACTTCGAGCGCGAAATTCCTGGGATCAGCCCCCGGAA	6504
Db	20602	AGTTTCCTCTACGACGCGGGGAGTTTCGAGCGCGGCTTCTTCGGGATCAGTCCGCTGAG	20661
Qy	6505	GCCTCGCATGACCCCGACGAAAGACTCTCTCGAAACCGCTGGGAAACATCGAA	6564
Db	20662	GCACTGGCATGACCCCGCAGCAGGATTCGCTGGAGGCTTCATGGGAGCCATGGAG	20721
Qy	6565	CACGCGGGATCAACCCCGACACCTTCACGCGCACCCCGAGTCTTCACCGGACCC	6624
Db	20722	CAGGAGGTATTGACCTACGACCGTACGCGGAGGACGACGAGGCTTCGCGGCTC	20781
Qy	6625	AAACGACGAGGACTACGACTTCGCGTGAC---AAGCGGGGACAGTCAACCGATGTTTC	6681
Db	20782	ATTTCGACGCGCTATGGAACCGAGCTGCAGGAAACCGCGACGACACCGAGGCTAT	20841
Qy	6682	GCACTGACCGGAACCGCGGAGGCTCATCTCGGTGCTATCTGTCACAGTTGGTTTT	6741
Db	20842	GTCTGACCGGCACATCCGGGAGTGGGCTCCGGTCTGATCTCTGTCACAGTTGGTTTT	20901
Qy	6742	GAGGTCCTCGGTGCGTGACAGCGTGTCTCTGCTGTTGGTGGCTTTGATCTG	6801
Db	20902	GAGGTCCTCGGTGCTGCTGACACCGGTTGTTCTGCTGTTGGTGGCTTTTACATCTG	20961
Qy	6802	GCTGTACGCGCTGCGTCCGGTGAGTCTCGATGGCGCTTCGCGGGGTGACGCTG	6861
Db	20962	GCTGTACGCGCTGCGTCCGGTGAGTCTCGATGGCGCTTCGCGGGGTGACGCTG	21021
Qy	6862	ATGTGCTCTCGGGTCCCTCTGAGAGTTTTCGCGCAGCGGGGTTCGCGCGGACGCGG	6921
Db	21022	ATGTGCTCTCGGGTCCCTCTGAGAGTTTTCGCGCAGCGGGGTTCGCGCGGACGCGG	21081
Qy	6922	CATTGCAAGCGTTCTCGCGCGCGGACCGGCTGGGCTGAGGCTGTGGGATG	6981
Db	21082	CATTGCAAGCGTTCTCGCGCGCGGACCGGCTGGGCTGAGGCTGTGGGATG	21141
Qy	6982	CTGCTGGTGGAGCGGCTCTCCGACGCCATTCGCAACGCTCACCGTCTCTCGCGGCTG	7041
Db	21142	CTGCTGGTGGAGCGGCTCTCCGACGCCCTCGTCCGCAACGCTCACCGTCTCTCGCGG	21201
Qy	7042	CGTGGAGTGGCTCAACAGAGCGTTCGAGCAACGCTGTGACCGCGCCGCAACGCGCGG	7101
Db	21202	CGTGGAGTGGCTCAACAGAGCGTTCGAGCAACGCTGTGACCGCGCCGCAACGCGCGG	21261
Qy	7102	TCCAGCAGCGTGTCTATCCGCGAGCCCTCGCCAAACCGCGGCTTGTGCGCGGTCGATGTC	7161
Db	21262	TCCAGCAGCGTGTCTATCCGCGAGCCCTCGCCAAACCGCGGCTTGTGCGCGGTCGATGTC	21321
Qy	7162	GACCGGTGGAGGCCACCGCACCGGACCACTTTTGGGCGACCCGATCGAGGCCAGGCC	7221
Db	21322	GATCGGTGGAGGCCACCGCACCGGACCACTTTTGGGCGACCCGATCGAGGCCAGGCC	21381
Qy	7222	CTCTCCGCGACTACGGACAGGACCGTCCGCGAGGGCGCTGTGGCTGGGCTCGGTC	7281
Db	21382	CTCTCCGCGACTACGGACAGGACCGTCCGCGAGGGCGCTGTGGCTGGGCTCGGTC	21441
Qy	7282	AAGTCCAATGTGCGTTCACACACAGCGTCCCGCGGCGTTCGCGGGGTGATCAAGATG	7341
Db	21442	AAGTCCAATGTGCGTTCACACACAGCGTCCCGCGGCGTTCGCGGGGTGATCAAGATG	21501
Qy	7342	ATGCGGCTGCGGATGTGCTGCTCCGCGAGCGTTGATGTGATGAGCCGTCGCGGAT	7401
Db	21502	ATGCGGCTGCGGATGTGCTGCTCCGCGAGCGTTGATGTGATGAGCCGTCGCGGAT	21561
Qy	7402	GTGACTGGTCCGCGGCTGCGTCTGCTGACGAGAGCGTCCCTGCGCCGCGGCGG	7461
Db	21562	GTGACTGGTCCGCGGCTGCGTCTGCTGACGAGAGCGTCCCTGCGCCGCGGCGG	21621
Qy	7462	GAGGCGGCTTACGCGCGGCGAGGAGTGTCTATTCATTCGCGGCTCAGCGGCACCAACGCCAC	7521
Db	21622	GAGGCGGCTTACGCGCGGCGAGGAGTGTCTATTCATTCGCGGCTCAGCGGCACCAACGCCAC	21681
Qy	7522	GTCTCTCTCGAAGG-----CACCGCGCAGCAGCGTT	7554
Db	21682	GTCTCTCTCGAAGGACCGCGCCACAACTCCCGTCAGACACACCGCGCGAGCGTT	21741
Qy	7555	CGGCGGACACCGCGCGGAGGCTGACCGCGGCGAGCGATGAGGCTGTCGCGGC	7614
Db	21742	CGGCGGACACCGCGCGGCGGAG---GATCCCGGTAGTGGCGAGAGGCTGCTGCGCGC	21798
Qy	7615	AGTCTGCGGCTGCGCGGCTGCTGCTGCGCAAGTGCAGCGCGGCTTCGCGCGCCAG	7674
Db	21799	AGTCCAGGCTGCGCGGCTGCTGCTGCGCAAGTGCAGCGCGGCTTCGCGCGCCAG	21858
Qy	7675	GCCAGGCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	7734
Db	21859	GCCAGGCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	21918
Qy	7735	TACACCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	7794
Db	21919	TACACCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	21978
Qy	7795	CGCGACGCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	7854
Db	21979	CGCGACGCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	22038
Qy	7855	ATCCACAGCGGCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	7914
Db	22039	ATCCACAGCGGCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	22098
Qy	7915	ATCTGCTCCGAGAGGACCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	7974
Db	22099	ATCTGCTCCGAGAGGACCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	22158
Qy	7975	CCGCTTCGCGCGGCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	8034
Db	22159	CCGCTTCGCGCGGCTTCGCGCGGCTGCTGCGCAACCGCGGCTTCGCGCGGATGTCGGA	22218
Qy	8035	CCCTCTCTCCCGCTTCGCGCGGCTTCGCGCAACCGCGGCTTCGCGCGGATGTCGGA	8079
Db	22219	CCCTCTCTCCCGCTTCGCGCGGCTTCGCGCAACCGCGGCTTCGCGCGGATGTCGGA	22278
Qy	8080	CGGCGGCTTCGCGCGGCTTCGCGCGGCTTCGCGCAACCGCGGCTTCGCGCGGATGTCGGA	8139
Db	22279	CGGCGGCTTCGCGCGGCTTCGCGCGGCTTCGCGCAACCGCGGCTTCGCGCGGATGTCGGA	22338



15745 GGTGGTTCGAAATGGGTTGACGGCGCCGAATGGTCTCGGCTCAGGAGCGGGTGATCCGGCAG 15804  
Db  
2323 GGGTTGGCGAAGCGCGGGTTGTCCTGGCGGATGTGGATGGTGGAGGGGACCGGACG 2382  
Qy  
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RESULT 6

RESUL 6  
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ID AAH79278 standard: DNA: 31422 bp.XX  
01761744

AC AAH79278;

XX  
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DT 04-DEC-2001 (first entry)

XX

DE Streptomyces avermitilis c

XX

KW Avermectin aglycone syntha

KW drug production; veterinary

XX

OS Streptomyces avermitilis.

100

FH	Key	Location/Q
FM	and	1. 1ACAC

FT CDS 1.14646

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PD 30-AUG-2001.

XX

PF 23-FEB-2001; 2001WO-JP0138

XX

PR 24-FEB-2000; 2000JP-004740

XX

PA (KYOW ) KYOWA HAKKO KOGYO

CC of avermectin aglycone synthase (AAS) derived from *Streptomyces*  
CC avermitilis. The activity of an acyl carrier protein (ACP),  
CC beta-ketoacyl carrier protein synthase (KS), acyltransferase (AT),  
CC beta-ketoacyl carrier protein reductase (KR), dehydratase (DH), enoyl  
CC reductase (ER) and/or thioesterase (TE) domain may be reduced or  
CC suppressed. The process can be used in the production of drugs, veterinary  
CC drugs and pesticides. The present sequence is a fragment of the *S.*  
CC avermitilis genome.

SQ Sequence 31422 BP; 4136 A; 10237 C; 11677 G; 5372 T; 0 other;  
Query Match 21.0%; Score 6437.2; DB 22; Length 31422;  
Best Local Similarity 69.9%; Pred. No. 0;  
Matches 9934; Conservative 0; Mismatches 2928; Indels 1350; Gaps 39;

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Qy 17572 CTC-----CACCAGCACACCCAAACCTCACTACCAACCCCGCCACACCCCGCTC 17622  
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Qy 17623 ATCACCGGACACCCGACCGGACCACTCTCAACCCCGCGCTACTGAGACCAACAGCC 17682  
Db 16834 GTCACCGGACACGAGCTCGAGCGCTCCGAGCTCGAGCGGCGTACTGATCGAAACCTC 16893  
Qy 17683 CGCAACCGTCTGACTAGCGCACACACCCCAACCCCTCCACCAACAGCGGCTACACACC 17742  
Db 16894 CGGCAACCGTCTCTGAGCGGACCGAGCGGCTCTCGAGATGGGATCGCTTC 16953  
Qy 17743 TACATCGAATCGGACCGGACCAACCTCTCAC-----CAGCCTCACCCACCAACCTCCCC 17799  
Db 16954 TTGCTCGAGGTACGCTCATCCGCTGCTCAGCTCGCGCTCCGAGACCTCGAGCGC 17013  
Qy 17800 AACACCCCGACACACCTCACTCAACCCCGGACCAACCCCGGACCCCAACCCACCTC 17859  
Db 17014 TCACGCTCGATCCCGCTGCTGCTGCTTTCGAGCGGACGAGGCGACCTCCCGCT 17073  
Qy 17860 CTCACCACTCGCCAAACACACACCTGCGACCCCGGACCTACACCCACCAACAC 17919  
Db 17074 CTCCTGCTCTTGGGCGGAGCTCTATGGCGGCGCTTCA CGCGCGAGTGGAGGCGCTTC 17133  
Qy 17920 AACCAACCCCGACACACCTCGACCTTCCCGACCTTCCCGCTTCCCAACACCAAGCAC 17979  
Db 17134 TTGCGCGCTTGGCTCCCGGAGAGTCTCATCTCCCGACCTACGCTTCCAGGCGAGGT 17193  
Qy 17980 TACTGGCTGAAAGACACAGCGCGGCTCGGATCGGGTTCGGGTTCGGGTTCGGGCGG 18039  
Db 17194 TTCTGGCTCGAGCGCGCGGACACACACCCGAA-----GGCGTGGCTCCCGCTGCG 17244

Qy 18040 GCAGGGAAGTGGCGGGAAGGAGAGTGGAGTGGCGTCTTGGGACGCGGTGGCGCGC 18099  
Db 17245 CCGATCGATGGCGGTTTTGGCAAGCCATCGAACCGGGGAGCTCGACGCGCTCAGCGG 17304  
Qy 18100 CAGGACTCGGAAACGGTCCGACACGCTCGCGTGGCGGCTCCCTCGCGCGGCTGGAACG 18159  
Db 17305 CAGCTCC-----ACGCGACGCGGAGAGCGCGCGCTCGCGCTG 17349  
Qy 18160 GTGGTGGCGGACATCTCGCGCTGGGACCGCGACCAACGACCAAGCCGCGATCAACACC 18219  
Db 17350 CTCTTCCACCTCTCGAGCTTTCACCAACGCGCCCAAGAGCAGACGCTCGACACC 17409  
Qy 18220 TGGAGCTTACAGGAAACCTGGAAACCTTCACTCTCCACCA-----CCACCAACCCAC 18276  
Db 17410 TGGCGCTACCGATACGTTGAGGCTCTGACCAACGCGCGCACGCGCGCGACCTCGCC 17469  
Qy 18277 CAACCTGGCTCATCGCCATCCCGAAACCCAGACCCACACCCCGCCACATCAACCAATC 18336  
Db 17470 GGCACCTGGCTCTCTGCTGCTGCGGCTCGGCGAGAGCGCTCTCCCTGCGACGCTC 17529  
Qy 18337 CTCACCACTTCACCAACGCGATACCCCGCTCCCTCATCCCTCACCTCAACACCAACCC 18396  
Db 17530 ACCGATGCGCTTACCGCGCGCGCGCGCTGCTCTCGCGCTGCGCTGAGCGAGGTTCA 17589  
Qy 18397 ACCAACCCCAACACTCTCACACACCGCAACAAAGCCCAAAACCAACCAACCGGACCC 18456  
Db 17590 ATAGCGCGCGGCTCTCACGAGACCTGCGGAGGCTGTGCGGAGACTGCC---CG 17646  
Qy 18457 ATCACCGGCTGCTCTCTCTCTCGCCCTCGACGAAACACCCACCCCGCCACACCCCGC 18516  
Db 17647 ATTGCGGCGGCTCTCTCTCTCTCGCCCTCGACGAGCGCGCTCGCGGACCATCGCGC 17706  
Qy 18517 ACACCAACCGGACCTCTCTCAACCTCACTCTACCCAAACCAACCAACCAACCAACCC 18576  
Db 17707 CTGCGCGCGGCGCTTGGCTCTCTGCTCGCGCTCTGCTCAAGCGCTCGGCGACCTCGCC 17766  
Qy 18577 CCAACCCCGCTCTGCTAGCGCACCAACCAACCGCACCAACCCCGCCCAACGAGCCCTC 18636  
Db 17767 GAGGCTCTCTGCTCTTTCAGCGCGCGCGCTCTCGATGGAGACTCGGACCACTC 17826  
Qy 18637 ACACACCCCGGACCAACCTTGGGGAAGTGGGGAAGTGGGGAAGTGGGGAAGTGGGGA 18696  
Db 17827 GCGCATCCACCGAGGCGCTGATCTGGGCTTGGGCGCGCTGCTGCGCTCGAGACCC 17886  
Qy 18697 ACCACACCGCGGAATCATGCTCTCCGACGACCGCCCGCCCGCCACCGCTCCACAC 18756  
Db 17887 GAGCGGTGGGCGGCGCTGCTGACCTCGGCGAGCGCTCGAGCGCGCGGCGCGGCGC 17946  
Qy 18757 CTCACCAACCCCTCACCCACCCCGCACCAACCAACCAACCAACCAACCAACCGGCG 18816  
Db 17947 TTGCTCCCGGCTCTCGCCAGCGCACGAGAGACGCTCGGCTCGCGCGCGCGCGCGC 18006  
Qy 18817 ACCACACCGCGCGCTCACCCCGCACCGCTCACCCCGCACCAACCAACCAACCGCC 18876  
Db 18007 CTCTAGCAGCGCGCTTCTGCTCGCGCGCGCTCGCGGATGCGCTCGCGCTCGCGGCTC 18066  
Qy 18877 ACCCGCGGGAACCACTCATACCGGCGGAACCGCGCGCTCGCGCGCGCTCGCGCGCT 18936  
Db 18067 ATGCGCGGAGGACCATCTCATACCGGTGGTACCGCGCGCATTTGGGCTTCACTCGC 18126  
Qy 18937 CACCACTCACCGACCGACCGACCGACCGACCGACCGACCGACCGACCGACCGCGCC 18996  
Db 18127 CGATGGCT---CGCTCGAAAGGCGCTGAGACCTCTCTCATAGCGGAGGCGCC 18183  
Qy 18997 CACACCCCGGACGACCAACCTCACCGCGCTTCCAAACAAAGGATCCACTCACC 19056  
Db 18184 CAGCGGAGGCGGCTGAGCTCCAGCGGCTCACCGCGCTCACCGCGCTCGCGCGGCTCACC 18243  
Qy 19057 ATCAACACCTGCGGACACAGGACCGGACCACTCCAAACAACTCTTCAACCAACATCCC 19116  
Db 18244 TTCCCGCGTGGATGTGCGCGACGAGGCGCTGTGCGCACGCTTCTCGAGCAGCTCGAC 18303

CC attack by phytopathogens.

Sequence 28958 BP; 4084 A; 11863 C; 8356 G; 4655 T; 0 other;

Query Match	10.2%	Score 3140.6;	DB 18;	Length 28958;
Best Local Similarity	54.11%	Pred. No. 0;		
Matches 8239; Conservative	0;	Mismatches 6284;	Indels 698;	Gaps 63;

[illegible]

Qy	14872	ACGACCCCAACAAACCCCGCTCGGTGATGTCCTCGTGGGCAAGTCTCCGAGGAGCGAGAC	14931
Db	14236	ACTGCCCTCGCTCGTCTGACAGACACCTCTCTCCCTCCCGCCGCGAAGCGAG	14295
Qy	14932	GAAGAGCTGTGGCCTGTGGCAGCCATGGGCGGTGCTCGGCGCATGCCACTCCC	14991
Db	14296	CGCGTCTCTCGATCTCGTCGCGACCGAAGCGCGCTCGGTCTCGGCTCGCCTCGTTC	14355
Qy	14992	GAAGTGATCGTTCGGAACAAGGCCTTCAAAGAGCTGGGTTTTGATTTCTTCGCCCAATT	15051
Db	14356	GAATCGCTCGATCCCATCGCCCTCTACAAGAGCTCGGCTCGATTCCCTCATGSCCCTC	14415
Qy	15052	CAGCTTCGTAAACGACTGCTGTGTGAGTGTGACTGTCGCGTTCGGCGCACGGTGTATCTTC	15111
Db	14416	GAGCTCCGAATCGACTCGCGCGCGCGCGGCTCGGCTCGAGCTACTCTCTCTCTTC	14475
Qy	15112	GATTTACCCACATCCGATGGCGTTTGCAGTTCTCTCGGCGCGCGATCGTCGGAGCGGAC	15171
Db	14476	GACTATCCAAACCCGACTCGGCTCTCACGCTTTTTCACAGCCGATCTCTTTCGG---GGGA	14532
Qy	15172	ACAGGCACGACCACTCGTCTGCGCGTTAACTGGCGTCCCGCGCGAGCGCATCGCCATC	15231
Db	14533	ACCACCAACGCGCCGCGTACGCTCACCCGGGGGAGCGAAGACCTATCGCCATC	14592
Qy	15232	GTCCGATGCGCTGTGCGTATACCCCGGTGATGTACGAGCGGTGATGATCTCTGGCAGGTG	15291
Db	14593	GTGCGATGAGCTGCGGCTTCCGGCGCAGCTGCGCACGCCCGAGGATCTCTGGAAGCTC	14652
Qy	15292	GTCAGTGTGGCCATCAGCGGATCGCGGATTTCCGAGCAACCGTGGGTGGGACCTCGAC	15351
Db	14653	TTGCTCGACGGACAAATGCGATCTCGGCTTCCCAAAATCGCGGTGGAGTCTCGAT	14712
Qy	15352	ACGCTGTACAACCCGACCGGACCGGACCAACCGAAACAGCTACACCGGAGCGGCGGATTC	15411
Db	14713	GGCGT-----CGAGCCCCCGGTGCGTTCCTCCAGTCCGGAGGGGGGCTTC	14757
Qy	15412	CTTTACGACGCGGCAATTCGATCCGACTTCTTCGGTATCAGTCCCGGTGAGGCACTG	15471
Db	14758	GTCTACGACGCGACGCCCTTCGATCCGGCTTCTTCGGGATCAGTCCAGTCCGAAGCGTTC	14817
Qy	15472	GCGATGACCGCGACGAGCGGCTGCTGTGGAAACAGCGTGGAGAGCATCCAAACGCG	15531
Db	14818	GCGTTGATCCCAACAGCGCATTTTGCTCGAGATCACATGGGAAGCCTTCGAGCGTGA	14877
Qy	15532	TGCATCAACCCGACAGCCTTCGTGBCACACCAACCGGCTCTTCGCGGGCTGACCTAC	15591
Db	14878	GGCATCGACCGGCTCCCTCCAAAGGAGCAAGAGCGGGTCTTCGTTGGGTATGGCAG	14937
Qy	15592	CAGCACTACGCGGGGCTTCCACAGCTCCGGCAGGGTTGAGGGGTATCTCGGGAC	15651
Db	14938	AGGCACTACCAATGCAATCGCTGTGAAACGCACTGGCGAATCAAGGACTCGTTGCCACC	14997
Qy	15652	GGAAGCGCAGGAGTATCGCTCGGGTGTGTGCGCTACGCTCTCGGCTGGAAGTCCG	15711
Db	14998	GGTAGCGCAGCGGT---CGGTCCGGCGGAATCGCATACAGTTCCGACTTCAGGGGCC	15054
Qy	15712	GCCTCACAGTGCACACTGCTGCTCTTCGTCCCTGGTTCGTCTGCACCTGCGCTGTGAG	15771
Db	15055	GCCATCAGCGTGGAGACGGCGTGC---AGCTTCTCGTCGCGGTTCACTCGCTGCCAG	15111
Qy	15772	GCCTCGGTCGCGCGAGTCTTCATGGCCCTCGCGGTGGCGTCACTGATGTCAACC	15831
Db	15112	GCCTCCCCCAACGGCGAATCTCCCTGGCGCTGCTGGCGGGGTGACCATATGCGCCAG	15171
Qy	15832	CCGCGCGGGTTCGTGGAGTTTTCCGGCGCAGCGGGGCTTGGCGTGGAGCGGGCGTCAAG	15891

Db 63759 AGTCTCCGCGAGGGTGTTCGACCTGTGTGATGCTGCTGTGGGGTGTGTGCGTTC 63818  
QY 28977 GCGCAGTCCGAGCACCCGACCGCATCACGCTGTCTGGACTTCGACGGGGGACACAGGC 29036  
Db 63819 GCGCAGTCCGAGAACCCGACCGATTCGTTGTGTCGATGTGAGCGGAACCGCCGATC 63878  
QY 29037 GGAGCCCGTCACTAGTCGCGACCGCGCTGAACTGCGGGGAGCGCAGCTTGTCCGTCGCGCC 29096  
Db 63879 ATGCG---GTGCGCTCGCGCGCGCTGCGTTCCGGAGAACCGCAGCTGCGGTTCGCGC 63935  
QY 29097 CCGAGGGCTTTCACGCAAGGCTGTGCGCGGCCACGTGTGCGCGACCGCTACCCGC 29156  
Db 63936 CGGTGAAGTCCCGGTTCCTCGCTGCGCGCATGTGTTCGCGCGAGCAGCGGATCCC 63995  
QY 29157 CGTACCCGCGTGGCGGTACCGTCAAGCGGTCAAGCGCGTACCGGAGCGGTCCTT 29216  
Db 63996 AGTGCCCGTG----- 64006  
QY 29217 CTTTCGCGCGAAACCGTCTGATCACCGCGGAAACCGTGTCTGCGCGCGCTCGTGC 29276  
Db 64007 -----CGGATGGACCGTGTGATTTCCGCGGTACGGCCCTGCTGGCGGGTGTGTC 64061  
QY 29277 CCGGCTCTGTGGAGCGCACCGGTACCGCATCTGTCTGTGGCGGTGCGCGCGAC 29336  
Db 64062 CCGGCTTTGGTGGCGAGCGCGGTGTCCGCGCCCTGTGTCTCGCGGGCGACGCGGTG 64121  
QY 29337 GGAACCGGAGGTGCGCGGAGTTGCGGCGAGCTCGGTGGCTCGCGCGACGCTGA 29396  
Db 64122 GAGCGCCCGGGTCAACGACTGTGTGATGATGATGTTGGTGGCTTGGAGCTGCGGTGA 64181  
QY 29397 GTCTGTGCTCGAGCGCGGACCGGACGAGCTGCGCGACCTGCTGTACACGATCCC 29456  
Db 64182 CGTGGCGAGCTCGATGTGCGGATCGGCCCACTGTGACCGCTGCTGACGACGATCTC 64241  
QY 29457 CGACGATCGCGCTGACCGGTGTGTGACAGTGGCGGATCTGAGCAGCGGTGAT 29516  
Db 64242 GCGAGATTTCCGCTGCGCGAGTGTGATCGCGCGCGGACATGCGCGACGGGTCT 64301  
QY 29517 CAGCTGCTGTGCGCGAGCGCTCGGGCGCTGCTCGCGGCAAGGCGAGCTGCGT 29576  
Db 64302 CGAGTCTGTACACGAGCAGTGTGCAAGTGTTCGGCCGAGAGCGCGCGTGTG 64361  
QY 29577 GCTTCTGACGAGTCAACCGCGCGGACGAGCTGTGCGCTTTCGTCATGTTCTCTCCG 29636  
Db 64362 GCACCTGCAAGTGTGACTCTTGTATCTGATCTCTGTTCTTCTGCTCTCTCTCTCT 64421  
QY 29637 GTCCGGGTGTGCTGCTGCTGCGCGGAGGCACTACGCGCGCGGACGCGCTCTGA 29696  
Db 64422 CTCGCGGTGCGCGGGGCTGCGGGTCAAGGAACTACGCGCGCGGAAACGCGTTCCTGA 64481  
QY 29697 TTTCTTGTCTATCGCGCGCGCGAGGGGCTGCGCGCTCTCTCTGCGCTGCGGCT 29756  
Db 64482 CGGCTGTGCTAGCAGCGCGAGCGCGGGTGTCTGCGGTGTCTGCTGTGGGGCTT 64541  
QY 29757 GTGGAAGAGGACACAGGATGACGGGCCACCTCGACGCTCGACGACCATGCGCGATCAG 29816  
Db 64542 GTGGAGACGCCACCGGATGACCGAGCGCTCGATGCGCGGGCGCTAGCGGATTCG 64601  
QY 29817 CCGCGGGATGCGCGCGCTGCGACGTGCGAGGCTGTGGCGCTGTTCGACGCGGCTT 29876  
Db 64602 GCGCACCAATCCGCGCGATGTCCGCGCGGACGGTGTGCGGTGTTCGAGATGCGGTTTCG 64661  
QY 29877 GCGCGAGCGGAGCGTTCCTGATCGCGCTCGGCTCGACCTCAAGCGGCTGCGTGG 29936  
Db 64662 GTTTCGGGCGAATCGTTCTGTTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGTT 64721  
QY 29937 TGCCGCTGCGACCGGTCGCGCGCTGTGCAAGGTTCGTTTCACTGCTGCTGCTGCTG 29996  
Db 64722 TGCGCGCGAGCGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64763  
QY 29997 CTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 30056  
Db 64764 ---GCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 64820

QY 30057 TGAGCGTCTGCGCCCGCAGAGTGCCTGAGCGCAGGCGGCTGCTGCGCTGCTGCG 30116  
Db 64821 TGTGCGCTGCGAGGCTGCCGACCTGATCAGGAACCCAGCTGTTGGGTTTGTGCG 64880  
QY 30117 GTTCGATGTGCGCGCGGTGCTGCGCATAGCGGTGCGGACGGAATCGACGATCGCGGC 30176  
Db 64881 CGAGCATGTTTCGCGCGTCTGCGGCAATTCGGGTGCGGTTCGAGGTCGCGGCGCATCTGC 64940  
QY 30177 GTTCCGCGAGCTGGGGTTCGACTCGCTCAGCGCGTTCGAGTCCGCAACCGTCTCACGC 30236  
Db 64941 TTTCCGGGATTTGGGTTTGTATTCGTTGTCGGTGTGAGTTTCGAAACCGCTTGGCG 65000  
QY 30237 CCGCAGCGCGCTGCGCGCTGCGGCGCACCTGCGCTTCCGATTTCCCGACCGCGCAGCGCT 30296  
Db 65001 GGTGCTGGCGTTCGTTGCGCGCTACTGCGGTGTTCCGACTATCCGACACCGCGGCGTT 65060  
QY 30297 GCGCGAGCATTTGGCGGAGCGTCTGCTTCCGACACGAGGCGCACG 30342  
Db 65061 GGTTCGCTTCTGCTCGACAACTGATTTGGTGGCGTGGAGGCTCG 65106

## RESULT 15

AAT89956

ID AAT89956 standard; DNA; 28958 BP.

XX AC AAT89956;

XX DT 12-MAR-1998 (first entry)

XX DE Sorangium cellulosum soraphen gene cluster genomic DNA.

XX KW Soraphen; polyketide synthase; PKS; antipathogenic; antibiotic;  
XX KW transgenic plant; phytopathogen; resistance; ss.

XX OS Sorangium cellulosum.

XX PN US5662898-A.

XX PD 02-SEP-1997.

XX PF 01-JUN-1995; 95US-0457342.

XX PR 20-AUG-1990; 90US-0570184.

XX PR 02-JUL-1992; 92US-0908284.

XX PR 31-AUG-1992; 92US-0937648.

XX PR 01-JUL-1993; 93US-0087636.

XX PR 08-JUN-1994; 94US-0258261.

XX PA (CIBA ) CIBA GEIGY CORP.

XX PI Beck JJ, Gaffney TD, Hammer PE, Hill DS, Lam ST;

XX PI Ligon JM, Ryals JA, Schupp T, Uknes SJ;

XX WPI; 1997-447901/41.

XX PT Protecting plants against pathogens with genetically transformed  
XX PT biological control agent - which expresses all polypeptide(s)  
XX PT involved in pyrrolnitrin biosynthetic pathway

XX PS Ex 16; Column 104-128; 88pp; English.

XX CC This genomic DNA sequence encodes the Soraphen gene cluster. This  
XX CC sequence encodes two open reading frames (ORF's), the positions of which  
XX CC are not given in the specification. ORF1 is approximately 25.5 kb in  
XX CC size and encodes 5 biosynthetic modules homologous to the erythromycin  
XX CC genes of *Saccharopolyspora erythraea*. Each module contains a  
XX CC beta-ketoacylsynthase (KS), an acyltransferase (AT), a ketoreductase  
XX CC (KR) and an acyl carrier protein (ACP) domain. ORF2 is immediately  
XX CC adjacent to ORF1 and is thought to contain 3 modules. Soraphen is a  
XX CC type I polyketide synthase (PKS) which has antibiotic activity.  
XX CC Transgenic plants containing such antipathogenic genes like those  
XX CC encoded in the Soraphen cluster should have enhanced resistance to



QY 26760 GCGCAGCCGCGCAGTACGAGCGCGGCGCCTACGTCGCCCTGCC 26819  
DB 61833 CCGCTGCCATGCGGTGTCGCGCTGACCGGGAAGGAGGATGCTCGCGATGCTTCC 61892  
QY 26820 CCGCCAGGACGTCGAGCAGCTCATTTCCGAACCGTGGGAAGGCGAGTTGTGGGTGGCAGC 26879  
DB 61893 GGAAAGCGCGGTGTGAAGCAATCGCAGGCCCTGCCG-----AGCTGACCGTTGCGGC 61946  
QY 26880 CCTCAACGCCCCCACTCCACACCGTCTCCGCGACACCAAGCGGTGGATGAGTGCT 26939  
DB 61947 GGTCAACGGAACCCGCTCCACTGTCTGTTTCCGCGCAACCGTCCGCTCTGGAGCGTCTGCA 62006  
QY 26940 GCGCAGCTGCACGACACCGGCTTACGGGCCAAAGCATCCCGCTCGACTACGCTCCCA 26999  
DB 62007 GACCGNACTGACCGCGGAACAGTGCAGACCCGCGGGTGGAAATTGATTAGCCCTCGCA 62066  
QY 27000 TTGCCCCCAGCTCCAAACCCCTCCAGAGAAATCTCTGCACTGCTGGAGAGATCACCCC 27059  
DB 62067 TTGCGCCGAGATCGGCGAGGTCCAGGCGCGCTTCTGACCCGCTGGGCGAAGTCGGGTC 62126  
QY 27060 CCAGCGCTCCAGTCCGCTTCTTCTCAACCGTGGNAAGCACCCTGGCTGGACACCAAC 27119  
DB 62127 CGAACTGTGAGATCGCTTTCTACTCGACGCTCACCGCGAGCGGACACCGGCG 62186  
QY 27120 CCTGACCGCGCTACTGTGATCCGCAACCTCCACAGCCCGCTCCGCTTCAGCCAGCCAT 27179  
DB 62187 ACTGACGCGGACTACTGTGATCAGAACTTCCGAGCCCGTCCGTTCCAGCAGCGT 62246  
QY 27180 CCAGACCTTGACCGAGCAGACCGCGCTTTCATCGAAATCAGCCCCCAACCCCT 27239  
DB 62247 CGCCCGGATGGCAGATCAGGCTATCGGTTCTTCGTGAGGTGAGCCCGACCCGCTGCT 62306  
QY 27240 CGTCCCGCATCGAAGACACACCGAANAACACCCAGGAAACATCACCGGACCGGAG 27299  
DB 62307 CACCGCCGGAATCCAGGAACCTCGAAGCCCGGACCGGCGGGTGGTGGTTC 62366  
QY 27300 CCTCGCCCGCGGACAGCAGACACCGCTTCTCAGCGCCCTCGCCACACCCACAC 27359  
DB 62367 GCTGCGGCTGGGAGGGCGGCTCCGCGGCTGGTGATCTTCGTTGGCGAGTGCAGGT 62426  
QY 27360 CACCGGATCGGACACCCACACCTGGCACCACCACTACACCCCAACCCACCC 27419  
DB 62427 GCGCGGACTCGCGGTGAATTGGGAACAGGTATTTCTCAACCGGAGCCCGAGCGGTGCC 62486  
QY 27420 CAAACCCACACCCACTCGACTCGCCACTTACCCCTTCCACACCGACTACTGCT 27479  
DB 62487 -----GTGCGGACCTACCGGTTCCAGCGGCGAGCTACTGTT 62525  
QY 27480 CCAACCAACCC---ACCACAAACAGACCTCACACCGGCTCACCGCCCTCACCCCAACCA 27536  
DB 62526 GGAGTCCGCGAGTACGACCGGGCGATCTCGGTTGGTGGGCTTCTCCGCGAGCA 62585  
QY 27537 CCGCTCTCTACCGGCACACTCACCTCGCGGACAAACACAACTACTACCGGCG 27596  
DB 62586 TCCCTCTCTCGGGCTGCGGTGACGTGCGGATGCGGCGGCTTCTCTGACCGGCA 62645  
QY 27597 CTTCTCCCTACGACCAACCTTGGCTCACCGACACCGTTCGCGGATGGTCTCT 27656  
DB 62646 GTGTCTGGTCAAGACCCCTTGGTTGGCCGACCACTGGTTCGCGGGCGATCTGCT 62705  
QY 27657 GCGGCGACCGGCTCTCGAACTCGCCCTCAAGCGCGGAAAGGCTGGAATGCGCCCTCG 27716  
DB 62706 GCGCGCACCGGCTTCTGGAATGCTGATACGCGCGCGGACAGGTGGGTGCGATCT 62765  
QY 27717 GTTGGAGGAATGACCTTGAACGCACTGTTGTGATCTCCGCAACCGAGGACGTGACGTT 27776  
DB 62766 GATCGAGGAGTTGCTCTGACGACTCCGCTGTTTGGCCGCGACCGGTGCGGTGCGGT 62825  
QY 27777 GAGGTTCAGGTTGCGGAGCCGATGAGATGGCCATCGGCCCTCGCCATCCATCTGTA 27836  
DB 62826 GCAGATCGCGGTTGGCGGTCCGAGACGAGCCGCGGCCCTCGGTCGCGTGCATTTCTG 62885  
QY 27837 CTCCGCGACCGGCTCTCGGCGGACCGGAGTGGACCCCGTCAAGCCGCGGCTCTCTAC 27896

DB 62886 TCGAGACGACGCGCGTCCGCGAGAC-----TCGTGACCTGCCACGCGACCGCAGCTTGAC 62942  
QY 27897 ACACCAACCGGACACCGATCACCGTCCGACACGACACCGACCGCTTGGCGGAG 27956  
DB 62943 -----CTCCAGCGATCACAGGACCGCGGCGCGGCGCCGATGGAT 62984  
QY 27957 CTGSCCCCGCGCGCGCAGCCATCGAACTTGGGCGAGCTCTACGCTGCTATGGGCGC 28016  
DB 62985 TTGSCCGCCCAACGATGCTGTGCGGTTCCGCTGGACAGCTTCTACGCGC---CGAGC 63041  
QY 28017 GGACTCGGACATCCCTACCGGCGCGCTTCCAGGGGCTGCACCGCCTGGAGGTTCCG 28076  
DB 63042 TGACGCGGCTTCGATTTCCGCGCGCTTCCAGGGGTTGCAGCGCTTGGAAAGCGCG 63101  
QY 28077 CGACGATGCTCTGCGCCAGGTGCTCTCCGGAAGAGGCTCTGCGCATGCTCCGCGCGC 28136  
DB 63102 AGACGAGATCTTCCCGAGGTGCGCCTGCCC-----CACCGCACACCGCGAAGACGCGCG 63155  
QY 28137 GGCCTTCGCTGTTCAACCGCGCTTCTCGAGCGCGCCTTGACCGCCACGCGCTCACCCC 28196  
DB 63156 CAGGTTGGGAATCCACTGCTGCTGCTGATGCGGCACTGACGGGCTGGCGGAGCGCA 63215  
QY 28197 CCAGAACGGGACGCGCTCGACGGAJACGTGCCCCAGAGAGCATGCTGACCGCGCAGC 28256  
DB 63216 AGAGGATCCGAGC----- 63229  
QY 28257 CCACAGCGCGACTGCGCTTACGTTGAGGGGCGTGTCTCTGACACAGCGGCGGAGTTC 28316  
DB 63230 -----AGGGAATGGCTCCCGTTCCGCTGGCAAGGTGTGTCTCAAAGCGAGCGG----- 63278  
QY 28317 CGTGTGCGGTACGCTGTCGCGAGTCCGACAGCAGTAAATGCGTGGGCTTCACCGC 28376  
DB 63279 CGCACTTCTTCCGCTGACCTGTTCCGCGCGGCGGAGTGGGTGTCGTTGTTTAC 63338  
QY 28377 GCGCAGAGGACGCTCGGCGGTGGTGAAGATCGAGTCTGCTGCGCTGCGCGCGGTGTC 28436  
DB 63339 GACCGACAGCTGCGCAAGCGTCTCTCATGATTCGCTGCTGCTGCGCCAGATTC 63398  
QY 28437 CACGAGGAGTCCGCGGCGCGGATCGTACCGCGGACGAGTCTGCTTCCGACT 28496  
DB 63399 GGACAGCAGTTGGCAGCGGCG-----CGTGCAATGGAAACAGAGTCTTCTTCCGGT 63452  
QY 28497 GGACTGGGTTTTCGTAACAGTCCCGCGCGCAACCGCCCTTCCGCCACCGCGACCGGCTG 28556  
DB 63453 CGACTGGAGCGAAT-----CTCGCGCGGCGCTGCCAAGCGGCTCTCTG 63497  
QY 28557 GCGGCTCATCGCGCGGCGCTTCCCACTCCCGGCTGACGAGACGAGCAGTGCAC 28616  
DB 63498 GGCAGTGATCGC----- 63516  
QY 28617 CGGCTATGACGAGCGCGGAGCTGCTTCTGGCTCTGACCGCGGTGCTCCGCGCGCGG 28676  
DB 63517 GAACCTCGCGCGGCTTGGGCTCGGCACTTGGGCAACCTTCCACCGGACTGACCGCGG 63576  
QY 28677 TGTGCTGCTGATGCTGTCGCGCAACCGAAGCCGCGAGTATTCGCGCGGAGCGCC 28736  
DB 63577 TTGGCT----- 63590  
QY 28737 CCGGAGCGCGGAGCCGAGGCTCGAGGCGCGCGCGGACGCTGCTGACGTGGGGCTGCT 28796  
DB 63591 CCGGAGCTGCTGTTGGTGGTCCATGCGGTGCTCTCGCCAGGACTTGGACGTTG----- 63643  
QY 28797 GCACAGGCTGCGCTGACAGCGGCTGCGCGCGAGATGTTGGCCAGGCTTCCAGGCTGCT 28856  
DB 63644 -----CTTCCAGGACGCTGCGCGGACAAACGATGCTTACCTGATCCAGGATTTGTT 63698  
QY 28857 GGGCGACAGCGCTTCGACAGACAGCGGCTGCTGCTCTGACGTGCGCGCGGCTGCGCGC 28916  
DB 63699 GCGCGCGCGGATTCGCGCGGATCTCGGCTGTTGAGTGTGAGTGTGGGTGCGGCTGAC 63758  
QY 28917 CGCTTCGCGGACGATGCGACGGAACCTTCCCGGCGCGCGCTGCTGTTGGGGCTGCTGCTTC 28976

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Db 59661 ACGGCACGGCCAGAGCGACGTCAACCCCAATCGCTGACGGCGGCCACGAGACGAAATCT 59720
Qy 24748 ----- 24747
Db 59721 TCGACCTCATCGACCGGAAGTTCCGGCGCTGACCGCCCTTTCTCGCCTCAGCTCCCTG 59780
Qy 24748 -----CCGCAAGTG 24756
Db 59781 ATTACTGGAACGGTGTATTTCGATGGCCAAATGAAGAAAGCTCCGCGAGTACCTCAAGCG 59840
Qy 24757 GCCCATCGCGTAC-----CGTCGAGA 24779
Db 59841 TGTGCTGTCGAACTGGAAGAGCGGCGACGAACCCCTGCGACGAGTTGGAGCGCCAGAGCA 59900
Qy 24780 CGAACCGATCGGCATCATCGGTATGGCATGTCTGCTTCCCGCGCGCTACGTTCTGCGGA 24839
Db 59901 CGACCCCATCGGATCGTGTGATGGATGTGTTATCCCGTGGGTTCTCACTCCGGA 59960
Qy 24840 CGACTGTGGGAATTGCTCGCTTCGGGTAAAGACGCTATCGCGCTCTTCCCGACCGACCG 24899
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Qy 24900 CCGCTGGGACCTGGACACCTCTACGACCCGACCCGACACCCCGGACCTGCTACAC 24959
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26581 ACCTCGGCGGACCAACCGCTGCTCGGCGCGCTGCTGCGCGCTCGCGCGCGCGCGCT 26640  
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27763 GAGGAGGTGAGCTTTCAGGTTCAGGCTTCGCGGCGCGGATGAGAGTGGGCGCATCGCGCG 27822  
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Db 28788 CGCTCGCACCGTACGCAAGGCCGCCAGCAACACCGCCCCAGG 28828

Search completed: June 18, 2003, 21:35:33  
Job time : 9370 secs

THIS PROJECT IS A SERVICE (COST 10)

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2003, 03:36:49 ; Search time 894 Seconds  
(without alignments)  
10527.863 Million cell updates/sec

Title: US-09-914-286-1  
Perfect score: 30690  
Sequence: 1 gtcagagatggacgcgg.....acgaagtgagacagcgtga 30690

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3194.8	10.4	49377	1 US-08-764-233A-1	Sequence 1, Appli
2	3142	10.2	80161	3 US-09-036-987A-1	Sequence 1, Appli
3	3142	10.2	80161	4 US-09-370-700-1	Sequence 1, Appli
4	3140.6	10.2	28958	1 US-08-258-261B-6	Sequence 6, Appli
5	3140.6	10.2	28958	1 US-08-456-837-6	Sequence 6, Appli
6	3140.6	10.2	28958	1 US-08-457-342-6	Sequence 6, Appli
7	3140.6	10.2	28958	1 US-08-457-646A-6	Sequence 6, Appli
8	3140.6	10.2	28958	1 US-08-458-076A-6	Sequence 6, Appli
9	3140.6	10.2	28958	1 US-08-764-233A-4	Sequence 4, Appli
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13	2956.6	9.6	38506	3 US-09-320-878-19	Sequence 19, Appli
14	2951.8	9.6	36778	4 US-09-105-537-5	Sequence 5, Appli
15	2939.8	9.6	43280	2 US-08-804-227C-1	Sequence 1, Appli
16	2663	8.7	44377	2 US-08-804-227C-7	Sequence 7, Appli
17	2663	8.7	44377	2 US-08-804-198-1	Sequence 1, Appli
18	2342	7.6	13842	4 US-09-105-537-30	Sequence 30, Appli
19	2304.2	7.5	50937	4 US-09-428-517-1	Sequence 1, Appli
20	2188.4	7.1	15872	4 US-09-105-537-1	Sequence 1, Appli
21	2140.6	7.0	11220	4 US-09-105-537-32	Sequence 32, Appli
22	1852.8	6.0	13987	2 US-08-804-227C-13	Sequence 13, Appli
23	1800.8	5.9	33529	1 US-09-144-085-3	Sequence 3, Appli
24	1783	5.8	20235	1 US-07-642-734C-3	Sequence 3, Appli
25	1783	5.8	20235	3 US-08-439-009A-3	Sequence 3, Appli
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28	1007	3.3	71989	4 US-09-443-501A-2	Sequence 2, Appli
29	1004.4	3.3	4041	4 US-09-105-537-36	Sequence 36, Appli
30	992.4	3.2	4689	4 US-09-105-537-34	Sequence 34, Appli
31	985	3.2	68750	3 US-09-335-409-1	Sequence 1, Appli
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45	371.6	1.2	1010	3 US-08-858-003-29	Sequence 29, Appli

ALIGNMENTS

RESULT 1  
US-08-764-233A-1  
; Sequence 1, Application US/08764233A  
; Patent No. 5716849  
; GENERAL INFORMATION:  
; APPLICANT: Ligon, James M.  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Beck, James J.  
; APPLICANT: Hill, Dwight S.  
; APPLICANT: Neff, Snezana  
; APPLICANT: Ryala, John A.  
; TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ciba-Geigy Corporation  
; STREET: 520 White Plains Road, P.O. Box 2005  
; CITY: Tarrytown  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/764,233A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/258,261  
; FILING DATE: 09-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/258,261  
; FILING DATE: 08-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: 1506/CIP6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8587  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 49377 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:





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QY 19474 ATGTTCCCATTCGCGCGCGGAGTTGGCGGTCAAGCTGTGTGACGGCGGATCGCGAGGG 19533  
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QY 19594 AAGTCGTGGTCTGTCTCGAG---GACCTTCCCGAGCAGAGGAACTGAGAGCGCGCG 19650  
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QY 19651 -----AGTACCGTTGAGCAGACGAGAGCAACAACCTCCGCGCAACTCTCATGGTGG 19704  
Db 35147 GCGGATGGTCTCTCGAGCAAGACGCGGCGCACAGGCTCTCTCGAAGCTCCGAAACCG 35206  
QY 19705 TCAGTTCGAGCAGAGAGAGAGTCTGCTAGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 19764  
Db 35207 TCGAGAGCAGCAGATCCACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 35266  
QY 19765 CTGCGCGCAGCAGCTCCGAGGCGCATCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 19824  
Db 35267 CTGCGCATACCGAGCGCTCCAGGTGACCCCAAGGGCTTCATGGACCTCGGCTC 35326  
QY 19825 GACTCGCTTGGCGGCTGAGCTTCGCAACACCTCCGACAGACAGAGAGCTGGCTGTG 19884  
Db 35327 GATTCTGCTATGACCGCTGAGCTTGTGCGGCTTTCGAGAGGCGCACCGGATCAAGCT 35386  
QY 19885 CCGACGATCTCTGCTTTCGATATCCCGAGCGCCACCAAGCTGCGCCAAATTTCTGCTCTC 19944  
Db 35387 CCGGCCACCTCGCTTTCGACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 35446  
QY 19945 GAGATCCGCGAGTTCCAGCCGACA-----ACTCAACTCCGCTTCCG 19986  
Db 35447 TCGCTCCCGACCGCTTCGCGCGAGGCTCTCGTCCAGCGCGAGCGCGCGCTCCG 35506  
QY 19987 CGACCCCGGCGAGCTTCGATGAGCGGATCGCCATCGTTGGCATGGCTGTGCTTCC 20046  
Db 35507 GCGCTTCTGCTCGCGAGCGAGCGGATCGCCATCGTGGCATGGCTTGGCTTGGCT 35566  
QY 20047 GCGGAGTACTCTGCGCGAGGCTTCTGGATCTGATCTCTCCGAGCAGGAGCGGATC 20106  
Db 35567 GCGGCGATCGCGATGTCGACGCTCTTTGGAGTTCTCTGCGCCAAAGGAGCGGAGCGCT 35626  
QY 20107 GCGGATTTCCCGACCGCGCTGGAGCTGAGACAGCTCTACGACCGCGACCCCGAC 20166  
Db 35627 GAGCCCATTTCCCATGCGCC---GATGGAGTGGCGGTGCTCTACGACCCCGACCCCGAC 35683  
QY 20167 CACCCCGGCGCTCTGTACACCCGAAACGCGGATTCCTCTACGACGCGAGGCGCATTCGAC 20226  
Db 35684 GCGAAGCGAAGAGCTAGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGAT 35743  
QY 20227 GCGAATTTTGGCATCAGCCCGCGGAGGCTCTGCGCATGAGCCCGGAGCAAGCACTC 20286  
Db 35744 CCGCTCTTTTGGCATCAGCCCTCGGAGGCGCAAAATACCTCGACCCCGGAGCGGCTG 35803  
QY 20287 CTCTTCAAAACCGCTCGGAAACCATCGAAGCGCGGCTCAACCCCGGAGCGGCTCCAC 20346  
Db 35804 CTCTCGAATCTGCTGGCTGGCTCGGAGCGCGGCTGCTGCTCTCTCTCTCTCTCTCTCT 35863  
QY 20347 GGCACCCCGGAGTCTTTCACCGGCAACCGGACGAGGACCGGCGGACACATCGGT 20406

Qy	21484	TACACCTCGCCACAGCGCCGCGCTGTTCGACCAACCGCGCCACACCTCATCGCCCGGAC	21544
Db	36980	TACTCGCTCGCCACACACCGGGGTACTCTTCGAGCACCGGTGCCGTCTCTGTTGTTCCACGAC	37039
Qy	21544	CGGACACCTTCCTCTGCAAGCACTTCCAGGCACCTCGCGCAGGCGAAACCCACACCGCCCGCTC	21603
Db	37040	CGCGAGAGCTCTCTCCGCGCTCGATTGCTTCGCCACGGAAGCCCGCCCGAGACCC	37099
Qy	21604	ATCCACGACAGCCCGCAGCGGGACCGGGAACGGGGAGCCCGAGGAAAGACCGCATTC	21663
Db	37100	GTGCTCGAAGCAAGCGGAAG-----CCACGGCAAGGTCTGTTCTTC	37138
Qy	21664	ATCTGCTCCGGACAGGGCACCCAAACGCCCGCATGGCCACCGCTCTTACCACACCCAC	21723
Db	37139	GTCTTTCTGGGCAAGGCTCGAGTGGGAAGGATGGCCCTCTCTCTGCTCGATACCTCG	37198
Qy	21724	CCGCTTTTCGCCGCCGCACTCAACAGCATCTGCAACCACTCGACCCCGACCTCGACAC	21783
Db	37199	CCGCTTTTCGGGCAACAGCTCGAAGCGTGCAGCGCGCTCTCGCGCCCAACGTTGACTGG	37258
Qy	21784	CCCTCTCTCCCTCTCTACCCCAAAACGACACGACAAAGAGACGCGGCCGA	21843
Db	37259	TCGCTGCTCGCGTGT-----CCGCGGAGGAGGGCGCGCCCGCTCGAC	37306
Qy	21844	CTGCTTCAGCAGACCCCGTAGCGCCACCGCGCTCTTCGCTTCCAGTTCGCGCTTCAC	21903
Db	37307	CGGTCGACGTGTCAGCCCGCTGTTCTCGATGATGGTCTCTGCTGCGCCCTGTGG	37366
Qy	21904	GCGCTCTCACGACAGGCTACACATACACCCCGCACTACGCGGGAACCTCCCTCGGC	21963
Db	37367	CGCTCCATGGGCG-----TCGAGCCGACGCGGTGTCGCGCATAGCCAGGCG	37414
Qy	21964	GAATCACCGCCGCCACCTCGCGGCATCTCACCTCACCGACGCGCACCACTCATC	22023
Db	37415	GAGATCGCGCGGCTGTGTGGCGGCGGCTGTGCTTCGAGGAAGCTCCAAAGTTGGTG	37474
Qy	22024	ACCCAAACGGGCCA---CCCTCATGCAAAACCATGCCCCCGGCAACATGACCACTTCAC	22080
Db	37475	GCGCTGCGACGCGTTCGCTCGTGGAGCTCGCGCGCCAGGGGGCCATGCGCGGTGGAG	37534
Qy	22081	ACACCCCAACACATCACCCACACCTCACCGGCCACGAAACGACCTCGCCATCGCC	22140
Db	37535	CTGCGGAGGCGAGGTTCGACGCGGCGCTTCAGAGCTATGGCGATCGGCTCTTCATCGGG	37594
Qy	22141	GCCATCAACACCCCACTCCCTCGTCTACAGCGGCACCCCCCAACACGCTTCCAAACATC	22200
Db	37595	GCGATCAACAGCCCTCGTTTCAGAGATCTCGCGGAGGCCCTCGCGCTCGCCGCCCTG	37654
Qy	22201	ACACCCCTTCGCCAAACAAAGGATCAAAACCAAAACCTCCCAACCAACACGCGCTTC	22260
Db	37655	CTCCGCGATCTGAGTTCGAGGGCGTCTTCGCGCTCAAGCTGAGTTACGACTTCGCTCC	37714
Qy	22261	CAGTCCCCCACACCAACCCCATCTCTCAACCAACTCCACACGACACCAACACCTTCACC	22320
Db	37715	CATTCGGGAGGTTCAGTGTGATTCGACAGAGTCTCTCGATCTCTGTCGTGGGTCGAG	37774
Qy	22321	TACACCCCAACCAACCCCTCTCATCCGCGCAACACCCCAACCGACCAACTC-----	22374
Db	37775	CCGCGCTCGAGGCGGTTCGCTTACTTCACGGTGAGCGGCGCCGATCGACGGGAGC	37834
Qy	22375	---CTACCCCCCACTTACTGGACCCCAAGCGCCGCAACACGTCGACTACGCCACAC	22431
Db	37835	GAGCTCGAGCGCGCTTACTGTGTCGGAACCTTCGGGACCGGTCGCTTTCGACAGCGCT	37894
Qy	22432	ACGCAAAACCTTCCACCAACACGCGGTTCACCACTCATCTGAACCTCGGACCCGACAAAC	22491
Db	37895	GTGCAAGGCTCTCTTCGCGGAGAACATCGCTTCTTCGTGGAGTTCAGGCC---CAGTCT	37951
Qy	22492	CTCACACCGTCAACCAACCAACTCTCCCAACACCCCAACCAACCACTTCACCTCACC	22551
Db	37952	GTGCTGACCTTGGCTTTGACAGAGTCTTCGAAGGCTTCGAGCGCTCGGCGCGGTGTC	38011



Db 40124 CACGCCCTCGGACGAGGCTCTCCCGCGAGGCGA-----CGCCGCCCGCGCTCCGGC 40174  
Qy 24766 CTTACCGTCGAGAGCAAAACCGATGCCCATCATCGGTATGGCATGTCTCCCGCGCGC 24825  
Db 40175 CGCGCTCGAGCGACGAGCCCATCGCATCTGTGCGCATGGCCCTCGGCTTCCGGGCGGC 40234  
Qy 24826 GTACGTTCTGCGCGACGACTGTGGGAAATGCTCGTTCGGGTGAGGACGCTATCGGCGTC 24885  
Db 40235 GTGCGCATGTGACGCTCTTTGGGAGTTCTCTCCACCAAGGCGCGAGCGGTGAGGCC 40294  
Qy 24886 TTCCCGACCGACCGCGCTGGGACCTTGACACGCTCTAGGACCCCGACCCCGACACCC 24945  
Db 40295 ATTTCAC---AGAGCGCTGGGACGCGGTGCGCTCTAGACCCCGACCCCGACCGAC 40351  
Qy 24946 GGCACCTGTCTACACCCGAAACCGCGGATTCCTCTACGGCGGAGGCACTTTCAGCCCGAA 25005  
Db 40352 GCCAAGACTAGTCTCGGCATGCGCGGATGCTCGACCATGCACTCTTCGACCCCTGCC 40411  
Qy 25006 TTCTTTGGGATCAGCCCGCGGAAAGCCTTGGCCATGGACCCCGACGACGACTCTCTCTC 25065  
Db 40412 TTCTTTGGGATCAGCCCGCGGAGGCAAAACACTCTGACCCCGACGCGCTGCTCTCTC 40471  
Qy 25066 GAAACCGCTGGGAAACCATCGAACACCGCGGATCAACCCCGACACCTTCCAGCGCAC 25125  
Db 40472 GAATCTGCTGGCTGGCCCTCGAGACGCGGCGATCGTCCCGACCTCTCAAGGACTCC 40531  
Qy 25126 CCCACCGGAGTCTTCGCGGAAATCAACGCTCAAGACACGCGCGCATATCGGCCAAAGC 25185  
Db 40532 CTCACCGGCTTCTGTGGCATCTGCGCGCGGATACGCGATG-----CAAGAG 40582  
Qy 25186 CGTGATGGAGACCATCAGGGCTACGCGCTTGACCGGCGATTCGGGAGTGTGGCGTCC 25245  
Db 40583 GCGAGCTCGGAAGTTTCGAGGTTTACTTCTCAACGAAGCACTTCGCGCTCTTTGGCGG 40642  
Qy 25246 GCGCGGTGGCTACACGCTCGGCTCGAGCGCCCGCGGTCTCGGTGATACGCGGTGT 25305  
Db 40643 GGGGCTTTGGCCATACGCTCGGCTTCCAGGGGCGCGATCTTCGGTTCGACACCCCTGC 40702  
Qy 25306 TCGTCTGCTTGGTGGCTGATTTGGGCGGCGAGGCTTCGCTGCGGCTGAGTGTTCG 25365  
Db 40703 TCTCTCTGCTCTCTCTCTCACTCGCTCGCTTCCAGCGCTTCGACAGGCGAGTGCAAC 40762  
Qy 25366 ATGGCGCTTGGCGGGGTGACGATGATGCTCTCGGCTGACGTTTGTGGAGTTCTCA 25425  
Db 40763 CTCGCCCTCGCGCGGGGTGCTGCTCATGCTCTCCCGACAGACTTGTCTATCTTTCC 40822  
Qy 25426 GCTCAGCGGGTCTGGCCGCGACGCGGCTCGAAGGCTATTCGCGGCTCTCAGCGT 25485  
Db 40823 CGTCTGCGGCTTGGCGCCCGACGCGCGCTCTCCAGACCTTCTCGGACAAACCGCACGCG 40882  
Qy 25486 ACCGCTGGGCGAGGCTGTGGGATGCTGTGGTGGAGCGCTCTTCGACGCCGTGCG 25545  
Db 40883 TAGGACCGGAGAGGCGTCTGCTCTTGGCCCTCGAGCGGATCGGCGACGCCCTTCGCC 40942  
Qy 25546 AACGCTACCGGTCTTGCGCGTGTGTGCGTGTGCGGTCAACACGAGCGGTGCGAGC 25605  
Db 40943 CGGAGACACCGGTCTCTGCTCTCGTCTCGCGGACCGCCATCAACACGACGCGCGTGC 41002  
Qy 25606 AACGCTACCGCGCCCAACCGGCGCTTCCAGCAGCGGTGATCTCGTCAAGCCCTTGGC 25665  
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Qy 25666 AATCGGAGTACACCGCGCGATGTGACGAGTGTGGGCGCACGGACCGGGACCACT 25725  
Db 41063 GACGCCCGGATCACCCCGCGGACGCTGACGCTGTGATGTCATGGCATGGCACCGGCACTCG 41122  
Qy 25726 CTGGGGGACCCGATCGAGCGCCAGGCACTCTCTGGCGCGCTACGAGCAACACCGCCCGCAC 25785  
Db 41123 CTGGGAGACCCCATCAGGTGTCAAGCCCTTGGCGCGCTCTACGCGACGCGACCGCT 41182  
Qy 25786 CACCGCGCTTGTGGTGGGATCTCTCAATCAACATCGGGACGCAACGCGCGCGG 25845  
Db 41183 GAAAGCCTCTCTCTCGCGCGCTCAAGACCAACATCGGCCATCTCGAGGCGCGCTCC 41242

Qy 25846 GGCGTGGCGGAGTCACTAAGATGGTATGCGCTTGGCGCAACGGGCTCTCTCCACAGACC 25905  
Db 41243 GGCCTCGCGGCGTTCGCAAGATGGTGGCTCGCTCGCTCGCGCACGAGCGCTTCCCGCCACC 41302  
Qy 25906 CTCCAGTGGAGAGAGCCACCCCGAGGTGCACTGTGTCCAGGCGGAGTACAACTCTGT 25965  
Db 41303 CTCCAGCGACCCACGCAATCTCTCATGAGTGGGAGGCGCTCGCCATCGAGTCTGT 41362  
Qy 25966 ACACAAACCGTCTGCGCGCGCGACCGCGCGCGCGCACGCGCGCGGTGTCA 26025  
Db 41363 GATACCCCGAGGCTTGGCCCGCGCAAGAGATGGAGTTCGCCCGCGCGGATCTCC 41422  
Qy 26026 TCATTTCGGCGTTCAGCGGACCAACCCCGCATCATCTCTGAAAGAACACCACTTCCCAG 26085  
Db 41423 GCTTTGGATTTCTCGGCGACCAACGCGCATCTCTCGAAGAGGTCTCCCGCGCGCTG 41482  
Qy 26086 GACAGCATACGACGAGCAACCGCTGCGCAACGCAACGCGCTTCCCGCATCTCTCT 26145  
Db 41483 CCGCGCGAGCGCGCATCTACAGCGG-----CGTCCGAAGCGCTTCCCGCGCG 41533  
Qy 26146 CTTCCCGTTCGGGTTCGGCGAGGTCTGAGGCGGGTTGCGGCGGAGGCGACAGCGGTG 26205  
Db 41534 TGGCCGCTGCTCTGTTCGCCAGAGGAGGCGCGCTCGCGGCCAGCGGCGGCTC 41593  
Qy 26206 CGCAGTACGTGGCAGCGCGCGGACATGTCCTGCGGACATTTGGTGCGGGTCTGCGC 26265  
Db 41594 CGCGACCACTCTGTCGCCCGACGACCTCACCTCGCGGATGTGGCTATTTCGCTGGC 41653  
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Qy 26326 CGCAGGCACTGACAGCCCTGCGGCGGCAACCCCGACCATCACACAGCGGCAC 26385  
Db 41714 CTCTCGCGCTCGACTGCTCGCCAGGACGAGCGCGCGC-----GAGCACCTCTC 41767  
Qy 26386 ACCCGGCGGTGACCGCGCGGTCTGCTTCTGCTTTTCCCGGACAGGCGCGCGTGG 26445  
Db 41768 GACGAGCGGAGGACGACGCGAAGCTGCTCTTCTGTTCTTGGGCAAGGCTCGCAGTGG 41827  
Qy 26446 GCGCGGATGGCGCTGACCTGCTCACTCTCTACCGCTGTTCGCGGATTCGCGGAAACATCGACGCA 26505  
Db 41828 GAAGGATGGCGCTCTGCTGCTGACTCTCTCGCGCGCTTTCGCGGCTCAGCTCGAAGCA 41867  
Qy 26506 TCGGAGAAAGCCCTACCCCTCGGTGCTCTGCTGCGACGACATCTTCACCGCGAC 26565  
Db 41868 TCGAGCGCGCTGCTCTCAGCTGAGTGGAGCTTCTGCGGTCTTGGCGCGCGAC 41947  
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Db 42008 GTCTCTCTGCGCGCTTGTGGCTTGTGGCTGAGCGCGCGCGCGCTTTCGCGCGCAC 42067  
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Qy 26746 AAAACCGTTGACCTGCGGCGCGGCACTGGCGCGCTGACGAGGCGCGCGCGCATGCGC 26805  
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Db 42245 CTCTCATCTCGCGCGCTCAAGCGCGCGGCGCTGCTGCTCGGCGAGCGCGCGCGC 42304





Db 44254 GATCGCCCTCCGAACGGCAACCCCTCTTCAAGGCTCTCACGGCTGCCCCCAGCGGCC 44313  
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Db 44314 CACGAGCA----- 44321  
Qy 29202 GGCAGCGGTCTCTTCTTCCGGGGGGAACGGTGTGATACCGGGGGAACCGGTGTCT 29261  
Db 44322 --CAGCGTCCCGCGAGGCTCGAGGCAACCGTCTCTCATCGGAGGACACCGCACGCT 44379  
Qy 29262 GGGCGGCTCGTGGCGCGCATCTGTGAGGCGACGCGTACGCGATCTGTGTGGC 29321  
Db 44380 CGCGCCCTGTGCGCGCGGCTCTGTCTAAACACAGCGCAAGCACTCTCTCTAC 44439  
Qy 29322 GGGTGGCGGACCGGACCGGAGGCTGCGCGAGTTGCGGGGCGAGCTCGGTGGCT 29381  
Db 44440 CTCGCGCAGGCGGAGCGCTCCGGTGTCTGTTCGAAGGAGCTCGAGCTCT 44499  
Qy 29382 CGGCGGAGGTGGAGGTGCTGCTCGACCGCGGGAACCGGAGAGCTGGCGACCT 29441  
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Qy 29442 GCTGACAGGATCCCGAGATCGCGCGTGTGCGCGGCTGCTGTCACAGTGGCGGATCCT 29501  
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Qy 29502 GGACGAGCGGTGATCACGCTGCTGCGCGAGCGGCTCGGGGCGCTCTCCGGGCAA 29561  
Db 44620 CGACGGGATCTGCTCGCGGCTGAGCTCGAGCGGATCGACGGGTCTTCCGCCCA 44679  
Qy 29562 GCGGAGCTGCGGTCTTCTGACGAGTGAACGGCGGGGAGAGCTGTGGTTCGT 29621  
Db 44680 GATGATGCGGCTGCGACTTGCATCAGCTCAACCAAGATAAGCCCTTGGCGGCTCAT 44739  
Qy 29622 CATGTTCTCCGCTGCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 29681  
Db 44740 CTTCTTCTGCTGCGCGGCTGCTGCGGAGCTGAGTCACTCAACTACGCGGCTGC 44799  
Qy 29682 CAACGCGCTCTCGACTTCTTCTGCTCATCGCGCGCGCGGAGGCGTCCCGCGCTCTC 29741  
Db 44800 GAGCGCTTCTCGATGCGTTCGCAACACCGCGCGCGGAGGCTCCCTGCTCATC 44859  
Qy 29742 TCTGCTGGGCTGTGGGAAGAGGCAACAGGATGACGGGCACTCGAGCTGACGA 29801  
Db 44860 GCTCGGTGAGGCACTGGGCGGAGCGAGCGCAATGACAGAGCAGTCAAGCGCGCGG 44919  
Qy 29802 CATGCGGATCAGCGCGCGGATGCGGCGGCTGCGAGTCCGAGCTCGGCGT 29861  
Db 44920 CGCCCTCGATGAGCGCGCGG---CCTTCTCGACTCTGAGGAGGCTCGCCCT 44976  
Qy 29862 GTTCGACGCGGCTTGGCGGACGCGGAGCGGTTCTGTGATGCGGCTCGGCTCGACTAC 29921  
Db 44977 CTTGATGGGCGCTTTCGAAACGAGACCGCCCTGTTCCTCGCGGCTTCGACTGAG 45036  
Qy 29922 GCGGTACGCTGTGTCGCGCTCGCACCGGTGCGCGCTGCTGCTCAAGGCTCTCTCA 29981  
Db 45037 CGCGCTCAGGCGGAACCGCGGAGC-----GTCCCGCGTGTGTTCCAAAGCTCTCGTCG 45090  
Qy 29982 GCTGCTCGTCCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 30041  
Db 45091 CGCTCGACCGTACGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 45129  
Qy 30042 GCGCGCGGCTGCGGTGAGCGTCTGGCGCGGAGAGTGGCGGTGAGCGGAGCGCGCT 30101  
Db 45130 GGCCTGTCTTACAGAGCGCTCTACGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCG 45189  
Qy 30102 GCTGCGCTGTGTCGCTGCTGCTGCGCGGCTGCTGCGGCTGCTGCGGCTGCGGAGT 30161  
Db 45190 GCTGATCTCATCGCACGAGCGCGCGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCT 45249  
Qy 30162 CGACGATCGCGGCTTCCGCGAGCTGGGCTTGAATCTGCTCAAGCGGCTGAGGTGGG 30221  
Db 45250 CGATCCGATCGCTCTTCAAGAGCTTGGGCTGCACTTCCATCATCGCGCTCGATCTCGG 45309

Qy 30222 CAACCGTCTACGCGCGGCGGCTGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30281  
Db 45310 AAATCGGCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 45369  
Qy 30282 GACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30301  
Db 45370 AACCCAGCTGCGCTCGCAG 45389

RESULT 2

US-09-036-987A-1  
; Sequence 1, Application US/09036987A  
; Patent No. 6143526  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H.  
; APPLICANT: Broughton, Mary C.  
; APPLICANT: Crawford, Kathryn P.  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Merlo, Donald J.  
; APPLICANT: Treadway, Patti J.  
; APPLICANT: Turner, Jan R.  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dow Agrosciences LLC Patent Department  
; STREET: 9330 Zionsville Road  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: USA  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/036.987A  
; FILING DATE: 09-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stuart, Donald R.  
; REGISTRATION NUMBER: 28,479  
; REFERENCE/DOCKET NUMBER: 50,608  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317)337-4816  
; TELEFAX: (317)337-4847  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80161 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-09-036-987A-1

Query Match 10.2%; Score 3142; DB 3; Length 80161;  
Best Local Similarity 49.2%; Pred. No. 0;  
Matches 15063; Conservative 0; Mismatches 12830; Indels 2753; Gaps 147;  
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Db 35494 CACGAGGCGGAGTCCGAGAGCGGGAACCCATCGGATCGTGGCGATGGGCTCCGGTAC 35553  
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Db 35614 ATCGGTGAATTCGCGCTGATCGTGGTGGCACTTCGAGAGCTCTACGATCCCGACCGG 35673

1597 ACAGAGCCGACGCTTCTATCCGACGAGGAGCGGTTCTCTTACAGACGCGCGACTTC 1656  
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2017 TCGGCTGAGTGACGCTCGCGCTGCGCGCGCGCTCTCGGTCATGTCCACCCCTCGGCGATG 2076  
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2137 GCTGACGCGACGCGACCGGCTGCGGCGAGGCGCTGCGGATGCTGCTGCTGAGCGGCTG 2196  
2197 TCGGATGCGGCTGCGGCGATCGGCTGCTGCGGCGTGTGTAACGCGGAGTCCGCTCAAC 2256  
2257 CAGGACGCTGCTCGAAATGGGCTGACGCGCGCGCAACGCTGCGGCTGCGGCTGAGGCGGCTG 2316  
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2437 CAG---CGGCGCGTGAACGCGCGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTGCTGCGGCTG 2493  
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2614 GCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2673  
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2794 GCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2853  
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2974 CTTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3033  
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3094 CCGGATCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3153  
3154 GTGTTCCCGACACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3213  
3214 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3273  
3274 TCTGCTGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3333  
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3454 GGGCGCTGAGCTGAAAGGACGCGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3513  
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3574 CTCTGCTGCGGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3633  
3634 ACOCGCTGCTGCGGCGGATGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3693  
3694 GGGGCTGCGGCGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3753  
3754 CTGCGGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3813

Db	37708	GTTCGAGCGGTCTGCGCGCCCGCCCGCGGGTGCACACCGGGAGCGGCAGGTGCGG	37767
Qy	3814	TTCTTCTCCAGGTGGAGGGACCTGGCTTGGACACCAACCCCTGGAGCGCGCTACTGG	3873
Db	37768	TGGTGGTTCGAGCGGTGATCGCGGACCTGGGTGGATCCGGCGAGGCTGGACGGCGAGTATTGG	37827
Qy	3874	TACCGCAACCTGCACACCGCGTTCGTTTTCAGCGATGCGCTCCAGGCGCTTGGCGGATGAC	3933
Db	37828	TATCGGAACCTCCGCGACGCGGTTCGGTTTCGAACACGCGCTGCAGGGCTTGGTCGAGCGG	37887
Qy	3934	GGACACCGCGTCTTGGTTCGAAGTACGCGCCCAACCCCAACCTGCTGCTCCCGCGCATTCGAGAC	3993
Db	37888	GGATTTCGCGCTGTTTCATCGAAATGAGTGGCATCCGGTGTCTGACACACGCGCGTTCGAGGAA	37947
Qy	3994	ACCACGGAAGACACCGCGGAGACCTACCGGATCGCGAGCTCCGCGCGGGCGGACAC	4053
Db	37948	ACCGGTGCGGAGTTCGGAACCGCGCTGGCGCGGTAGGTACTTTCGACGTGACTTCGGGC	38007
Qy	4054	GACACCGCGCTTCTTCACCGCCCTCGCCACACCCATACACCGGATCGGCACACCC	4113
Db	38008	GGCTCCGGAGTTGTTGCAATTCGCTGGCGGAGGCTACGTGCGCGCGCCACCGTGGAC	38067
Qy	4114	ACCACCTGGCACCACTATACACCAACCAACACCCACCCCAACCGGACGACCTC	4173
Db	38068	TGGCGCGTG-----GGTTTCGGGGCGCGGGCGGACGGCTG	38103
Qy	4174	GACCTGCCACCTACCCCTTCCAACACGAGCACTACTGCTCGAGAGCTCACAGCGGGT	4233
Db	38104	GACCTGCCGACCTACCCGTTTCAGCGCGCAGCGGTACTGGCTGGACAAAGGAGTCCCTCC	38163
Qy	4234	GCCGATCCGGTTCGGGTGCGCGTTCGGGTGCGGTTCGGGTCGGGCGGCGAGGACT	4293
Db	38164	GACGAGGCTCGTTCGGTTCGGACCGCGGGCGGCT-----	38200
Qy	4294	GCGGGCGGACGGCAGAGTGGAGTTCGGGTTCGGGACGCGGTGGCGCGCGCAGAGACTG	4353
Db	38201	-----GGTTCTGGCAAGCGTGGCGCGCAAGACCTG	38232
Qy	4354	GAACGGTCGGACCACTGCGCGTCCCGCTCGCGGGCTGGACACGGTGGTGCC	4413
Db	38233	AAAGCGTGTCCGATGCGCTCGATCTCGACGCGAGCGACCGCTGAGCGCAACACTTCCA	38292
Qy	4414	GCACCTCTCGCTGGCACCGCCACCAACACGACCAAGCGCGCATCAACACCTGGACCTAC	4473
Db	38293	GGCTGTTCGCTGCGACCGTTCAGGACGAGAAAGGTCTTGGCAGACGGTGGCGGTAC	38352
Qy	4474	CAGGAAACCTTGAAACCCCTACCTTCCCAACCAACCAACCAACCAACCAACCTGGTTC	4533
Db	38353	CGAGTCGACTGGGTACGGGTGCGCGCGCGGACCGCGTCCGAGAAACGCGGAAACCTGGCTC	38412
Qy	4534	ATCGCATCCCGGAAACCCAGACCCACCAACCCCAACCAACCAACCTTACCAACCTC	4593
Db	38413	CTGGTCTTCCCGGGGGGATCGAGGAAGCGTGGTTCGAACGGCTGACCGATCGGTG	38472
Qy	4594	CACCAACGCGGATCACACCCCATCCCTTACCTTACCTTACCTTACCTTACCTTACCTT	4653
Db	38473	ACACCGGAGGATCAGCAACCTTGGCTTCGAGTGGCATCCCGCGCGGCGGAGTGGGNA	38532
Qy	4654	CACCTTCAACCAACCTTCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCA	4713
Db	38533	CTCG-CAACCGAACTCCGCGCGGACCGCGGTCGAGCGGTGACCGGTGAAGGCA-----	38581
Qy	4714	ATCACGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	4773
Db	38582	-----TCCTGTGCTCACCGGTTGGAGCGGACCGACCCACCGGATTCGAAGGAC	38631
Qy	4774	ACACCAACCGGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	4833
Db	38632	GTCCCGAGGGGATTCGCTTGTCTGTAACCTTGGTCAAGGCGCTGGTGAAGCGGACCTC	38691
Qy	4834	CCAAACCCCTCTGTGTACGCCACCAACCAACCGCACCAACCAACCAACCAACCAACCC	4893
Db			
Db	38692	AGAATTCCTCTGTGGACCATCAACGCGTGGTGCAGGACGCGCCCGGAGATCGCGTG	38751
Qy	4894	ACACACCCCAAGCCCAAACTCTGGGACTCGCCCGCACCACTCTCTCTCGAAACACCC	4953
Db	38752	CTGGCCCGATGAGGGCGAAGCATGGGTCTGGGGGAGTACCGGCACTCGAACACCC	38811
Qy	4954	ACCACACCGCGGAAATCATGACCTCCCAACACCCCAACCCCAACCCCTCCAGCAC	5013
Db	38812	GAGCGCTGGGTGGCTGATCGACCTCGCGGATTCGTGAGCGGAGCGTCTCTCACGAG	38871
Qy	5014	CTACACCAACCTTCAACCAACCCCAACCAACCAACCAACCTCGCATCCGACCAACCGG	5073
Db	38872	CTGGGCAAGCGCTCAACCAACCGCTTGGGAGAACCACTGGGATTCGCACTCGGCG	38931
Qy	5074	ACCACACCGCGCGCTCACCCCAACCACTCACCCCAACCAACCAACCAACCAACCC	5133
Db	38932	GTGTGGCGCGGACTGTTACCGCCCGCGGGAATC---AGCCCGTGGAGTAAAGTGG	38988
Qy	5134	ACCCCAACGGAACCAACCTCATCACCGGGGAACCGGCGCTCTCGCACCCACTTACC	5193
Db	38989	CGCCCGGAGGGAGCGGCTGATCACGGGCGGACTCGGCGCGTGGCGCACAGTGGCG	39048
Qy	5194	CACCACTCACCAACCAACCAACCAACCAACCACTCTCTCACGAGCGGCAACCGGCCCC	5253
Db	39049	AGTGTGGCGGAAATCGGA---GCCGAGCGAATCTGTGCTCACAGTCGAGCGGGCAAC	39105
Qy	5254	CACACCCCAACGACCAACCACTCACCAACCACTCCAAACAAAGGCACTCACCTTACC	5313
Db	39106	CAACGAGCGCGCGGAGCTGGAGCGCACTCGGGCCCTTGGAGCGCAAGTGTCC	39165
Qy	5314	ATCACCACTTGGACACCAACCAACCAACCACTCCAAACAACTCTCTTAAACCACTCCCC	5373
Db	39166	ATCGTGGCTTGGACAGTGAACCGATCGTGCAGATGTCCGCACTACTTGGCGAGTTGC--	39223
Qy	5374	CCACAAACCCCTTCAACCGTCTATCCACACCGCAGGCACTCTCGACGACCGCACCTC	5433
Db	39224	-----ACGTCAACCGGGTGTTCACCGCGCGGAGTCTGGTGGCTCTCGCGGTG	39273
Qy	5434	ACCAACTCACCCCAACCACTCAACCAACCTCTCGCGCGCAAGGCAACGAGCGGCCAC	5493
Db	39274	GCGGAGACGACGAGAGCGCTGGCGGCAATATGCGGGGCGAAGGTCCGCGGCGCTAG	39333
Qy	5494	CTCTTCAACCACTTCAACCAACCAACCAACCTTCTTCTTCTTCTTCTTCTTCTTCTT	5553
Db	39334	GTGTGGAGCACTTGGACAGCACCGATCTCGATGCTTCTTCTTCTTCTTCTTCTTCTT	39393
Qy	5554	GCCGCACTTGGCGGACCGCGCAACCACTACCGCGGAGCGCAACCGCTTCTTCTTCTT	5613
Db	39394	GCCGGGTATGGGGCGGGGGCGGTTCAGGGCGCTTACCGCGCGGCGAAGCGCATTTT	39453
Qy	5614	GCCCTCGCCCAACCGCACACCAACCACTTCCCGCGCACGATCGCTGGGGGAC	5673
Db	39454	ACACTCGCGGAAACCGCGGAGCGGCTTGGCGGCACTCGATCTCTTGGGGAGT	39513
Qy	5674	TGGCAAGGAAACGCACTCGTGTATTCGGAACGCGCGCGCATATCTCGACCGCGCGG	5733
Db	39514	TGGCGCGCGCGCATGGCCGA---CGGCGCGCGGCGAAGCACTTGGCGGAGCGG	39570
Qy	5734	TTCGACCATGTCAACCGAGTTGGCCACGCGAGGCTACGCGAGGCGATCGCGGAC	5793
Db	39571	ATACGTTCGATTCGCGGGCGTTCGCGCATCTTGGCTCT---GCAGGAAGTACTTGA	39627
Qy	5794	GAACGGCGTATGTGTCATCGCGCATCGCACTGGAGCAAGATCGAACA-----	5845
Db	39628	GATGAGAGTGGTGTGATCGCTGTGATGTGACTTGGGACCGATTCGTTCCACGTTCC	39687
Qy	5846	-----CCTCTCAGACGAGCACTGGTGAAGCGCGCGCGGAAAGGAGGAGCACT	5895
Db	39688	GCGACTCGCGCAACCGGTTGTCGAGAAAGTGGCGGCGGAGAAAGCGGATGCGCG	39747
Qy	5896	GTCGAGCGCCCACTTCAACCG---CGGAGTTGACAAACGCTGGCGCCATCAGACGTC	5952
Db	39748	AATGGCGCGGAGAACCGAGGGGCTCGCGCTTCCCGCGCAATCTCGCGGAGCTGCGGAA	39807

















Qy	17759	CCGAAACAACCTTCAACACCCTCACCGAACAACACTCCCAAACACCCCACCAACACCC	17818
Db	52737	CGGATGGGTGTGTTCGGCCTGGTGAGGAGTGCAGCGCCGGATCCGATCAGGGCGGAC	52796
Qy	17819	TCACCTCTACGCCACCCCAACCAACCCCAACCACTCTCAACCACTCGCCAAA	17878
Db	52797	GGGTGGCGGGTTTCGGCTCATCGCAGCAATCGCAGAGGCGCACACGGTGACACGG	52856
Qy	17879	CCACCAACACTGGCAGCCCCCAACCACTAACCCACCAACCAACCAACCCACACCA	17938
Db	52857	CATTGGGCGAGATCCATGTGCGTGTGCTGAGGTGGACTGGCGGTGTTTTTCGCGGTA	52916
Qy	17939	CC-----CAGCTCGACTCCCACTTAACCCCTTCACCAACAGACATACTGGCTCG	17989
Db	52917	CCGGGGCAAAAGCAGGTCTGAGCTGCCACGCTATGCTTCACAGCAGACGAGTACTGGCTTG	52976
Qy	17990	AAGCACACAGCGGGTTCGGGATCGGTTTCGGGTTCCGGTTCGGGGCGGACGGGACTG	18049
Db	52977	ACTCACCAT-----CCGAACCGGT-----CGGGCAATCCGCGCATC	53012
Qy	18050	CGGGCGGGACGGCAGAGTGGAGTTCGGGTTCTGGGACGCGTGGCGCCCGCAGACCTGG	18109
Db	53013	CCGGCGCCAGTCTGGGCTTCTGGGAACCTGTCAGCAGAGAAATGTCAGCGGCTCAGCG	53072
Qy	18110	AACGGTGGCGACACGCTCGCGTGCCTCCCTTCGCGGGCTTGACACGCTGCTGTCGG	18169
Db	53073	CCGCTCTGCACATTACCGCGCATCAGAGGTGCGAGCGTCCCTGGAACTCGGTGTTCCGG	53132
Qy	18170	CAGTCTCGGCTGGCAGCGCACCAACAGACGACMACCGCGCATCAACCTTGGACCTACC	18229
Db	53133	TCTCTCTCTCGCATTCGGCGATCCGGAACGAATCCCTGGTGACACAGTGGCGGTACC	53192
Qy	18230	AGAAACCTTGGAAAACTCACCTCCCAACCAACCAACCAACCAACCAACCAACCTGGCTCA	18289
Db	53193	GGATTTCTTGGCATAGCGGGCAGATTTCGACAGCCCTCTGTCGGGGACATGGCTCG	53252
Qy	18290	TGGCATCCCGGAAACCGAGACCAACCCCAACATCAACAAATCTCTCAACCACTCC	18349
Db	53253	TCGTCGTGCGGAGGGGTGGTGGCGAGTGGCAAGTCTCTGGTTTCAACGAGATGTTTCG	53312
Qy	18350	ACCACACGACATCACCCCATCCCTCAACCTCAACCAACCAACCAACCAACCAACCAAC	18409
Db	53313	AGNACGGGTTTCGCGGCMGTTCTGTTGAGCTCGCCGGGACAGCAGAGAGCCCTGG	53372
Qy	18410	ACTTCACCAACCCGCAACAGCCAAACCAACCAACCAACCAACCAACCAACCAACCAAC	18469
Db	53373	CGC-----AACGATTCCGCTCTGCTGCTGCTGCGTCAAGGGGAATAAGCGCGTGT	53423
Qy	18470	TCTCCCTCTCGCCCTCGAGAAACACCCCAACCCCAACCAACCAACCAACCAACCAAC	18529
Db	53424	TGCTCTGTGTCGGCTGGATGAATCGCCGCTCTCGCCGAAACGCTCTTTCGGAATGGCG	53483
Qy	18530	CCCTCTCTCAACCTCACCTCACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	18589
Db	53484	CGCTGAACTCGTTGTTACTGCTCGAGCTCTGCGGGCCGCGGATGTGTGCGGCGCATGT	53543
Qy	18590	GGTAGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	18649
Db	53544	GTTTGGCGACGTGTGTGTGTGTCGCGT-----CGGGGATGTGCGGTGAACCCGGGGC	53597
Qy	18650	AAGCCNAACCTGGGACTCGCCGACCAACCTCTCGAAACACCCCAACCAACCAACCGCG	18709
Db	53598	AGCGCTGTGTGGGACTGGGTGCGGTGCTGGGTCTGGAGCATCCGGCTGTGGGGTG	53657
Qy	18710	GAATCATCGACCTCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	18769
Db	53658	GCCTGTGTCAGCTGCGCTGCTGCTGATGAGGACGCTCGAGAACGCTTGTGCTGCTGT	53717
Qy	18770	TCACCCNAACCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC	18829
Db	53718	TGGCAGATCTTGGCGAGGA---CGAGATCGGGTAGCTCCCGGTGGTGTGTTGTCGTCGGC	53774

[illegible]

Db	54849	ATTATCCGAGCCCATCCGCGCTGGCTGAGCAGCTGGTCGGGAGCTGTGGGAGCGCAGC	54908
Qy	19964	CCGCAAACTCAACTCCGCTTCGCGACCCCGGCGAGAGCTCATGAGCCGATCGCCATCG	20023
Db	54909	CCG-----CGACCAACCGTCGTGGCCGGGGCCGATCCAGTGATCCGGTTGTCTGG	54962
Qy	20024	TTGGCATGGCTGTGCTTCCCGCGCGAGTGACCTCGCGCGGACGACCTTCCTGGGATCGA	20083
Db	54963	TCGCGATGGGATGCCGGTATCCGGGCGAGCTGTCTGCTCGCCCGAGGAGCTGTGGCAGCTGG	55022
Qy	20084	TCTCTCCGAGCAGGACCGGATCGCGGATTCGCCACCGACCGCGCTGGGACCTGGACA	20143
Db	55023	TTTCTGCGGGACGTATCGGGTATCGACGTTTCCCGCTCGATCGGGTTGGGACTGCAACA	55082
Qy	20144	CGCTTAGACCCCGACCCGACCAACCCCGGACCTGCTACACCCGAAACGCGCGATTCC	20203
Db	55083	CGTTGTTCCGACCCCGATCCGATCGGCGAGGACGTACCTATGTGCGAGAGGTGCTTCC	55142
Qy	20204	TCTACGACGCGAGGCCATTCGACGCGGAAATTCCTCGGATCAGCCCCCGGAAAGCCCTCG	20263
Db	55143	TGACCGGTGCTGATCGGTTGACGCGCGGTTTCTCGGCATCAGCCCTCGCGAGGCGCGC	55202
Qy	20264	CCATGGACCCCGAGCAACGACTCTCTCGGAAACCGCTCGGAAACCATCGAACGCGC	20323
Db	55203	CAATGGATCCGACGAGAGGTTGTCTCGAAGTGGCGTGGGAGGTTTTCGAAACGAGCAG	55262
Qy	20324	GCATCAACCCCGACACCTCCAGCGCACCCCGGAGGAGTCTTACCGGACCAACGAGAC	20383
Db	55263	GAATCGCTCCGTGTCTGTTGGGGTAGGAGCCGGTGTTCGCGGGGACCAATGGGC	55322
Qy	20384	AGGACACCGCGCACATCCGTAGGCCCCGAGCGGTACCGAGGATTCGTCTTGACCG	20443
Db	55323	AGGACACCGGTGCGAAAGTGGCT---GCCGCGCGAGCGCGGGTCACTCTCTGACCG	55379
Qy	20444	GGGACGACACAGCATCGCTCCGCGCGGACCTCTCTACATCTCGGTTGGAGGGCCCTG	20503
Db	55380	GAACCGCGGAGTCTCTGCGCGCGCGGCTTCTTACACGTTTCGCGCTTGAGGGGCGCTG	55439
Qy	20504	CGGTCAACCTCGACACAGGTGTTCTCTCTGCTCGTCCCTGACACCTCGCTGCCAGT	20563
Db	55440	CGGTGGCGGTGATACCGGGTGTCTGCTGCTGGTGGCTTGATTTGGCGTCCAGT	55499
Qy	20564	CCCTCAGTCCGGTGAATGCAACATGGCTTTGGCGGGGGGCCACGGTCATGACACCC	20623
Db	55500	CGCTCGTTCGGGTGAGTGATATGGCGTTGGCAGGTGGTGTGACGGTGATGTCGACAC	55559
Qy	20624	CGATCACCTTCAACGAAATTCGCCCCCGCAACCGGAGACTCGCCCCCGACGGGCGTTGCAAGG	20683
Db	55560	CCCTGGCTTCTCTGAGTTCTCTGTCAGCGCGGTTTGGCGGCAGATGGTCGGTCAAGT	55619
Qy	20684	CGTTCTCGCGCGCGCTGACGATACCGGTGGGGTGGGGTGGGGATGCTGCTGGTG	20743
Db	55620	CGTTTGGCGCGCTCGGATGACCGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGGGGTGG	55679
Qy	20744	AGCGCTCTCCGACCCCGCGCAACGGTCACTGCTGCTGGCGCGTGGTGGTGGCAGTG	20803
Db	55680	AGCGGTTGTGCGATGCTCGTGGGAATGTCACCGGGTGTGGCCGGTGTGGCGGGTCTG	55739
Qy	20804	CGGTCAACAGGACCGGTGGAGCAACGCTGTGACCGCGCGCCAAACGGGCGCTCCGAGAGC	20863
Db	55740	CGGTGAATCAGGATGGTGGTGGATGGCTGACCTGCGCGCAATGGTCCGTCGACGAGC	55799
Qy	20864	GGTTCATCCGCGAGCCCTCGCAACCGGACCTGACCCCGCGCGACCTCGATGGGTGG	20923
Db	55800	GGGTGATTCGGGAGCCCTCGGGAATGGGGCTGTGGGCTGTGGGCTGTGGATGTCTGG	55859
Qy	20924	AGGCCACGGCACCGGACCACTTTTGGGCGACCCGATCGAGGCCAGGCCATCTCTCGGGA	20983
Db	55860	AGGCGCAGGGACCGGTACCGGGCTCGGGATCCGATCGAGGCGGAGGGCTGATCGGGA	55919
Qy	20984	CCTACGGACAGGACCGTCCGCGCAACGGGCGGTTGTGGCTGGGCTCCGTCAAGTCAAACG	21043
Db			
Db	55920	CATATGGGCGAGGACCGGGATCCTGAGCGGGCCCTGTGGCTGGGGTCAATCAAGTCCAAACA	55979
Qy	21044	TCGGACACACACAGCGCGCGCGGGCGTGGCCGAGTGATCAAGATGGTATGGCCCTCC	21103
Db	55980	TCGSCCAACACGACGCGCGCGGGTGTGGCGGGGTCAATCAAGATGGTGTGAGGCCATGC	56039
Qy	21104	GCACACCGGACACTCCCAACCGACTCTCAACGGGATGAGCGGTCCCGCATGTGACTGGT	21163
Db	56040	GGCACGGGGAGTTTGCCTCGACAGCTGTGACGTGGGCAAGCCCACTCCACAGTGGACTGGT	56099
Qy	21164	CCGCGGTGGGTGCTGCTGACGAGACGGTGCCTTGSCCCCGGGGAGGGCGGC	21223
Db	56100	CTGCCGGGCGGTTCCGCTCTTACCGGGAACACGCTCTGGCC---CGAGAGCGCGCGTC	56156
Qy	21224	CGCGCGGGCAGGAGTGTCTATTCGCGGTGACGCGCACCAACGCCCAACGTCATCTCTCG	21283
Db	56157	CTCGTCGAGCGGGGTGTGCTGTTTGGGATCAGCGCACCAACGACACCTCATCTCTCG	56216
Qy	21284	AAGAAGCACCGCGCGACGATTCGCGGGGACCAACCGCGGACGAGATCCCGGTAGTG	21343
Db	56217	AACAACCAACGTCGGA-----ACGAGCGGAGATCGACCAAT	56252
Qy	21344	GCAGAGGAGTGTGCGCGGACGCTTGGGGTGGCGGTGTGGCTGTGGTGGCCAAAGTCCG	21403
Db	56253	CGGATCGCGGGTCACTGCGCATCCAGCGTGATCCCGTGATGTTGTGCGCTAGGAGTC	56312
Qy	21404	AGCGCGGCTTCGCGCGCCAGCGCCCTGACGCGCCACCTCACGACACCAACCCCGGCC	21463
Db	56313	TCGACGCTGCAGGCCCAAGCGCTGGCTGACGAGCCCGGCTGGAACGGGGTCTTGCGC	56372
Qy	21464	TCGACCTCGCGGACGTCGGATACACCTCGCCACGCGCGCGCGGTGTTCGACACCGCG	21523
Db	56373	CTTCTCGCGTGGATTTGGGGTATTCACCTCGCGACCACTCGTTCTGTGTGCGACCAACGCG	56432
Qy	21524	CCACCTCATCGCGCGCGACCGCACCTTCTGCAAGCACTCCAGGCACTCCGCGCAG	21583
Db	56433	CCGTGTTGGGGTGGCGATCGGAGGACATGCTGTCCAGGCTGGGAGCGCTCGCCGATG	56492
Qy	21584	GCGAACCCCAACCCCGCGCTCATCCACAGACGCGCCCGGCGGACCGGACCGGGGAGG	21643
Db	56493	GCCGGAACCGCGCGGGGTGATA-----ACGGCTCTCGGAAT	56531
Qy	21644	CCGCAAGAAAGACCGCATTTATCTGCTCGGACAGGGCACCCCAACGCGCCCGGCACTGGCCC	21703
Db	56532	CCGGTGGCGCATCGGATTCGTTTTTCGCTCAGGCGAGTCAGTGGCTGGGATGGGAA	56591
Qy	21704	ACGCGCTTACCAACACCAACCGCTTCGCGCGCGCACTCAACGACATCTGACCCACCC	21763
Db	56592	AGCGTTTGTGCGCGCTTTCCCGCGTTTCGCGGACGCTTCGAGGAAGCTTCGACGCGC	56651
Qy	21764	TCGACCCCACTCGACCAACCCCTCTCTCCCTCTCACCCCAAAACGACAAACGACAAACG	21823
Db	56652	TAACGGCACACTGGGCGCGGACGTTGGGGTGTGCTTTCGGTGTGATGAGCAGA---	56708
Qy	21824	ACAAACGAGGACGCGCGCGCACTGCTCAGCAGAGACCCCGTACGCGCAGCCCGCTTTCG	21883
Db	56709	-----TGCTCGACCGGACGCTGTGGGCGCAGTCGCGGATCTTCG	56747
Qy	21884	CTTTCAGGTGCGCCTCCACCGCTCTCTCACCGAGGGGTACCAATACCCCCCACTACT	21943
Db	56748	CGGTTCAAGTCGCGCTCTCTGGGATTTGTA---GGTGTGGGGGTGGCGCGCGCGCG	56804
Qy	21944	ACGCGGACACTCTCTCGGCGAAATCACCGCGCGCCACCTCGCGGCACTCTCACCTCA	22003
Db	56805	TGCTGGGCACTCGGTGGCGAGTTGGTGGGCGACGCGGCTGGTGTGTGTTGTTCTTGC	56864
Qy	22004	CCGACGCCACCACTCATCAACCAACGCGCCACCTCATGATAAACCATGCCCCC---CG	22060
Db	56865	CGGACGCTGACGCTGTGTTGCGGCTCGGGCCACCTGATGACAGGATTTGCCACCGCGC	56924
Qy	22061	GCACCATGACCACTTCAACACCAACCCCAACACACATCACCCACCACTCACCGCCACG	22120
Db	56925	CGCAATGCTCGCGTCCGCAACGAGCGCGGTGGGACCGCTGCTTTCCCGGGTGT	56984



Db	59097	AAACGCCATC---ACCCTCGCAGATGTGGACTGGAGCGATTCGCCGCTCTTTCAACCG	59153	Db	60141	TCCCGCGAGGCA CAGGCGATGSGACCCGCAACAGCGGTGTGCTGTGGAGATCTCGTGGA	60200
Qy	24317	CTCGACGCCACAGCCCGCTCATCGAGGACATTCGCGAGGTTCCGCAAGCGGCTCAGGAGC	24376	Qy	25080	AACCATCGAAACACGCCGCGCATCAACCCCCACACACCTTCACGCGCACCCCCACCGAGTCTT	25139
Db	59154	CGGCCGCCGCGACCACTGTTGGAGAGATCGTGGATCTACGCC-----	59198	Db	60201	GGTGTTCAGCGCGCGCGCATTTGACCGGTTCTTTTGGGGGTACCAAGACCGGTGTCT	60260
Qy	24377	TGGAAGCAGCTGCTGCGACGGCAAGACGACACAGCTCAGCCGATTCGACGCTCTCTCC	24436	Qy	25140	CGCCGGAATCAACGCTCAAGACCAACGCGCGCATATCCGCCAAAGCCGTGATGTGGAGAC	25199
Db	59199	-----CCGACACCGAGACCGAGGAGACACGCTGCCGCGAGCTGG	59240	Db	60261	CGCGGCGTGTATCTACACGACTACGCGTCCGCTCGCGTTTCGCAAGACCCCGCGGAG-----	60315
Qy	24437	GTGAGCGATTGGCCCGACTGACGCTCTCAAGCAGAAACGAGTGTCTGCTCGCCTGATTC	24496	Qy	25200	CATCGAGGCTACGCCCTGACCGGACGTTCCGGGAAGTGTGGCGTCCGCGGGGTGGCCCTA	25259
Db	59241	GGCAGCAGTGGCCCGCACTGCCCGCGCTGAGCGCGACACCTGCTGTGGAGTGGTGC	59300	Db	60316	-TTCCAGGGTTACTTCGCGCACCGGCAACGCGGGCAGCGTCGATCCGCGCGGGTGGCTTA	60374
Qy	24497	GGACAGGCATCTGACCGGTTCTCGGCTTCGTAATCCGGAAGGCATCGAGGACCAACGAG	24556	Qy	25260	CACGCTCGGGCTCGAAGGCCCGCGGTCGCTCGGTGATACCGCGTGTTCGTCGTCTCGT	25319
Db	59301	TGGCGGAACCGCCAGACCCCTGGGGCAGGATTCGGCGAGGCTGTGCNACCCGATCGA	59360	Db	60375	CACCTTCGGGTTAGAGGGCCCGCGGTACCGTGGACACCGCCTGCTCTGCTCCTCGT	60434
Qy	24557	CTCTCCGCACTCGGCTTCGACTCGCTGACGTGCGCTCAGTTCAAGAGAACTCGCA	24616	Qy	25320	GGGTTCGATTGGCGCGGCGCAGGGCTTCGCTGCGGGTGAGTTTCGATGGCGCTTCGCCG	25379
Db	59361	CTCTCCGCACTCGGCTTCGATTGCTGACCGGCTAGAGCTGCGCAACAGGTTGAACG	59420	Db	60435	GGCGTGCACCTGCGCTGCCAGTCCCTCGCGCTGGCGAAATGCGACCTTGGCCTTGGCGG	60494
Qy	24617	AGGAACCGGACTGCACTCCCGCCGCTCGCTGCTTTCGACTATCCACCCCGCAGGAAT	24676	Qy	25380	GGGTGTGACGCTGATGCTCTCGGGTACGTTTGTGGAGTCTTCACGTCAGCGGGTCT	25439
Db	59421	CGGTGACCGGGCTTCGCTGCGCGCGACGCTGGTTTTCGACCAACCGCAGCGCTGGCT	59480	Db	60495	TGGCATTTTCGGTGTGATGCGCACCGCGGGAGCCCTTCGTGAGTTTCAGCGGCAACGCGCACT	60554
Qy	24677	GTGCTGCCCATCTCGGCACACAATCTGTCG-----	24706	Qy	25440	GGCGCGGACGGCGGTCGCAAGGCTTATTCGGCGGCTGCTGACGCTACCGGTCGGGCCGA	25499
Db	59481	TGTCGAAACAGTTGGTTTCGGGCCCTGGTCGCGGAGCCGCGAACCGGCATCGAATCGCTGC	59540	Db	60555	CGCTTCGATGGCGGTCGAGCCCTTCGCGGATGCCCGACGCGCACCGCTTGGGGCGA	60614
Qy	24707	-----ACCTAG	24712	Qy	25500	GGGTGTGGGATGCTGCTGTGGAGCGGCTCTCGACGCCGCTCGCAACGCGTCAACGCTACCCGTGT	25559
Db	59541	TCGCGAGCTCGACAGGCTGGATACACGTTGGCGCAAGGGCTTCGATCCCACTGGAAG	59600	Db	60615	GGCGCGCGAATGCTGCTGTGGAACGCGCTCTCGACGCGACGACGCAACGCGCCACCCGCT	60674
Qy	24713	ACGCAAGAGGACCGCGGCACTGTGCAATGCTCTC-----	24747	Qy	25560	CTTGGCGTGTGCTGCTGGCAGTGGCTCAACAGGACGCTGCGAGCAACGCTTCGACCGC	25619
Db	59601	ACGAGCCAAAGTGGCGAGGCGCTTTCGACGCACTCTCGCACTCTCGCCAAAGTGGGACGGCGCGTG	59660	Db	60675	GCTGGCGCGTGTGCTGGTTCCCGGATCAACAGGACGGGACGCTCAACGCGCTGACCGC	60734
Qy	24748	-----	24747	Qy	25620	GCCCAACGGGCGCTCCACAGCAGCGTGTTCATCCGTTCAGCGCTTCGCGCAATCGGGACTGAC	25679
Db	59661	ACGGCAGCGGCAGAGGAGTCAACCCCAATCGCTGACGGCGGCGACGAGCAAGCAATCT	59720	Db	60735	GCCGAGCGTCCCGCANGCAGCAGGATGATCCGCCNAGCCCTTGGCGAACGCGGGTTGTC	60794
Qy	24748	-----	24747	Qy	25680	CCCGCGCATGTGACGAGTGGAGGCGCACCGGACCGGACCACTCTTGGGGGACCCGAT	25739
Db	59721	TCGACCTCATCGACCGGAAGTTCCGGCGCTGACCGCCCTTTCTCGCCTCAGCTCCCTG	59780	Db	60795	GCCCGCGAGTCTGATGTGTCGAGGCGCACCGGACCGGCGCTTGGGCGACCCGAT	60854
Qy	24748	-----CCGCAAGTG	24756	Qy	25740	CGAGCCCGAGGCACTCTTGGCGGCTTACGAGACACACCGCCCCCACCACCGCCCTTGTG	25799
Db	59781	ATTACTGGAA CCGTGTATTTTCGATGGCCAAATGAAGAAAGCTCCGCGAGTACTCAAGCG	59840	Db	60855	CGAGCGCAGGCGCTGTATCGCCACCTACGGGGCGAACCGGTTCGGCGGATCATCCGCTGCT	60914
Qy	24757	GCCCATCGCGTAC-----	24779	Qy	25800	GCTGGGATCCCTCAAAATCCAAATCGGCGACGACAGCCCGCGCGGCGTGGCGGAGT	25859
Db	59841	TGTCGCTGCTGMACTGGAGAGGCGCACGAAACGCTGACGAGTTGGAGCGCCAGAGCA	59900	Db	60915	GCTGGTTCCCTCAAGTGAACATCGGCCACACCGAGGCTCGCCGCGTGTGGCCGGGT	60974
Qy	24780	CGAACCGATCGCCATCATCGGTATGGCATGTGCTTCCCGCGCGGCTACGTTCTGCCGA	24839	Qy	25860	CATCAAGATGTGATGGCCCTTCGCAACGGGCTGCTGCGACAGACCCCTCCACGTGGACGA	25919
Db	59901	CGACCCATCGGATCGTGTGATGGATGTGTTATCCCGGTGGCGTCTCCACTCCGA	59960	Db	60975	GATCAAGTGGTCTCTGGCCATCAGGACCGGGAGATGCCCGCGAGCTGCACATCGACCA	61034
Qy	24840	CGACTGTGGAAATTCGCTTCGGGTAAAGACGCTATCGGCGTCTTCCGACCGACCG	24899	Qy	25920	GCCCAACCCCGAGTGTGATGCTGTCACAGGCGGAGTACAACTCTCTGACACAAACCGGTGCC	25979
Db	59961	GGAGCTGTGGGACTGGTCTGCGAGGAGGAGACGCGATCGCGAACTTCCCGGAAGACCG	60020	Db	61035	GCCATCGCAGCACGTGGACTGTGCGGGGCGCGGTGCGGTGCTTCACGAGCAGCGTTGA	61094
Qy	24900	CGGCTGGGACCTGGACAGCTCTACGACCCGACCCGACCCGACCCGCGGACCTGTGTAC	24959	Qy	25980	CTGGCCCGCGACCCCGGCGCGCCGCGCACGCGCGGTGTCTCATCTTCGGGCTCAG	26039
Db	60021	TGGCTGGAACTGGACAGAGCTGTTCGATCTCTGATCCGGCGCGAGCCGGGACCTCTACGT	60080	Db	61095	CTGGCGCG-----ATCTCGGACGCGCGCGGAGAGGGGTGCTCTGTTCCGGATGAG	61148
Qy	24960	CCGAAACCGCGGATTCCTCTACGCGCGAGGCGCACTTCGACGCGCAATTCCTCGGATCAG	25019	Qy	26040	CGGCACCAACGCCACATCATCTCGAAGAAAGCACCACTCCCGAGGACAGCGATACCGA	26099
Db	60081	CGCGAGGGTGGTTCTCTCGCGGGGTGCGGCACTTCGATGCGGGGCTCTTCGGGATCAG	60140	Db	61149	CGGTACCAACGACACCTGATCGTCGAGGAAGTATCCGACGAGCGGCTCTCGGGCAGTAC	61208
Qy	25020	CCCCCGGAAAGCCCTCGGCATGGACCCCGACGAAACGACTCTCTCTCGAAACCGCTGGGA	25079	Qy	26100	CGAGAAACCGGCTGCGCAACGCAACGCGCTCGCCCATCTCCCTCTCTTCCTCGGTCGCGGT	26159
Db				Db	61209	CGA-----GCCGACCGGGGCAATTTCCCTGCGCGCT	61238

Qy	26160	GTCCGCGAGGCTGAGCGCGGTTGCGGCGCAGSCACAGCGGTTCGSCCAGTAGTGGC	26219
Db	61239	GTCCGCGAAGACGGAGACGGCAATTCGGCGAGAGGCTCCGAGTTGCTCTCCGTAGTAC	61298
Qy	26220	AGCCCGCCGAGCATGTCACTTCGCCGACATTTGGTTCGGGTCTGGGCCCGCGCCGCGCCGT	26279
Db	61299	CGAGCACCCGGAGCCGGGACTGGGGGACGTCCGGTACTTCGCTGGGCCACCGGTTCGGCTGC	61358
Qy	26280	ACTGGAAACACCGCGCGCTCATCTCTGGCCGGGACCGCGAGGAACTGGCGCAGGCACTGAC	26339
Db	61359	GATGAGACACCGGCGTGTCTGGTTGCGGACGATCGGGACTTTTCGTTCGCGCGGACTGAC	61418
Qy	26340	AGCCCTGCGAGCCGGCGAACCACCCCAATACACACAGCCACACCCCGGGGGGTGA	26399
Db	61419	GGCGTTGGCTGGGGCGTTTCGGGAGCAAGT-----GGTGCAGGGCGGGCGGACTG	61472
Qy	26400	CCGCGCGCGCGTCTGCTTCCTGCTTCCCGGAGCAGGGCGGCCAGTGGGCGGGATGGGCT	26459
Db	61473	CAAGGGAAGGTGGGTTGCTGTTCCCGGCGCAGGGCTCGCATTTGGCAGGGATGGGAG	61532
Qy	26460	GACCCGTCTCACTCTCACTCCCGGTGTTCCCGGACACATCGACGCGATCGGAGAAAGCCCT	26519
Db	61533	GGAACTGTCCGAAATCTCGCGCGTGTTCGGCGGAAGCTGGCGGAATCGCGCGGGCTAC	61592
Qy	26520	CACCCCTGGGTCCCTGCTCCCTGACCGACATCTGACCGCGACCCCGGACGCCGCGC	26579
Db	61593	GGCCCTTACGTGGAGTGGTGGCTCTCGGCGTCTTCGGCGGTATCCCGATGACCCGCG	61652
Qy	26580	ATGGCAACAAGCCGAGTGTCTCAGCCGCTGCTTTACGACTCATGTGCTCTCCCTCGCGCG	26639
Db	61653	GCTGATCGCGAGCGTATTACGTGCGCTGTTCCGCAATGATGTTGCTGGCGGA	61712
Qy	26640	CCTGGGCGCTCTTACCGGATCGAAACCGGACCGCGGTCTTCGGCCACTCCCAAGGAGAAAT	26699
Db	61713	ACTGTGGGTTGCTGGGAGTGGAGCCCGCGCGGTGCTCGGTCTATTCCAGGCGGAGAT	61772
Qy	26700	CGCGCGCCACATCTCGGCGCACTCAGCTCGAAAGACCGCGCCCAAAACCGTTGCACT	26759
Db	61773	CGCCCGCCCAATGTGGCAGGCGCTTGTCTTGACTGATGGGTGGCATCATCGCTGC	61832
Qy	26760	CGCAGCGCGCACTGCGCGCGCTACGAGCGCGCGCCCATGGCCTCACTGCCCCCTGCC	26819
Db	61833	CCGCTGCGATGCGGTGTCCGCGCTGACCGGGAAGGAGGATGCTCGGATTCCTTGCC	61892
Qy	26820	CGCCAGAGCTGCGAGCTCATTTCCGACCGGTGGGAAGCGCATGTTGGGTGGCAGC	26879
Db	61893	GGAAAGCGGTGTGAAGCAATCGCAGGCTGCGCG-----AGCTGACCGTTGGCGC	61946
Qy	26880	CCTCAACGGCCCCACTCCACACCGTCTCCGGCGACCAAGCGGTGGATGAGTGTCT	26939
Db	61947	GGTCACAGACCCGGCTCCACTGTCTTCGGCGAACCCTGCGGTCTGGAGCGTCTGCA	62006
Qy	26940	GGCGCACTGCACACACCGGCTACGGGCGCAACGCAATCCCGGTGCACTACGCTCCCA	26999
Db	62007	GACCGAACTGACCGCGGAACGTCAGACACCGCGGGTGGGAATTGATTACGCTCGCA	62066
Qy	27000	CTGCCCGCAAGTCCAAACCCCTCCAGACGAATCTCTGCACTCTGCTGGAGACATCACCCC	27059
Db	62067	TTCCCGCGAGATCGCGCAGTCCAGGGCGCGCTTCTGACCGGCTGGGCGGAAGTGGGTC	62126
Qy	27060	CCAGCGGTCCACCGTCCGTTCTTCTCCACCGTGGAGGCACTGGCTGGACACCAAC	27119
Db	62127	CGAACTCTGATGCTGCTTTCTACTACCGGTACCCGGAGCGGACCGGCGC	62186
Qy	27120	CCTGAGCCCGCTACTGTGATCCGCAACTCCACCGAGCCGCTTCGCTTTCAGCCAGCCAT	27179
Db	62187	ACTGACCGCGACTACTGTACCAAGACCTTCGGCAGCCCGTCCGCTTTCAGCAGACCGT	62246
Qy	27180	CCAGACCTGACCGGACGAGACCGCGCTTTCATCGAAATTCAGCCCGCCCAACCCCACT	27239
Db	62247	CGCCCGGATGCGAGATCAGGGCTATCGGTTCTTCTGCTCAGGTGAGCCCGCGCATCGCT	62306
Qy	27240	CGTCCCGCATCGAAGACACCAACCGAAAAACACACCGAAAAACATCACCGCAGCCGCGAG	27299
Db	62307	CACCGCGGATCCAGGAAACGCTGGAAGCGCGGACCGCGGCGGGTGGTGGTTCGGTTC	62366
Qy	27300	CCTCCCGCGCGGAGAACACACACCCACCGCTTCTCACCGCCCTTCGCCACACCCAC	27359
Db	62367	GCTCGCGGTGGCGAGGCGGCTCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	62426
Qy	27360	CACCGGATCGGCACACCCACCTGGCACCACTACACCAACCAACCAACCAACCAACCC	27419
Db	62427	GGCGGAGTCCCGGTGAATTTGGGAACAGGTTTCTCAACACCGGAGCCGACCGGTGCC	62486
Qy	27420	CAACCCCAACACCCACCTCGACCTGCGCACCTACCTCTTCAACACCAACCAACCAACCA	27479
Db	62487	-----GCTGCCGACTTACCTCCGTTCCAGCGGCGAGCGGTACTGGTT	62525
Qy	27480	CCAAACACCC-----ACCAACAAACCGACCTTACCAACACCGGCTTCAACCCCAACCA	27536
Db	62526	GGAGTCCGCGAGTACGACGCGGCGATCTCGTTCTGCTGGGCTTGTCTCTCCGCGAGCA	62585
Qy	27537	CCGCTCTCACCGCACACTACCTTCGCGGACAAACACACAACTACTTACACCGGCGG	27596
Db	62586	TCCCTCTCGGGCTCGGTGACGCTGGGCGGATGCGGGCGGGTTCTTGTGACCCGGCAA	62645
Qy	27597	CCTCTCCCTACGACACCCCTGCTTACCGACACACCGTTCGCGCGGATGCTCTCT	27656
Db	62646	GCTGTGCTCAAGACCCAGCCCTGTTGGCGACCACTGGTTCGCGCGGCGGATCTCTGCT	62705
Qy	27657	GGCGGCGACCGCGCTCTCGAACTGCGCTTCAAGCGCGGGAACGGGTGGAATCGCCCTCG	27716
Db	62706	GGCGGCGACCGCGTTCGTGAAATGCTGATACGCGCGCGGACACAGTTCGGGTGCGATCT	62765
Qy	27717	GGTGGAGAACTGACCTGTCAGCGACCGTTGGTGTATCCCGCACACCGGAGACGTGAGTT	27776
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Qy	27777	GCAGGTCAACGCTTCGGGCGACCGATGAGTGGCATTCGCGCCCTTCGCGATCCACTCGTA	27836
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Qy	27837	CTCGGCGACCGGCTGCTGCGCGGACCGGGATGGAACCGCTACGCCACCGGCGCTCTCAC	27896
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Qy	27897	ACACCAACCGCGACACCGATCAACGCTGCGGACACGCAACCGAGCGCTGCTTGGCGGAG	27956
Db	62943	-----CTCCAGCGATCACAGGACCGCGGCGGCGGCGGCGGATGGAT	62984
Qy	27957	CTGGCCCCCGCGCGCGCGACCCATCGAACTGGGCGAGCTTACCGGTCTATGGCGGC	28016
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Qy	28017	GGACTCGGACATCGCTTACCGGCGCGTCTTCAGGGGCTGACCGCGCTGGAGGTTGCG	28076
Db	63042	TGAGCGGCGTTCGATTTCCGCGCGGCTTCAGGGGTTGCGAGCGCTTGGAAAGCGCG	63101
Qy	28077	CGAGGATGCTTGGCGGAGGTGCTGTCGCGGAGAGGCTCTGCGCGATGCTCCGCGGC	28136
Db	63102	AGAGGAGATTTCCCGGAGTTCGCGCTTGC-----CACCGCACCGCAAGACGCGCG	63155
Qy	28137	GGCTTCGCTTTCACCGCGCTTGTCTGACGCGGCGCTTCGACCGCGCGCTCACCCC	28196
Db	63156	CAGTTTCGGAATCCACCTCTCTGCTGATGCGGCACTGACGCGCTGGGCGGACCGGA	63215
Qy	28197	CCAGAACGGGAGCGGCTCGACGGAAGACGTCGCCAGGAGCATGCTGACCGCGCAGC	28256
Db	63216	AGAGGATCCGGAACG-----	63229
Qy	28257	CCACGAGCGGAGTTCAGTGGAGGGGCTGCTGCTGACACCGGCGGCGAGTTC	28316
Db	63230	-----AGGGATGCTCCCTTCGCTGCGGAGGAGTGTGCTCTTCAAGCGAGCGG	63278
Qy	28317	CGTGTTCGCGTACGCGCTGTCGCGAGTTCGCGAGCAGGTAATGCGCTGGCCCTCACCGC	28376



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QY 28377 GCGCGACGAGGACGGTCCGGCGGTGGTGAAGTTCAGATCGAGTCCGCTCGCGCTCGCGCGGTGTC 28436  
Db 63339 GACCGACACGACTGGCCAGACCGTGTCTCTCATCGATTGCTGTGGTGTGCTCGCGCAGATTTC 63398  
QY 28437 CACCGAGGAGTCCGCGCGCGCGCGGATCGTACGCCCGAGCAGAGTCCGCTCTTCGGAATC 28496  
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QY 28497 GGAATGGGTTCCGTACCAAGTCCCGCCAAACGCCCTTCGCCCAACCGCGGACCGGCCCTG 28556  
Db 63453 CCACTGGAAAGCGAAT-----CTGCGCCCGCGCTGCCAAGCCGGTCTCCCTG 63497  
QY 28557 GCGCGTCACTCGCGCGCGGGCTTCCCAACCTGCCCGCGCTGACGGAGCACGAGCAAGTGCAC 28616  
Db 63498 GGCAGTGATCGGC-----AATGAC 63516  
QY 28617 CCGCATGACGAGCCGCGCGGACCTGCTTCGTGCTCTGAGCAGCGGTGCTCGCCGCCCGG 28676  
Db 63517 GAACTCGCCGAGCCTCGCGCTCGGCATTTGGCAGCGAACTCCACCCCGACCTGACCGGG 63576  
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QY 28797 GACACGGTCCGCTGCACGCGGCTGCCCGCAGATGTTGGCAGGCTCCAGGCCCTGGCT 28856  
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QY 29037 GGAGCCCGTCACTGGCGACCGCGCTGAACTGCGGGAGCGGACGCTTCCGCTCGGCC 29096  
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QY 29097 CGGAGGGCTGTTACGCCACGCTGTTGCGCGCGCACGTTGTCGCGGACCGGTACCCGC 29156  
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Db 63996 AGTGCCTCGTG----- 64006  
QY 29217 CTTTCGGGCGAAACGGTCTGATCACCGCGGAAACCGGTGTCCTGGGCGGCTCGTGCG 29276  
Db 64007 -----CGATGGGACGGTGTGATTTCGGCGGTACCGGCTGCTGGCGGGTGGTTGC 64061  
QY 29277 CCGGATCTGTGGAGGCGACCGGTACGGATCTGTTGCTGGCGGGTGGCGCGGACC 29336  
Db 64062 CCGGATTTGTGGCGGAGCGGGTGTCCGCCCTGCTGCTGCGGGGCGACCGGGTG 64121  
QY 29337 GAGCCCGAGGGTGGCGGAGTTCGGGCGGAGCTCGGTGGGCTCGGCGGACCGGTGGA 29396  
Db 64122 GAGCCCGCGGGTACCGACCTGTTGATGATGTTGGGCTTGGGCTGGGAGTGGCGGTGGA 64181  
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Db 64182 GGTGCGAGCTGCGATGTCGGGGATCGGGCCAGTTGGACCGGCTGTGTGACGACGATCTC 64241  
QY 29457 CGACATCGGCGCTGACCGGTGTCGTGCACAGTCCGGGCATCTCTGGACGACGGGCTGAT 29516  
Db 64242 GGCAGATTCCGCTGCGGGAGTGGTGCATGCGGCGGGGACATTCGCGACGGGGTCT 64301  
QY 29517 CACGTGCTGTCGCGCGAGCGGCTCGGGGCGTCTCCTCGGGCAAGGCGGACGCTGCGCT 29576  
Db 64302 CGAGTCGCTGACACAGAGCAGTGGCAAGAGTGTTCGCGCCGAAAGGCGCGGTCGCTG 64361  
QY 29577 GCTTCTCACAGCTGACGCGGGGAGAGTGTGCGCTTTCGTCATGTTCTCTCCG 29636  
Db 64362 GCACCTGACAGTTGACTCTTGATCTCTGTTCTCTGCTCTCTCTCTCTCTCTCTCT 64421  
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Db 64422 CTCGCGGTGCGGGGCTGCGGGTCAAGGAACTACGCGGGCGGACGCTTCTTGA 64481  
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Db 64482 CGGCTGCTCAGCACCGCGGACGCGGGGCTGCTCGGTGCTGCTGCTTGGGGCT 64541  
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Db 64542 GTGGAGCAGCCACGCGGATGACCGGAGCGCTCGATCGCGGGCGCTAGCCGATTC 64601  
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QY 29877 GCGCGACGCGGAGCGGCTTCTGATGCGCGCTCGGCTCGACCTCAGCGCGCTACGCTG 29936  
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QY 29937 TCGCGCTCGCACCGGTGCGCGCTGCTGCAAGTCTGCTTACGCTGCGCTCGCTCCG 29996  
Db 64722 TCGCGCGACGCGGCTGCTGCGTCTGTTGCGGACCTGCT----- 64763  
QY 29997 CTCGCGCGCGCGCGCGCCATGCGGCGCGCGCGGCGGCGCGGCTGCGG 30056  
Db 64764 ---GCCAGCGCGCTGCGCGCGGCGCGGTCAAAGTTCGCGGACGCTCAACGCTGCT 64820  
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Db 64821 TGGTGGCTGCGGAGGCTGCGGACCTCGATCAGGAAACCCAGCTGTTGGGTTTGGT 64880  
QY 30117 GTCGATGTCGCGCGGTGCTCGGCCATAGCGGTGCGGACGGAATCGACGATCGCGGC 30176  
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QY 30177 GTTCGCGAGCTGGGGTTCGACTCGCTCAGCGCGGTGAGCTGCGCAACCGCTCACGCG 30236  
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QY 30237 CGCAGCGGCTGCGGCTGCGGGCACGCTGCGCTTTCGATTTCGCGACCCCGGACGCT 30296  
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QY 30297 GCGCGACATTTGGCGAGCGCTGCTTCCCGACGAGAGCCGACG 30342  
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## RESULT 3

US-09-370-700-1  
; Sequence 1, Application US/09370700  
; Patent No. 6274350  
; GENERAL INFORMATION:  
; APPLICANT: Balez, Richard H  
; APPLICANT: Broughton, Mary C  
; APPLICANT: Crawford, Kathryn P  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Treadway, Patti J



Db 37231 TCGTTGGTCGACGTGTCGGCGGAGCGGAGAACTCCCAACCGGTGACCGCGGTGACGTG 37290  
Qy 3334 GTCCAGCCTGTGTCGTTCAGCGTCATGTGTCTTTTGGCTGCTCTGTGGCGTTCTTACGGT 3393  
Db 37291 CTCAGCGCGCTTCCTTCGCGGTGATGGTTCGCTCGCGGAGGTGTGGCTTCTTACGGG 37350  
Qy 3394 ATCGAACCGACGCGGTCTTTGGCCATTTCCAGGCGGAGATCGCGGCGCGCATGTGTGT 3453  
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Qy 3454 GGGCGCTGAGCTTGAAGAGACGCGGAAGACTGTTGGCTGCGAGCGCGCGCTGGCC 3513  
Db 37411 GGGGTGCTCGCTGAGAGATGCGGCCAGCTTGTGCGCATTTGCGACGAGAGCTTGAAG 37470  
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Db 41849 -----GGGATGTGTTCTCGGTTCCGATGGCAGCTGCTGGATCAGACGCTGTGGGG 41901  
Qy 8113 CAGCGCGGCTTTCGCTTTCAGGTGCGCTTCCACCGCTCTCTCACCGAGGCTACAC 8172  
Db 41902 CAGTCGGGTCTGTCGCGCTGCAAGCGCGCTCTTGGGGTCTCT--GGGTTCTGGGGC 41958  
Qy 8173 ATCACCCCGCTACTACCGCGACCTCTCTCGGGAAATCACCGCGCGCCACCTCGCC 8232  
Db 41959 GTTCGGCGGATGTGGTGATGGGCAATTCGGTGGGGAGTTGGCGCGCGGTTTCGGCT 42018  
Qy 8233 GGCATCTCACCTCACCGACCGCACACCCCTCATCACCAAGCGCGCACCTCATGCA 8292  
Db 42019 GCGTGTGTTGTTGCGGGATGCGGCTCGGTTGGTGGCGCGCGCGCGTGTGATGCA 42078  
Qy 8293 ACCATGCCCC---CGGACCATGACACCTTCCACACACCCCGCCACATACCCAC 8349  
Db 42079 GCGCTGCGCTCTGACGGCGGATGTGGCGGTGGCTGTGGTGAAGACCTTGTTCGGCA 42138  
Qy 8350 CACCTCACCGCCACGAAACACCTCGCCATCGCGGCATCAACACCCCGCTCCCTC 8409  
Db 42139 TTGCTGGCGGTTCGGGAGAGTCCGTGAGCGTTCGCGGCTCAATGCCCCCGGTTTCGGTG 42198  
Qy 8410 GTCATCAGCGGACCCCGCACACCGTCCAAACATCACACCTCTGCGCAACAAAGGC 8469  
Db 42199 GTGTTGTGGGCGATCGGAGGTGCTGGCAGCATGCTGGCGCGGTGACGAGTCCGA 42258  
Qy 8470 ATCAAAACCAAAACCTCCCAACCAACCGCTTCCATCTCCCCCGCACCAACCCCATC 8529  
Db 42259 GTCCGACGCGCGCTTGGGCTCTCCCATGCTTTTCATTGCAACGGATGACCCGATG 42318  
Qy 8530 CTCACCAACTCAACGACACCAACCTCTACCTACCACCCACCCACACCCCGCTC 8589  
Db 42319 TTGGCGAGTTCCGCCAGATCCCGAGTCTGCGGAGTTGCGTAAGCCAAACGACACCGCTT 42378  
Qy 8590 ATCACCGCAACAC-----CCACCCGACCACTCTCTACACCCCGCTACTG 8637  
Db 42379 GTGTCAGTTGACGGGTGAGTCTGACAGAGCGCGGAAATGAGCACACAGGGTATTGG 42438  
Qy 8638 ACCCAACAGCCCGCAACCGTTCGATACGCGCACCCACCGCCAAACCTTCCACCAACAC 8697  
Db 42439 GTGCGCAGCGCGTGAACCCGTCGTTTTCGCGGACGCTGTCAGGCGCTTGCAGCGCAG 42498  
Qy 8698 GCGTCAACCACTTCAATCGGACCCGACCAACCTCTACCTCACCGCTTCAACCCACAC 8757  
Db 42499 GGCATAGGACGCTGCTGAGCTCGCGCCCGGACCGGAAACGCTGGCGGCACTGGTTCCGGAG 42558

Qy 8758 AACCTCCCAACCC-----CCACACCAACCTTACCTTACCCACCCACCCACCCAC 8808  
Db 42559 TGTGCGACGAGTCCGATCGGTTGGCGGATTTCTGTCATCCCACTGATGCGCAGGAG 42618  
Qy 8809 CACCCCAAAACCACTCTCACCACCTCGCAAAACCAACCAACCACTTGGACCCCGCAC 8868  
Db 42619 CGGACGAGACCCGTTCTGCTGATGACAGCCCTGGCGCATCTCCACACCCGTTGGTGG 42678  
Qy 8869 CACTACACCCACGACAAACCCCAACCCCAACCCCAACCCCTCGACCTTCCCACTTAC 8928  
Db 42679 GTGACTGCGAGGCTTTTTCGCGGTACCGCGCTAGGAGCTCGAGTTGCCAAGTAT 42738  
Qy 8929 CCTTTCAAACCACTTCTGAAAGCAACACCCCGGTGCGCGCAACCGTGTCA 8988  
Db 42739 GCCTTCAAACGACGACTACTGATCGAGTCCAGTGCAGCGCAGCAGCGACCGCA 42798  
Qy 8989 GC-----AGCGGACTCGACCCCAACCCCAACCCCAACCCCTTCA 9021  
Db 42799 GACATCGCGAGGTGGCGAAACAGTTCTGGACCGCGTTGACCAAGGCGATCTGGCAAG 42858  
Qy 9022 CTCGCGCCACATTTGGAACTGCGACTGACGCTG---GAGCGCTTCTTTCAGAGCGCTT 9077  
Db 42859 TTGTCGCGCTCTGATCTTGGGCGGACGACACATGCGCATCTTTCGATGATGTA 42918  
Qy 9078 GTCTTTGAGGTGCGATCCGTCGCTGAGTCCGCTCGCGCGCACGCTGCTCTGCT 9137  
Db 42919 TTGCGCGGTTGCTCTCTCGGAGCGGACTCCGCAACCGTTCGCTGCTGATTCCTGCG 42978  
Qy 9138 GGGCGCCACCTTCTTCGAACTCGCCCTTTCATGCGGGCACATACGTGGGCTGCGACCGAGT 9197  
Db 42979 CGGTACCGAAATCAGTTGGCATTTCTCTCGGAGGTGCGCGCGCCGAAAGTTTCGCTACC 43038  
Qy 9198 GGATGAGCTGACGTGATCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9257  
Db 43039 TGGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43098  
Qy 9258 GGTGGGCTTTCGCGCTGCG----- 9276  
Db 43099 CTGCTCGAGGCGCGCGCGAGGTCTCGGATCGGCTGTCGGAAGAGGACCCCGACCGC 43158  
Qy 9277 GATGGGAGGCGCGCGTTTGTGATGTGATGCGCGGGGTGGAGTGTGTTGTGGTGG 9336  
Db 43159 GAGGACGCTCGACACGCGCTGCGCAATCGCTGACGATGCGGCTCAACTCGGTGGCGGTG 43218  
Qy 9337 GGTGTCGCTGCGGTGGGTGCGACGCT-----CATGCTCGGGG 9379  
Db 43219 CTTCGCTGTTGGGCTCGATGAATCGCTCTCGGGAATTCCTGCTTGCCTGCTGCT 43278  
Qy 9380 TGCTGTTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9439  
Db 43279 TTCGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43338  
Qy 9440 CGCGGGTTCGCGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9499  
Db 43339 TGGCGGTGACGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43398  
Qy 9500 GTGTTTGGGCG-----GGTGTTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9549  
Db 43399 CTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43458  
Qy 9550 GGGGATTTGCTGCTGA-----GGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9578  
Db 43459 ATCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43518  
Qy 9579 GGAGAGCGTGGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9627  
Db 43519 GATGTCGCGAGGATCAAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43578  
Qy 9628 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9687  
Db 43579 CGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 43638



QY 9688 GGGCGGGGTTCCGGAGGGTGTTCGGGTCCGGCTGTGTGGGTGGTGTGCTTCAC 9747  
Db 43639 GTGTGTA CGGGGGGTTTGGGGCGCATGTTGCCCGGTGTTGGCGGTGCTGAG 43698  
QY 9748 CGGGCGGGTGTAC-----CGGTGTCCGGGTGCGGTG 9780  
Db 43699 CACGTGGTGTTCACCAAGCGTCCGAGAGCGAGCGCTCCGGGCGCTGGGGAAATTGCGGCG 43758  
QY 9781 TCGGCTGTTCGGCGGGGGCGGGCGGTGAGGGGTGTGCGTGTGCGGTGAGGATGAGCG 9840  
Db 43759 GAGCTGGAGGGCGCTGGGTGCTCGGGTGTGATTTGTGCGCTCGAGCTGGCTGATCGTAC 43818  
QY 9841 GGTGTGCGCGTGGCTGCGTCCATCGTCTTGATTTGCGCTGTGCGCTGTGATGAGTGTG 9900  
Db 43819 GCAGTGGCTGGAGTGTGGCAGGATCGGTGGGGAGTGTGCTGACTGCGGTGTATAC 43878  
QY 9901 CGTGTGTCTCGGTTTCGGGGGGCGGGGTTCGCTGTATGCGGTGCAAGTGGCTGAG 9960  
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QY 9961 GTGGGTCTGTCCCGTGTGGCAGCG-----TGGCGTGGCAGAGAGCTGG 10012  
Db 43939 GTGTGTTCGGCAAGTGGTGTGCGCGAATCTGGACGATGCTGCGCGACTCGAG 43998  
QY 10013 GTGAGAGCGGTGGTGGGCTGTGCGGGGTGGTGTGGGTGCGCGATGCCGTG 10072  
Db 43999 CTGGATGCTGTGATGTTCTCTCGTGTGCGGGGTGGGGAGCGCGGACAGGT 44058  
QY 10073 CCGTGGCGGTGGCGGTGTGCGGTGTGGGTGGTGTGGGTGAGTGTGTTGGTGGGTGT 10132  
Db 44059 GCGTATCGGCTCGAAACGCTACTTGGATGCTTGGCGGAGCAGCGTGGCGAGGGGA 44118  
QY 10133 TGGGTGTGTCAGGGTGGCTGGG--CTGGAGCGGTTCGGGTTCGGGTGCGGTGTG 10190  
Db 44119 TTGGTGGGACCGCGGTTCGCTGGGGACCGTGGCGGTGACCGGATGCGCGCGCGAA 44178  
QY 10191 GGTGACCC-----GGGTGCGGTGGTGGCGCGCGCGCGAGAGCGCGCGGTG 10236  
Db 44179 ACCGGCGACAGCTGCACCGGATGGGCTGGCTGATGGAACGAGCGCGGTGCTG 44238  
QY 10237 GATGTGTGGGTGTC-----GTGCGTGTGGGGCT 10265  
Db 44239 GCATTCAGGGTGCATTTGACCGCGATGAGACCTCCCTCGTGGCGGATGTGATTTG 44298  
QY 10266 GTGTGTTCGGCGAGGTGAGCATCCGAC--CGGTTGTCTCTCGACTCGACACC 10323  
Db 44299 GCACGTTTCCGCCAGCTTACCTCGGACGTGACGCCCGCTGCTGGACACCATGAC 44358  
QY 10324 GACACCGGACCGACTCGACAC----- 10346  
Db 44359 GAGGCCGAGCGCATTTGMAACACCGCGGNAACAAGCGGGCACAGGCAACCCGTTGAG 44418  
QY 10347 -----CGGTGCTGTGTGCTG 10360  
Db 44419 CTGACGCAACGCTGGCGGACTGTGCGGAAGGAACGCGAGATGCGGTATTTGATCTG 44478  
QY 10361 GTTGGGCGTGTGATGGTGGCGGTGTGGCGG----- 10393  
Db 44479 GTGCGGCGGAGACGGCGGTGTGTGGGACGCGAGATGCAACGCGCCTGCGCGCATCG 44538  
QY 10394 -----TGGTGGCGGTGTGTCAGCGCGAGTGGCGG 10423  
Db 44539 CGGCCGTTCCAGAACTCGATTGCACTTCTGTGATGGCGGTGGAGCTGGGCAACCGGCTG 44598  
QY 10424 TCGTGGGAGCGGTGTGCGCGCACGCTGAAACGACTT----- 10464  
Db 44599 AACACCGCACCGGATCAGCTGCCCGCAGCAGATTTTCGACTACCCCAATGCCGAG 44658  
QY 10465 ----- 10464  
Db 44659 TCGGTGTCGCTCACTCTGCGCGCAGCTTTTCCAAAGGAGATACCGTGTGAGTGGCC 44718  
QY 10465 -----GAGTATCCGGTGTATGTTCCAGCCAGCGGTCCGCTGACACAGGCC 10512

Db 44719 CTTCCGAGCTCGATCGAATCGAGCAGCAGCTCTCGATGCTCAACCGGAAGCGCGCA 44778  
QY 10513 CGCGGTCCGAGCTGCTGCCAGCGCTCCGGTGGCTGCTGCTCGCGGTGCGGTGAT 10572  
Db 44779 CGGACCGAAATCGCGACACGACTCGAGCCCTCCACGAGAAAGTGAACAGCGCAGCTGAA 44838  
QY 10573 GTATCGGTGGGAGGTGTTGCGGTGTTGCGGTGGTGGTGG----- 10614  
Db 44839 GTACCGACCGAGCCGATGTCTGAGCAGCTCGATTGCGGCGACGACGAGATATTC 44898  
QY 10615 ----- 10614  
Db 44899 GAGTTTATCGACACGAGCTCGACCTGTCTGAGCAGTTCCTCGGAACTTCAAGCGCG 44958  
QY 10615 -----GTGTGGTGGAGCGGTGG 10631  
Db 44959 AAATCGGTGAAATCAATGGCAATGAAGAAAAGCTTTCGCTATCTGAAGAAGT 45018  
QY 10632 GACGGGTGCTGCGGTGCGCGGTGGCGGCATCTGCTGCTGTGTGTGGGTGCGGGA 10691  
Db 45019 AACTGCGACCTGATCAGACCCGCGAGCGCTCTCGCGCCGAGAGCCGAGTACAGA 45078  
QY 10692 TCTGCTGTGTGT--GAGCCGCGGTGCTCGGATGCTCGGGTTCGAGAGGTCTGGCGCG 10750  
Db 45079 GCCGATCGGATCGTCTCGCGAGCTGCCGACTGCCCGCGCGTFCGACTCTCCGGAAGC 45138  
QY 10751 AGCTGGCGGTGGGGCGGAGGTGCGG-----ATTGTTCGTGTGATGTGGGGAGCG 10805  
Db 45139 GCTTGGCAACTCGTGGCACTGGCACCGACCGCATCTCGAGATTCCCGCGCACCGGG 45198  
QY 10806 GCGGAGGTGCTCGGCTGCTGGAGGTGTTCCTCGCGGTGTCGCTGAG----- 10857  
Db 45199 CTGGGATCTCGCGGTGTGACGATCCGACCCGAAACACAGGGAAGCTGTACACCGC 45258  
QY 10858 -----GGTGTCTGATGCGGTGTGTGCTGAGAGTGCAGACGATCGCTCTCTCAC 10910  
Db 45259 GGCGCGGTGTTCTCGCAGAGCGGGGATTTTCGACCCCGCATGTTTCGGGATTTCCGC 45318  
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QY 10971 GCTACGCGGGTATGAGCTGTGCGGTTCGCTGCTGTTCTCTCGCGCGGGGATCCT 11030  
Db 45379 CCTGAAGCGCGGGCATAGACCCGACATCCTCGCGGAGCAAGACCGGTGTCTCGG 45438  
QY 11031 GGGGTGCGCGCGGAGGCAACTACGC----- 11057  
Db 45439 TGGTGTACGCCCCCGAGGATGAGCGGCGCTCTTCAGGAGATGAGCGAAACGCTGGGG 45498  
QY 11058 ----- 11057  
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QY 11058 ---CGCGGCAATCCGCTCTGAGCGCGTGGCGGTACCGCGCGGGCGGGTCTGCC 11114  
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QY 11115 GGGGTGTGCTGCGTGGGGGTGTGGGAAGAGCCAGCGGATGACCGGGCACCTTGGC 11174  
Db 45619 TTTGCGGTGTGAGTGTGCTGTTCCGGGAAATGCACTCGCGCTGGCGCGGTGTGAC 45678  
QY 11175 CGGCA-----CCGACCAACCGGCGCATCATCCGTTCCGG 11207  
Db 45679 GGTGATGCGGACACCGCGAGCTTCTGGAGTGTCTCCGTCAGCGTGGTTGGCTCCGGA 45738  
QY 11208 TCTCATCCCATGTGACCCCGGAGCGACTGG-----CCCTCTTCGATGCGGCCCTGCG 11261  
Db 45739 CGGGCGGTGCAAGTGTGCGGCTGCGCGGATGGGACCGGGTGGGTGAGGTGCGCG 45798  
QY 11262 TCTGACCGCGCGTCTGCTGCGCGCGGACCTCGCTCCCGCCCGCCCTTCGCGCCCT 11321

Db 45799 TCTGTTGTTCTGGAGCGGTTTCTCGATGCGCGGGAATGGCACGAGGTTCTGGCGGT 45858  
Qy 11322 GCTGAGGACCTC-----CTGCCCGCACCC 11347  
Db 45859 GTGCGGGTAGCGCGGTGAACAGGACGGCGGTCGAATGTTGACTGCGCCGAATGG 45918  
Qy 11348 GCCCGGACACACCGCCGACCACTACCGGT----- 11379  
Db 45919 TCCGTCGAGCAGCGGGTGATCACCCAGCGTTGCGAGTGGCGGGCTGTCGTTTCCGA 45978  
Qy 11380 ---GGTCGGACAAGCGGCCAGCTGCACCGCCGCTGGCGCCGACACACGACACA 11435  
Db 45979 TGTGATGCGTTCGAGGACATGAGACCGGGACACGTTGGGTGATTCGATCGAGGCACA 46038  
Qy 11436 ACAGCACACACCCCTCTCGCCCTGGTCCGCTCCACATCGCACCGCTCTCGGCCACAC 11495  
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Qy 11605 CCCACACCTCGCTTCGACCAACCCACCCACCCCTCACCCACACCTCCACACA 11664  
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Qy 11665 CAACTCCAGCCAAACCGCAACCGTGTCCGCCCGTGTGGCGGAGCTC----- 11715  
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Qy 11716 -GACAACTCGAATCGGCCCTCTCGCCCTCGACAAACCGACGCGCCGCGGAAG--- 11771  
Db 46339 TGTGATTTCTCGAACTCTCAGTCCAGTCCAGCAGGGCGAACCGCGCGCGGTCCGAGGCGA 46398  
Qy 11772 -----AGTCACCTCGGCTGAAGTCACTCATGTTGAGGTGAACGCCACCA 11819  
Db 46399 GCGGNAACCGGATGTAGCGTCCCGTGTGCTTGGGTGCTGTGGGTGAACACCGGA 46458  
Qy 11820 GCATCCGACAGCGGAAGCGTGTGAACGACGAGTTTC-----ACATCGGCAACA 11871  
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Qy 11872 GAGGCTGAGATTTCAAATTCATGACACGACCTCGGCTGTCTGAACCGGACGCTG 11931  
Db 46519 GCCGTGAGTGTGGCGTATTCGCTAGGAATGACACGCGCGGCTGGATGAACGCGCAT 46578  
Qy 11932 CCACTCCGCGCGTATCCGCTGGGCGCTGTAGGACG--TGAATGCAATGGCGAATGAAG 11989  
Db 46579 GGTGTTGGCTCGGACCGTCCCGCTCTGACCGGTTGAGGGCATTCGCCGACGCGTG 46638  
Qy 11990 CGAAGCTCTTGAATACCTCAAGCGGTCACTGCGGACCTGGAC----CGCACTCGCGGT 12045  
Db 46639 CGATGCGCCGAAGTGGTTTCGGGTCTGTGGGGCTGTGTGCGCGGTTCGTGTT 46698  
Qy 12046 CCCTGTACGAGTGTGACGAGTGTGACGAGGACCGATTCGATTTGGGGATGGCGGT 12105  
Db 46699 CTCGGGTCAAGGTGTGATGTCGGCGGGATGGCGCGGGGCTCTACTCGGTGTTCCGGT 46758  
Qy 12106 CGTTACCGAGGGGCGGACGTCACCCACGCACTGTGCACTCTGTCAAGTCCGACG 12165  
Db 46759 GTTCGCGNACGGTT--CGACGAGGCTTGGCGGAGTTGATGCAACCTTGGGCCAGGAAC 46817  
Qy 12166 GACGCTATCGGGAGTTCCGACCGACCGT--GGATGGAACCTGGAGCAG-CTCTACGAC 12222  
Db 46818 TCGCGGTTCGGGATGTGTTGTTCCGTTCCGAAGCGTGTGCTGGATCGGACGGTGGG 46877  
Qy 12223 CCGGACCCGACCGCTCAGGAACCAAGTTACACGCGCAGCGGAGGGTTCTCTATACGCG 12282  
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Qy 12283 GCGCAC-----TTGACGCGCGGTTCTTCGAGTTGTACCC----GCGTGAGGCGC 12328  
Db 46938 TTCGCGCGGATGTGTGTTGGGCGACTCGTGGGTGAGCTGGCTGCGGTGCATCGCGCTG 46997  
Qy 12329 TGGCAATGGACCCGACGAGCGCTGTCTGCTCGAACCACCTTGGGAAACGTTTCGAACAGG 12388  
Db 46998 GTGTGTTCTGCTGTGTCGAGGCGCGCGGTGGTGGCGGGTTCGCGCCGCGTTGATCGCAGG 47057  
Qy 12389 GCGGAAATCGACCCGAGGTTCATGCGCGGAAGCGGACCGGGTTCGTTGGGGATCAATC 12448  
Db 47058 GCTTGCTTCTGTTGCTGCCATGCTCGCGGTGCTACGCGGTGAGTTTCAGGTTCGATCTCT 47117  
Qy 12449 CCGAGGA----CTACACCACCGGATACACATCAGCCCTCAAAACGAGTCGAGGGCTAC 12504  
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Qy 12505 CTGCTCATGAGGCGCGGCAAGATTCGCTCAGGCGGCTATCTCTCAACTTTCGGGCTC 12564  
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Qy 12565 GAAAGSCC----- 12572  
Db 47238 GCGGACCCGTTGCGGTTGCGATGCTTTCATTCGCCCCCATATGAGAGCCGATGC 47297  
Qy 12573 -TGCGATCACTATCGACACCGCTGTTCTCTCTGCTCGTCCCTGCTGATCTGGGCTGCG 12631  
Db 47298 TGGAGGATTCGCGCAGATCTCCGAGGCGCGGAATATCACGACCGGACTGCCGATCA 47357  
Qy 12632 AAGCGCTCGGTCCGTTGA-----ATGACCATGGCGTCCGAGGC 12672  
Db 47358 TCTGACCTGATCGGTGAGCTGACGCGTGGTTCGAGTGTAGGGCACTCCGAGTACTGGG 47417  
Qy 12673 GCGGCTCGGTATGCGGACCTCCCTGCTCTTCAACGAGATGTTCTCGCAGCGGGGCTG 12732  
Db 47418 TGCGTCAAGTGGGTGAGCGCTGCTGCGCGAGGGTGTTCAGCGCTTGTTCGGTCAAG 47477  
Qy 12733 GCGCAGACGCGCGTGCA-----AGGCGTTTTTCGCGCGCGCGGACCGGACCG 12781  
Db 47478 GTGTGCGCACGATGTTTCGAATTTGGGTCCGACGCGGCGTGTTCGACGTTGTCGAGGAGT 47537  
Qy 12782 GCTGTGTCGAGGTTGCGGATGCTGTGTGTGAGAGCGGCTCTCGACGCGCCGCGCAACG 12841  
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Qy 12842 GTCACCGTCTCTGCGG----- 12859  
Db 47598 CCGGAACCGTGTGCGACGCTTTGGCGCAGATCCACACCGTGTGTGAGGTGGACTGGC 47657  
Qy 12860 -----TCGTCCGCGGACGCGCGTCAACACGAGGACGCGGCAAGCAACGCGCTGACCGCAC 12913  
Db 47658 GGTGTTTTTTCGCGGTACCGGGGCAAGTCACTCGCCACCTACGCTTCCAGC 47717  
Qy 12914 CCAAGCTGTTCAAGTCAAGTCAATCCGCGAGGCTTTGGCCTCAACGACACCTCTCC 12973  
Db 47718 GCGAGCGTACTGGCTGCGCATCACCGCGCGTGGGTGAGGTGACCGCGCGCGGATGG 47777  
Qy 12974 CTGCGGATGTCGATGCGGTGGAGCCACGCGACGCGGACCACTTCGCGGACCGCGATCG 13033  
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Qy 13034 AGGCTCAAGCCCTCGTCAAGCCTACGCTCAGGACCGCCCAACCGCGCGCCCTCTGCG 13093  
Db 47838 TGCTGACCGGTGCTGACGCGGTTTCGATCCGTGGTGTGCTCCATCAACCGGTGCTGG 47897  
Qy 13094 TCGGAACCTCAAGTCCAACTTCGGGCACTCCATGGCGCTGCGGGTGTGGCGGGGTCA 13153  
Db 47898 GCGAAATCGTCTGTCGCGGACCGGATCTGAGCTGTGTGCGACGCTGCGCGACGCGC 47957  
Qy 13154 TC-----AAGATGGTGTGCGGTAATGGTCTGCTGCCGCGACGTTGATCTGGAT 13209  
Db 47958 TCGGTTGCGCGGTGGAAGAACTGGGCTTTGGAAGCGCCCTGATCTCTGCCGATCATG 48017



Db 50178 TGCTGGGGTGGGTTGCGGGCGCATGCGGGTTCGATATCCGACGCGCGGGCGCTGG 50237  
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Db 50238 CGCGTTCTTCATCAGGAACCTGGCAGCGAGTCCGCTCCACGTGCGCGCGTGACCA 50297  
Qy 15197 TAACTGCGGTCCCGCCGACGAGCGATCGCCATCGTGGCATGCGCTGTGCGGTACCCCG 15256  
Db 50298 GGGCAGCGAGTCCGGAAGAGATCTTGTTCGCAATGTCGGGATGGGATGTCGTTTTCGG 50357  
Qy 15257 GTGATGTACGACGCTCGATGATCTCTGCGAGGTGCTCAGTGGTGGCCATGACGCGATCG 15316  
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Qy 15377 ACCAGGAACAGCTACACCCGAGCGCGGATTCCTTTACGACGAGGCAATTTGATC 15436  
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Qy 15437 CGAGCTCTCTCGGTATAGTCCGCTGAGGCACTGCGGATGACCCGACGAGCGGCTGC 15496  
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Qy 15497 TGCTGGAAACAGCTGGGAGAGCATCGAAACGCTGTATCAACCCGACAGCCTCCGTG 15556  
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Qy 15557 GCACACCAACCGGCTCTTTCGCGGGCTGACCTACACGACTACGCCCGCGG ---CTTTC 15613  
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Qy 15614 CCACAGCTCCGCGAGGTTGAGGGGTATCTCGGCAAGGAGCGAGCGAGTATCGCT 15673  
Db 50718 CCAGAGCACCGAGGCTTCGAAGGGCACCTTCGGACGCGGCAATTCGGGAGCGTGT 50777  
Qy 15674 CGGTCGTGTCGCTACGCTCTCGGCTGGAGGTTCGCGCTTCACAGTCGACACTGCT 15733  
Db 50778 CGGTCGGGTGCGTATTCGTTGTTGTTTCGAGGGTCTTCGCGTGACGTTGATACGGGT 50837  
Qy 15734 GCTTTGCTGCTGCTGCTGCTGCACTTGGCTGTGAGCGCTGCGGTCCGCGAGTGT 15793  
Db 50838 GTTCGTCGTGTTGTTGCGGCTTACACCTGGCGGCTCAAGCACTGCGCGCGGTGAGTGC 50897  
Qy 15794 CCAATGGCTCCGCGGTGCGTCAAGTGTATCAACCCGCGCGGTTCGTGAGTGT 15853  
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Qy 16154 CTTTGGGCGACCGATCAGAGGCCAGGCCCTCTCTCGCACTTACCGACAGGACCGCCCG 16213  
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Db 51318 CCGGTCCGCGCTGTGGCTGGGCTCGGTGAAGTCAAGTATTTGGTTCACACCGCAGCGCGG 51377  
Qy 16274 CAGTGTGGGCGGGGTCTCAAGATGTGTGATGGGCTCGCGAATGGTCTGTCTGCCCGGA 16333  
Db 51378 CCGGTGTGCTGTGATCAAGATGTGTGATGGGCTCGCGAAGGAGTGTGCCCGCA 51437  
Qy 16334 GGTTCATGTGATGAGCGCTCGCGCATGTGGATGTGTCTCGCGGGGCGGTGCAAGTGC 16393  
Db 51438 GGTTCATGTGATGAGCGCTCTCGCGCATGTGGATGTGTCTCGCGGGCAGGTTCGAATCC 51497  
Qy 16394 TGACGAGACGCTGCTTCGCGCGGAGGGGCGGCTCGCGCGGACGAGGTGTCTCAT 16453  
Db 51498 TCACGGAGAACACGCTTCGCGCGGACAGC ---GGTCTTCGCGCGGCGGTGTCTCAT 51554  
Qy 16454 GGTTCGCGGTGAGCGGACCAACCGCCACGTCTCTCGAAGAGACACCGCCCAACA 16513  
Db 51555 GGTTCGCGGTGAGTGGACCAACCGCACCTGATCTTTGAACAACCTCCG --- 51604  
Qy 16514 TCCGTCAGACACACCGCGCGACGACGCCCGGAGAGACGCGCGCATGTTCCGG 16573  
Db 51605 -----CGA 51607  
Qy 16574 GGGAGCGCGCGGACGACCGCGGTACCGCGGGGAGGACGTGCTCTGTCTGCCGCA 16633  
Db 51608 GAGTCGACGCTCAACAGACCGGATTCGG -----GTTCTGTCCGG 51650  
Qy 16634 GTCCAGGGTGTGCGGTGTGTGTCGCAAGTTCGACCGGCGCTCTCGCGGCCAAG 16693  
Db 51651 ATTTTCGGTGTGCGGTGTGTGTCGCGCAAAACACCGGAGCGTATCCGCCAGG 51710  
Qy 16694 CCCAGGCTTCGACCGCCACCTCACCGACACCGCGGCTCGACTCGCGACGCTCGGT 16753  
Db 51711 CAGATGATGATGTTCTTACTTGAGCAATCGGTTGATGTTCCCGCGAGATATCGGT 51770  
Qy 16754 ACACCTTCGCGCGCGCGCGCTGTTCGACACCGCGCGCACCTCATCGCGCGGAC 16813  
Db 51771 ATTCTGCTGCGGTGACCGTTCGCGGTTCGACACCGCGCTCTGTGTGGTGGGATC 51830  
Qy 16814 GCGACACTTCTCTGCAAGCACTCCAGGCACTCGCGCGAGGGAACCCACCGCGCGTCA 16873  
Db 51831 GTGCGGCTGCTGCGGGCTTGAAGCGCTGGCGCTTAGTAATAGACCTGCGAGGTGA 51890  
Qy 16874 TCCACAGCGCGCCGCGCGGACCGGACCGGAGCGCGGAGGAGGAGGAGGAGGATTC 16933  
Db 51891 TCACCGGCACTCGT -----GCCGCTGGGCGGCTCGGATTCG 51926  
Qy 16934 TCTGCTCCGACAGGCGACCCAGCGCGCGCATGGCCACGCGCTCTTACCAACCCACC 16993  
Db 51927 GTTCTCGGTCAAGTGGTCACTGGCCCGGGATGGGAGCGGCTCACCTCGGGGTTTC 51986  
Qy 16994 CCGTTCGCGCGCGCTCAACGACATCTGCAACCTCGACCCCGCGCTGCAACCG 17053  
Db 51987 CCGTTCGCGCGCGCGTTCGAGAGCGCTGCTGAGCTGATGCGCATCTCGGCGAGA 52046  
Qy 17054 CCCTCTCCCTCTCTCAACCGAGACCCCAACACCCAGGACACCAACCTCTCGAGAG 17113  
Db 52047 TGGCCCGGCTACGAGATGTGTGTC -----CGGTTCCG 52079  
Qy 17114 CGGCGGCACTCTCCAGCAGACCCCGTACGCGCGCGCTCTTTCGCTTCAGAGTTCG 17173  
Db 52080 ATAGCAACTTCTGGAACGACCTTGTGGGCGGAGCGGGCTGTTGCGGTTCGAGTTCG 52139  
Qy 17174 CCCTCCAACCGCTCTCACCGACGCTACCACTACCCCGGCTACTACTACCGCGACT 17233  
Db 52140 GACT ---CTGGAGTGTGTGGGTTCTGGGGTGTCCGCGCGCTGTGTGTGCTGGGCCACT 52196  
Qy 17234 CCCTCGGCGAATCAGCGCGCGCCCACTCGCGCGGATCTCTCACTACCGACGCGCACA 17293  
Db 52197 CCGTCTGAGTCTGCGCGCGCGTTCGCGGCTGGAGTGTGTTGTTGCGGATGCGGCTC 52256

17294 CCCTCATCAACCAACGCGCCACCTCTATGCAAAACCATGCCCC---CGGCACCATGACCA 17350  
Db  
52257 GGCTGGTGGGGCGTGGCCGGTGTATGCAAGCCCTGCCAATCTGGCGGTGCGATGCTCG 52316  
Qy  
17351 CCCTCCACACCAACCCCAACCAATCAACCAACCTCAACCGCCCAACCAACCAACCAACCTCG 17410  
Db  
52317 CTGCGGCTGCTGGAGAGGAGAGTGGCCCGTGTCTGCGCGCACTGCGGTGATCGTGTGG 52376  
Qy  
17411 CCATCGCGCCCATCAACACCCCACTCTCTGTCATCAGCGGCACCCCAACCCGTC 17470  
Db  
52377 GGATCGCGCGGTCAACGTCCTCCGGTGGTGTCTCTCCGGTGTATCGGGATGTGCTCG 52436  
Qy  
17471 AACACATCAACACCTCTGCAACCAACAAAGGATCAAAACCAAAACCTCCCAACCAAA 17530  
Db  
52437 ATGACATTTCCGGTGGTGGAGGGCAAGGATCCGGTCCAGGTGGTGGGGTTTCGCG 52496  
Qy  
17531 AGCGCTTCCACTCCCAACCAACCAACCACTCTCAACCAACCACTCAACCAACCAACCAACCA 17590  
Db  
52497 ATGCGTTTCATTCGCATCGATGGATCGATGCTGGCGAGTTCAACCGAATCGCCCGGA 52556  
Qy  
17591 CCCTCACCTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 17638  
Db  
52557 GCGTGGATACCGGTCGTGAGGGTCGCGATCGTGTCAACGTTGACGGTGAAGTCTGATG 52616  
Qy  
17639 CACCGACCACTCTCAACCCCACTACTGACCAACCAACCGCGCAACCAACCGTCGACT 17698  
Db  
52617 AGTTCGGATGCGGCTAGCGCGAGTATTGGTGGCGGAGTGGAGAACCGGTCGCT 52676  
Qy  
17699 AGCGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 17758  
Db  
52677 TCGCGACGCTGCTGCGCTCGCGGTACGCGTGTGAGCAACCGTCTCGAGGTGCGTGC 52736  
Qy  
17759 CCGACACCACTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 17818  
Db  
52737 CGGATGGGGTGTGTGCGCGTGTGTGCAAGAGTGTGCGCGCGCGGATCCGATCAGGGCGAC 52796  
Qy  
17819 TCACCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 17878  
Db  
52797 GGGTGGCGGGTTCGGTCTATGCGAGCATCGGACGAGGCGCACACGGTGTACACGG 52856  
Qy  
17879 CCACCAACCACTGGACCCCAACCACTACACCAACCAACCAACCAACCAACCAACCAACCA 17938  
Db  
52857 CATGGCGCAGATCCATGCTGCTGTGTGTGAGTGTGAGTGTGCGGTGCTGCTTTTCGCGGTA 52916  
Qy  
17939 CC-----CACCTGACCTCCCACTTACCTCCCTCCCAACCAACCACTACTGCTCG 17989  
Db  
52917 CCGGGGCAAGCAGGTGAGTGTGCGGTCACGATGTATGCTTCAACGACGAGCGTACTGCTTG 52976  
Qy  
17990 AAGACACACAGCGGTGCGGATCCGGTTCGGTTCGGGTTCGGGCGGCGGAGGACTG 18049  
Db  
52977 ACTACCAT-----CCGAACGGT-----CGGGCAATCCGCGGATC 53012  
Qy  
18050 CCGGCGGAGCGCAGAGTGGAGTCCGGTTCGGGACCGGTGCGCCCGCAGGACCTGG 18109  
Db  
53013 CCGCGCGCAGTCCGGCTTCTGGGAATCGTGCAGCAGGAAGATGTACGCGGCTCAGCG 53072  
Qy  
18110 AAACGGTCCGACACGCTGCGGTCGCGCTCCGCGGCTGCAACGCTGAGTGTGCGCG 18169  
Db  
53073 CCGCTCTGCATATACCGCGATACGACGTGACGCGCTCCCGGATCGGGTGTGCGG 53132  
Qy  
18170 CACTCTCGCGCTGGCACCGCAACCAACGACCAAGCCCGCATCAACCTGGACCTACC 18229  
Db  
53133 TCCTCTCTCTTGGATCGCGGATCGGACGAATCTCTGTGTACCACTGGCGGTACC 53192  
Qy  
18230 AGGAACCTTGAACCCCTCAACCTCCCAACCAACCAACCAACCAACCAACCAACCAACCTGCTCA 18289  
Db  
53193 GGAATTTCTGGATGAGCGGGCAGATTGGCCAGACCCCTCGTTGTCGGGACATGGCTCG 53252  
Qy  
18290 TCGCATCTCCGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCTCC 18349  
Db  
53253 TCGTGTGCGGAGGGGTGTGCGGAGTGTGCGCAAGTGTCTGCGTTTCAACGAGATGTTCG 53312  
Qy  
18350 ACCACAGGATCAACCCCACTCCCTCAACCTCAACCAACCAACCAACCAACCAACCAACCAAC 18409

53313 AGGAACGGGTGGCCCGCAGTTCTGTTCAGCTCGCCGGCACGACGAGGAAGCCCTGG 53372  
Qy  
18410 ACCTCCACCAACCCGACAAAGCCCAAAACCAACCAACCAACCAACCAACCAACCAACCAAC 18469  
Db  
53373 CGC-----AACGATTCGGTCTGTTCGTTGCGTTCAGGGGGAATAGCGCGCTGT 53423  
Qy  
18470 TCTCCCTCTCGCCTCGACGAACACCCACACCCCAACCCCAACCCCAACCCCAACCCCAACCCGCA 18529  
Db  
53424 TGTCTTGTGGCTGTGATGATCGCGTCTCGCGAAGCTGTCTTTCGCGATGGCG 53483  
Qy  
18530 CCCTCTCAACCTCACCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCCCTCT 18589  
Db  
53484 CGCTGAATCGTGTGATCTGCTGCGAGCTCTGCGGGCGCGGATGTGTGCGCGCATTTGT 53543  
Qy  
18590 GGTAGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 18649  
Db  
53544 GGTGGCGACGTGTGTGTGTGCGGT-----CGGGGATGTGTCGGGTGAACCCGGGC 53597  
Qy  
18650 AAGCCCAAACTCGGGGACTCGCCGACCAACCTCTCGAACACCCCAACCCCAACCCCAACCCGCG 18709  
Db  
53598 AGGCGTGTGTGGGACTGTGGTCCGTCTGTGAGCATCCGGCTGTGTGGGTG 53657  
Qy  
18710 GAATCATCGACCTCCCAACCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCC 18769  
Db  
53658 GCCTGTGCGAGTGGTGTGCTGATGAGGAGCTCGAGAACGCTTGTGCGTGTGT 53717  
Qy  
18770 TCACCAACCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCC 18829  
Db  
53718 TGGCAGTCTTGGCGAGGA---CGAGATCGCGGTACGTCCCGGTGTGTGTCGTGCGGC 53774  
Qy  
18830 GCCTCACCCCAACCAACCTCACCCCAACCAACCAACCAACCAACCAACCAACCCCAACCGAA 18889  
Db  
53775 GGTGGAAAGCGGTGTGTGGCGGTGCGGTGCGGGTGTGTGTGCG---GTCTCGGGGA 53831  
Qy  
18890 CCACCTCATCACCGGGGAAACCGGCGCTCTCGCCACCCCAACCTCACCCCAACCACTCACCA 18949  
Db  
53832 CGGTGTTGGTGACGGGTGTGACGGCGGTGTTGGGGCGCATGTTGCCCGGTGTGGCG 53891  
Qy  
18950 CCACCAACCCCAACCAACCTCTCTCTCACAGCGCGAACCGGCGCCCAACCAACCCCAAC 19009  
Db  
53892 GTGCC---GGGGCTGAGCATGTGTGTGTGACAGCCGTTCAGAGCGCGCGGTCTCGGGCG 53948  
Qy  
19010 CACAACACCTCACCAACCAACCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCTGCG 19069  
Db  
53949 CTGAGATTTTCGGGGCGAGCTGTGAGGGCTGTGGGCTGTGGGTTCGATCACGGCTGCG 54008  
Qy  
19070 ACACGACCAACCAACCAACCTCAACCAACCTCTCAACCAACCTCCCAACCAACCAACCC 19129  
Db  
54009 AGTGGCGCATCTGTGACGCTTTGGCCGAAAGTGTGGCGACCATTCGGATGATTTGCCGCG 54068  
Qy  
19130 TCACCAACCTCACCAACCAACCGAGGATCTCTGAGAGCGCAACCTCACCAACCTCACCC 19189  
Db  
54069 TGACCGGGTGTGATCATGTGCGGGGGTGTGAGTTCGGGACGTGTGCGGTGTGTGT 54128  
Qy  
19190 CCACCAACCTCAACCAACCTCTCGCCCAACCAACCAACCAACCAACCTCTCCACCAAC 19249  
Db  
54129 TGACCGATCTGTGGGGTGTGTGCGGAAAGGAGGAGGTGTGTGCGGCAATCTCATGAT 54188  
Qy  
19250 TCACCAACCAACCAACCTCAACCGCTTGTCTCTACTCTCTCGCGCGCCCAACCTCTCG 19309  
Db  
54189 TGCTCGCGATGTGAGCTGATGCTTGTGTGTCTCATCTGTCTCGGTGTGTGGG 54248  
Qy  
19310 GCGCACCGGCAACCAACCTACCGCGAGCAACCGCTACCTCGACCGCTCTCGCCAC 19369  
Db  
54249 GTGTGCGGCGAGGGGCTTATCGCGCGGGAATGCTACTTGGATGCGTGTGGCGAGC 54308  
Qy  
19370 ACCGCCACCAACCAACCTCCCGCCCAACCAACCTCTGCGTGGGCACTTGGCAAGCAACG 19429  
Db  
54309 AGCTCGGCAAGGGGGTGTGTGGGAGTGTGGGTGTGTGGGGCGCGGTGGCGCGTACG 54368  
Qy  
19430 GACTGGCGACTGTGATCAAGCGAAATCTCCCGCGCGCGGATGTTCGCCATGTGCGC 19489



Db	54369	GAATGGCGCAGGTGAAGCGGTGCACAGCTGCGCCGGCGCGCTGTGTGCCAATGGCTG	54428
Qy	19490	CCGAGTGTGGCGGTACAGCTGTGTGACGCGCGCATCGCAGCGGGCGCCGAGTCTCTCTCG	19549
Db	54429	CGGATCGGGCGTGTGCGCACTTCAAGGGCATTTGATCGTGACGAGACATCCCTGTGTG	54488
Qy	19550	TGCGCGATATCGACTGGAAGAAATTTGGGACCGGTTCTCTCCA---GCAAGTGTGTGGTCT	19606
Db	54489	TGGCCGATATGGCGTGGGAGAGTTTCGCCCGGTGTGCCATGTCTCCGTGGCGCTCGCC	54548
Qy	19607	TGCTCGAGGACCTTCCCAAGCA---CAGGNACTGAGAGCGCGCATCCGTTGAGC	19663
Db	54549	TGCTCGAGAGCTGCGGAGACACAGCAGGCGTTGGCGATTCGGAGAACCACTGTATG	54608
Qy	19664	AGACGGAGAGCAAAACCTTCCGGCACTCTCATGGGTGGTTCAGTTCGAGCAGGAG	19723
Db	54609	CTGCGGACTCGGCGGTCCCGCTACCGCGCTCGCGGCGATGGCAGCCCGCAACCGCC	54668
Qy	19724	AAGACTGTAGCTGTGCGCATCTCACTCGCGCGAGTGTCTGGGCGCGAGCACTCG	19783
Db	54669	GCGCGATGCTGGACCTGTGTGTGGCGAGGCTTCGATTTGTGTGGGACACAAACGGGTCTG	54728
Qy	19784	AGGCCATCCGCGCGGTGGTGTTCAGGATCTAGGTTTCAGCTCGCTTGGCGGTTGG	19843
Db	54729	ACCCAGTTGGTCCCGACCGGCGGTTCAGGAGCTCGGATTTGATTCGTGATGGCGGTG	54788
Qy	19844	AGCTTCGCAACCACTCGCAGCACAGCGGAGCTGGCTCTGCGGACGACTCTCTGTCTTCG	19903
Db	54789	AACTCGGCNAACAGTTGGCGGAGGCAACAGGATTCAGTCTCGCGGCGACGTTGATCTTCG	54848
Qy	19904	ATTACCCAGGCCCAACCAAGCTGCGCCAAATTTCTGTCTCTCGAGATTCGCGGATTTCCAGC	19963
Db	54849	ATTATCCAGGCCCACTCGCGCTGGCTGAGCAGCTGTCGGCGAGCTGTTGGGAGCGCAGC	54908
Qy	19964	CGCAACACTCACTCGCTTCGCGACCCCGGCGAGAGCTCGATGAGCGGATCGCCATCG	20023
Db	54909	CGG-----CGACCACTCGTGTGGCGGGCGCATCCAGTGATGATCCGGTTGTGTGG	54962
Qy	20024	TTGGCATGCGCTGTGCTTCCCGCGGAGTGACCTCGCGGCGACGACTTCTGGGATCTGA	20083
Db	54963	TCGCGATGGGATGCGGATATCGGGGAGCTGTCTGCGCCGAGGAGCTGTGGCAGCTGG	55022
Qy	20084	TCTCTCGAGCAGCAGCGATCGGCGGATTTCCCAACCGACCGCGCTGGGACCTGGACA	20143
Db	55023	TTTCTCGGAGCGTATCGAGCTTCCCGTTCGATCGGCGTGGGACTGCAACA	55082
Qy	20144	CGCTTACAGCCCGACCCGACCCCGGACCTGTCTACACCGAAACGCGGATTC	20203
Db	55083	CGTTGTTGACCCGATCCGGATCGGCGAGGAGTACCTATGTGCGAGAAGGTGCTTTC	55142
Qy	20204	TCTAGAGCGAGGCACTTCGACGCGCAATTTCTCGGATCAGCCCGCGAAGCCCTCG	20263
Db	55143	TGACCGGTGCTGATCGGTTGAGCGCGGGTCTTTCGGCATCAGCCCTCGCGAGGCGCGG	55202
Qy	20264	CAATGGAACCCAGCAAGCTCTCTCGAAACCCGCTGGGAAACCATTCGAACACGCG	20323
Db	55203	CAATGGATCCGAGCAGAGGTTGTCTCGAAGTGGCGGGAGGTTTCGAACGAGCAG	55262
Qy	20324	GCATCAACCCCAACCTTCCAGGCAACCCCGCGAGTCTTACCGGCACCAACGAC	20383
Db	55263	GAATCGCTCGTGTGTTGGGGGTAGCAGACCGGTGTGTTCGCGGGACCAATGGGC	55322
Qy	20384	AGGACACGCGCACATCTCGTACGGCCCGAGCGGTACCGAGGATTCGTCTTGACCG	20443
Db	55323	AGGACACGCGTGGAAATGGGT---GCCGCGCGAGGCGGGGTCACTCTCTGACCG	55379
Qy	20444	GGGAGCCCAACGACTCGCTTCGCGCGGAATCTCTACATCTCTCGGTTTGAAGGCGCTG	20503
Db	55380	GAACGCGCGAGTGTCTGCGCGCGCGCTTCTCTACAGTTCTGCGCTTGAAGGCGCTG	55439
Qy	20504	CGGTCACTCGACAGAGGTTGCTCTCTCGCTGTGCGCCCTGCACTCTGCTCGCAGT	20563
Db	55440	CGGTGGCGGTGATATCCGCGTGTCTGTGTGGTGGCGTTGCAATTTGGCGTGCAGT	55499
Qy	20564	CCCTCAGTCCGGTGAATGCACCATGCTTGGCCGCGGGGCCACGCTCATGACCACTC	20623
Db	55500	CGCTCGTTCGGGTGAGTGTGATGCTTGGCAGGTGGTGTACGCTGATGTGACAC	55559
Qy	20624	CGATCACTTTCACCGAATTCGCCGCCCAACGCGACTCGCCCCCGACGGGCTTGCAGG	20683
Db	55560	CCCTGGCTTCTCTCAGTCTCTCTCAGCGGTTTGGCGCCAGATGCTCGGTGCAAGT	55619
Qy	20684	CGTTCTCGCGCGCTGACGCTACCGCTGGGGTGAAGGTTGGGGATGCTGTGTGGT	20743
Db	55620	CGTTTGGCGCGCTGCGGATGGCACCGGGTGGGTGAGGGTCCGGCTGTGTGTCTGG	55679
Qy	20744	AGCGCTCTCGACCGCGCGCGCTCAACGCTCACTGTCTGTGGCGGTGTGTGTGGCAGTG	20803
Db	55680	AGCGTTGTGCGATGCTCTCGTGAATGCTACCGGCTGTGGCGGATGCTCGCGGTCTG	55739
Qy	20804	CGGTCAACGAGGCTGCGAGCAACGCTGTGACCGCGGCCCAACGGGCTTCCGAGCAGC	20863
Db	55740	CGGTGAATCAAGATGGTCTCGTGAATGGCTGACTGCGCGCAATGGTTCGCGAGCAGC	55799
Qy	20864	GCCTATCCGCGACGCTCTCGCCAAACGCGACCTGACCCCGCGAGCTCGATGCGGTG	20923
Db	55800	GGGTGATTCGCGACGCGCTCGCGAATGGGGCTGTGGCGTCCGATGCGATGCTGTGG	55859
Qy	20924	AGGCCACGCGCACCGGACCACTTTTGGGCGACCCGATCGAGGCCAGGCCATCTCTCGCA	20983
Db	55860	AGCGGACGCGACCGGTACCGGGCTCGGGGATCGATCGAGCGCAGCGCTGATCGCA	55919
Qy	20984	CCTAGGACAGGACCGTCCGGCAACCGGCGTGTGGCTGGGCTCGCTCAAGTCCCAACG	21043
Db	55920	CATATGGCGAGCGAGCGGATCTTGAAGCGGCGCTGTGGCTGGGCTCGATCAAGTCCAA	55979
Qy	21044	TCGAGACACACAGCGCGCGCGGTGGCGGAGTGATCAAGATGGTGTGATGCGCTTCC	21103
Db	55980	TCGGCCACACGAGCGCGCGCGGTGGCGGAGTGATCAAGATGGTGTGAGGCCATGCG	56039
Qy	21104	GCCACCGGACACTCCCAACCGACTCTCAACGCGATGAGCCCTCGCCGATGTGAGCTGGT	21163
Db	56040	GGCAGCGGAGTTGCTGCGAGCTTGCAGTGGACAAGCCCACTCCAAGTGGACTGGT	56099
Qy	21164	CCGCGGTGTGGTGCAGTGTGACGAGACGCTGCTGCGCGCGGCGCGGCGGAGGCGCGC	21223
Db	56100	CTGCGCGGCGCTTCTGCTCTCAACCGGAAACAGCGCTGCGC---CGAGAGCGCGCTC	56156
Qy	21224	CGCGCGGCGAGGAGTGTCACTATTTCGCGGTGAGCGGCAACAGCCCACTCTCTCG	21283
Db	56157	CTGTCGAGCGGGGTGTGCTGTTGCGGATCAGCGGCAACCAACGACCTCATCTCTCG	56216
Qy	21284	AAGAAGCACCCCGCGACGACGTTCCGGGGGACCAACCGCGGAGAGGATCCGGTAGTG	21343
Db	56217	AACAACCACTCGCA-----ACGAGCGGAGATCGACCAAT	56252
Qy	21344	GCGAGGAGGTGTGTCGGCGAGTCTCTGGGTGTGGCGTGTGCTGGTGTGCGCCAAAGTCCG	21403
Db	56253	CGGATCGCGGCTCACTGCGCATCCAGCGGTGATCCCGTGGATGTTGTGCGTGGAGTTC	56312
Qy	21404	AGCGCGCTCGCGCGCGCGCGCGCTGACGCGCCCTCACGACCCACCAACCGCGCC	21463
Db	56313	TCGAGCGCTCGAGGCCCAACGCGGTGCGCTGCGAGGCCCGGCTGAGACGGGGTCTTGGCG	56372
Qy	21464	TCGACCTCGCGAGTTCGGATACACCTTCGCGCCACGCGCGCGCTGTGTGACCAACGCG	21523
Db	56373	CTTCTCGCTGATTTGGGGTATTCACTCGCGACCACTCGTTCTGTGTGGAGCAACGCG	56432
Qy	21524	CCACCTCATCGCGCGCGACGCGGACACTTCTTGTGAGGACATCCAGGCACTCGCGGAG	21583
Db	56433	CGGTGTGTGGGTGCGGATCGGAGGCACTGCTGTCCAGGCTGCGAGCGCTCGCGGATG	56492
Qy	21584	GCGAACCCACCCCGCGCTCATCCACAGCGGCCCGGAGGACCGGAGG	21643
Db	56493	CGCGAGCGCGCGGGGTGATA-----ACGGGCTCTGCGAAT	56531

QY	21644	CGCAGAGAAAGACCGCATTTATCTGTCTCCGGACAGGGGACCAACGCCCCGGGATGTGCC	21703
DB	56532	CCGGTGGCCGATCGGATTCGTTTTTTTCCGGTCAGGGCAGTCAGTGGCTGGGGATGGGAA	56591
QY	21704	ACGGCTCTACCAACACCCGCTCTTGGCCGGCCGACCTCAACAGCATCTGCACCCACC	21763
DB	56592	AGGCGTTGTGCGCGGCTTTTCCCGGCGTTCCGGACGCTTCGAGGAAGCCTTCGACGGCG	56651
QY	21764	TCGACCCCCACCTCGACACACCCCTCTCTCCCTCCCTCAACCAAAACGACAAACG	21823
DB	56652	TAAAGGCACACCTGGGCGCGGAGTTTCGGGGTGTCTGTTTCGGTGTGATGAGCAGA---	56708
QY	21824	ACAAAGAGAGACGGCGCGCATGCTCTCAGCAGACCCCGTAGCGCCAGCCGCTCTTCG	21883
DB	56709	-----TGCTCGACCGGACGCTGTGGGCGCAGTCGGGATCTTCG	56747
QY	21884	CCTTCCAGGTGCGCTCCACCGGCTCTCTACCGAGGCTACACATCACCCCCCACTACT	21943
DB	56748	CGGTTCAAGTCGGGCTCTCTGGGATGTCGA---GGTCGTGGGGCGTGGGCGCGCGG	56804
QY	21944	ACGCCGACACTCTCCTCGGCGAAATCACCGCCGCCACCTCGCGGCATCTCTCACCTCA	22003
DB	56805	TGCTGGGCGACTCGGTGCGGAGTTGGCTGCGGGCGACGCGGCTGGTGTGTTCTCTTCG	56864
QY	22004	CCGACGCCACACCTCATACCAAAAGGGCCACCTCATGCAAAACCAATGCCCCC---CG	22060
DB	56865	CGACGCTGACGGTTGGTTGGCTCGGCTCGGGCCACCTGATGAGGATTCGCCACCGGCG	56924
QY	22061	GCACCATGACACCTTCACACCAACCCCAACACACATCACCCACCTCACCGGCCGAG	22120
DB	56925	GCGCAATGCTCGGGTCCGACACGAGCGGCGGTTCGGAACGGTGTCTTCGCGGGGTGT	56984
QY	22121	AAAAAGCACTCGCCATCGCGCCCATCAACACCCCCACCTCCCTCGTCATCACGGCACCC	22180
DB	56985	GCGATCGGTCAGATCGCTCGCATCAACGGGCCCGAGTCGGTAGTGTCTCTCGGCGACC	57044
QY	22181	CCCAACCGTCCAAACATCACACCCCTCTGCGCAACAAAGGCGATCAAAACCAAAACCC	22240
DB	57045	GCGATGTGCTCGTAGGACTCGCAGGCGAATTCGATGCCCGAGGGCTTAGGACCAATGTT	57104
QY	22441	TCCCCACCAACGAGCCTTCACTCCGCCCAACACCAACCCCATCTCTCAACCACTCCACC	22500
DB	57105	TGCGGGTCTCCCATGTCTTCCATCTCGCACCGGATGGAAACCGATTCTGGACGATGACGG	57164
QY	22301	AGCACCCCAAAACCTCACTACACCAACCCACACCCCTCTCATCACCGCCAAACAC---	22358
DB	57165	AAACCGCAGGTGGTTCGAGTTTCGGTGAAACCGGTGTGCGGATGTTCTCCGCGGACCG	57224
QY	22359	-----CCCAACCGACCAACTCCTCACCCCCCACTACTGGACCCAAACGACCGCA	22408
DB	57225	GTGCGCTGGACACCAACCGGACTGATGTGCGGCGCGACTACTGGACCGCCAAAGTCGTG	57284
QY	22409	ACACGTCGACTAGCCACACCAACCAACCCCTCAACCAACGCGGCTCACCTCTACA	22468
DB	57285	ATCTGTCCGCTTCGGAGACGGTGTCCGGGCGCTCTGCGGCCAAGCGGTGGACACGATCG	57344
QY	22469	TCGAACTCGGACCGGACCAACACCTCACACCTCCACCAACCAACCTCCCAACACCC	22528
DB	57345	TCGAGTTGGGCGCGAGCGGGCGTGTGTGGCCCTCTGTGTGAGCAGTGTCTTGGCGGGTCCG	57404
QY	22529	CCACCAACCCCTCACCTCACCAACCCCAACCAACCCCAACCCCAACCCCACTCTCACCA	22588
DB	57405	ACAGGCTGGAGGGTGGGGGATCCCGTGTGATGCGCAGGACCGCGATGAGGTCGAGA	57464
QY	22589	ACCTCGCAAAACCAACCACTGGGACCCCGACCACTACACCAACCAACCAACCAAC	22648
DB	57465	CCGCGGTGGGGCGCTTGGCGCACGTCGACGTCGCGGTGGTGTGCGGTGGACTGGTGGCTT	57524
QY	22649	CCACACCCACAC-----CCACTCGACTCTCCCACTTACCCCTTCCAAACCAACC	22699
DB	57525	GCTTCGCGCGCACCGGGCCCGCACCGTCGAGTTGGTCCCACTTACGCTTTCGAACGCCAGC	57584
QY	22700	ACTACTGGCTCGAACTACCCAGCGCCCAACCGAGCCCGGTCAAAAGGGGTTCTCGCCGCT	22759

Db	57585	GGTACTGGCTGG-----CGGGCAAGCGGACGGGGCGCGCGCGCGATG	57626
Qy	22760	CGGCTCCAGACACGCGAGTTCGTGGACGCGGTAAAGAGGAAGACCTCCAGA	22819
Db	57627	TGGTTGCCAGACCGGTGCGAGCGCGCTTCGTGGAGTTGGTCAGCGCGCGCATCGGAAC	57686
Qy	22820	GCCTCGCGGAAACCTTCGACATCGAC---GCCTCTCTCTGTGACACGGTGGTGGCCGAC	22876
Db	57687	CGTTGGTGGATGAACCTGCAACGACCGGACACGACCTTCGGGAGGTGCTGCCCGTTC	57746
Qy	22877	TCTCGGCTGGACCGGACCAACAGACGAAAGCCGCGCATCAACACTTGGACCTTACGAG	22936
Db	57747	TGGCTTCTGGCGGAGAAACAACGACGAGAGGCCCTCGCGAATCTTGGCGCTACCAAG	57806
Qy	22937	AAACCTGGAAACCCCTCACCTCCGCCACCAACCAACCCCAACACCTTGGCTCATCG	22996
Db	57807	TGGCTGGAGGTCGTGAGGTGCGTCGCGAGCGCCCTTCGGGGCGGTGGCTTGGTGG	57866
Qy	22997	CCATCCCGGAAACCCAGACCCACACCCCCACATCAACAACATCTCAACACCTCCACC	23056
Db	57867	TGCTTCAGCTGAGGTGCCCGGAGTCAAC-----CGGCGGTGGTCA	57908
Qy	23057	ACAAGGATCAACCCGATCCGCTCTACTGTCTCAACACCAACCAACCCCAACAC	23116
Db	57909	TCGACGCGCTGATCGCGCGCGCGAGGTGCGGTCTCTGGAATTGACCCGAGCAGGACC	57968
Qy	23117	TCCACACACCTCCACACACACCGGACAAAGCCCAAAACACACACCGGACCCATCA	23176
Db	57969	TCAACGCACTGGCGCTTGTGGACAGGTGCGCGCGTCAATTGCGGACCGCACCGAGTGA	58028
Qy	23177	CGGCGCTGCTCTCCCTCTCGCCCTCGAGAAACACCCACACCCCAACACCCCAACAC	23236
Db	58029	CGGCTGTGTCTCTGTTGGCGATGACGGCATGCCCTGCGGCGCATCGCACCTGT	58088
Qy	23237	CCACGGGACCTCTCTCAACTCACCTCCGCCAAACCAACCAACCAACCCCAACCA	23296
Db	58089	CCGCTGTGTGCGCGCTACCGTGATCTGACGAGGTGTGGGCGATCGGGTGTTCG	58148
Qy	23297	CCGCTCTGTTAGCGCACCAACGCGACCAACCAACCAACCCCAACACCCCTCACAC	23356
Db	58149	CCGCTGTGTGCGCGCACGACGCTGGGTGCGTGGGCGGAGACCGTTCGGCG	58208
Qy	23357	ACCCACCCAAAGCCCAAACTGGGACTCGCCGACCAACCTCTCTGAAACCCCAACC	23416
Db	58209	ATCGGACCAAGCTTGATCTGGGGCTCGGAGAGGTGTCGGCTTGAACATCGCAGT	58268
Qy	23417	ACACGCGGGAATCATGCACTCTCCCAACACCCCAACCAACCTCTCAACCACTCA	23476
Db	58269	GGTGGGTGGCTGTATCGACCTTCGGAGACACTGGAAGACGTCGGAACGGGTGG	58328
Qy	23477	CCAAACCTTCACCAACCCCAACCAACCAACTGCGCATCGCACACCGGACCC	23536
Db	58329	TGCGCGACTTCGCGGGAGCGGCGGAGATCACTCGCGGTGCTTCATCCGGGTGT	58388
Qy	23537	ACACCGCGCTTCACCCCAACACCTCACCCCAACCAACCAACCCCAACCCCAACC	23596
Db	58389	TGCTTTCGAGTGTGTCGGGAGCGCGGAAACCC-----CGGTCAAGACATGGCGTA	58442
Qy	23597	CCACGGAAACCACTTCATCACCGGGAACCGGCGCTCGCAACCACTCAACCCAC	23656
Db	58443	GCCGGGAAACGGTCTCTATCACGCGGAAACAGGCGGCTCGGTCCGAGTCCGACAT	58502
Qy	23657	ACTCAACCAACCAACCAACCACTCTCTCAACGCGGAACCGGCCCCCA	23716
Db	58503	GGTGGCGCGGGGAGCTG---AGCACTGGTGTGATCAGTCGCGCGCGCGGAG	58559
Qy	23717	CCCCAGCAACCACTTCACACCACTCCAAACAAAGGATCACTCACTCAACATCA	23776
Db	58560	CTCCGGCGCAGGACCTTAGGGGCGAGCTGATGTAACCTGGCGTGAAGTCAAGTCT	58619
Qy	23777	CCACTTCGACACCAAGCAACCCAGACCACTCCAAACACTCTCTCAACCACTCCCCAC	23836

Db	58620	TGGCTCGCATGTGACGACCGCGAGAGCTGGCGCGGTGCTGGCGCGCTTCCACGG	58679
Qy	23837	AAACCCCTTACCAACCGGTATCAACACCGCAGGGGTCAATCTCTTGCCTCCCGTGTGG	23896
Db	58680	AGTATCCGTGTGGCGGTGTGACACCGCGGTGGGACGCTGGCAACCTGGCG	58739
Qy	23897	AAACCGATGCCAATCTCTTCTTCCGTATACCGCAGCGAGCAACGGCGCGGCGATTC	23956
Db	58740	AGACGACCTTGGCGGAGTTCGCCGACGTGTTCGCCCAAGGTCTGGCGCGCGGAACC	58799
Qy	23957	TGCATGAGTGTCTGTGACCATGAAACGCTTTGAACATTTCTTCTTCTCTCGTGGGG	24016
Db	58800	TG--GACGGTGTGTGGCGGCAACGTTGCGACGCTTCTGTGTCTTCTCTGATCT	58856
Qy	24017	CGGCGCTTGGGCGAGCGGGAATAGTGCATATCTCGCGCGCCCAACGATACCTGGAGC	24076
Db	58857	CGGAGTTTGGGAGCGCGCGCCCAAGAGCCTATTTCGCGCGCCAAATGCTATCTCGATG	58916
Qy	24077	CGCTCGGACGATCGTCAACACATGACATTTCCCGGGGCATCGATCGCTGGGCGCCT	24136
Db	58917	CCCTTGGCGAGCGCGACGGGCTTGGCGCGCGCGGACGATGCAATCGCTGGGTCGCT	58976
Qy	24137	GGGCGGAAAGGCGATGTCGGCGGTGATGCGGCTCATGTTTACCTTGGAAGCGCGCA	24196
Db	58977	GGCGGGTTCGGGCATGGCGGTTTCAAGAGTAAACGAGCGCATCTCCGCGAAGGGGCC	59036
Qy	24197	TTCTCGCATGAGCAGCATGCGGCTCGCGGCATTTCCATGTCGCGGGCGAGCGGC	24256
Db	59037	TGGTACCGATGGAACCGCAGTCGGCCCTCTTCGCGCTGCAACAGCGCTGTCCCAACGAG	59096
Qy	24257	CGAATTCNAACCTGATCATCGGGGACATGACTGGGAGCGCTTCTGCTCCCGCTTACCG	24316
Db	59097	AAACCGCCATC--ACCCTGCGAGATGTGGACTGGGAGCGATTCGCCGCTCTTTCAACG	59153
Qy	24317	CTCGACGACACACCGCGCTCATCGAGGACATTCGCGAGGTTTCGGCAAGCGGCTCAGGAC	24376
Db	59154	CGGCGCGCGCGACACATGTTTGAAGAGATCGTGGATCTACGGC-----	59198
Qy	24377	TGGAGCAGCTGCGTCGACGGCAAGACGACACAGCTCAGCGGATTCGACGCTCTCTCC	24436
Db	59199	-----CCGACACCGAGACCGGAGAGACGCGTTCGCGCGAGCTGG	59240
Qy	24437	GTGACGGATTGGCCGACGATGCTCTCAAGCAGAAACAGAGTGTCTGTGGCGCTGATTC	24496
Db	59241	GGCAGCAGCTGGCCGACATGCGCGCGCTGAGCGCGGACACCTGCTGTGGAGTGTGTC	59300
Qy	24497	GGACAGGACATGCAACCGTTCGCGCTTCGTAATCGGAGAGGATTCGAGGACCAACGAG	24556
Db	59301	TGGCGGAAACCGCCAGCACCTTGGGGCAGATTCGGCGGAGGCTGTGCAACCCGATCGGA	59360
Qy	24557	CTTCCGCGACCTCGGCTTTCGACTCGCTGACGCTCGGCTCAGTTTCAAGGAACTCGGCA	24616
Db	59361	CTTCCGCGAATCGGCTTCGATTCGCTGACCGCGGTAGAGCTGCGCAACAGTTGAAACG	59420
Qy	24617	AGGAACCGGACTGCACTCCCGCTTCTGCTGCTTCTGCTGATATCCCAACCGCGAGGAT	24676
Db	59421	CGGTGACCGGGCTTCCCTGCGCGGACGCTGCTTTTCGACCAACCGACCGCGCTGGCGT	59480
Qy	24677	GTGCTGCCATCTGCGCACACAACTCTGCG-----	24706
Db	59481	TGTCGAAACAGTTGTTTCCGCGCTTGGTTCGGGAGCGGACCAAGCGCATCGAATCGGTGC	59540
Qy	24707	-----ACCTAG	24712
Db	59541	TGCGCGAGCTCGACAGGCTGATACCAAGTTGGCGCAAGGGCTTCGATCCCATGGAAG	59600
Qy	24713	ACGAGAAAGAGACCGCGGACATGTTCGAATGCTCTC-----	24747
Db	59601	ACCAGCCAAAGTGGCGAGGCTTGCACGCACTCTCGCAAGTGGGACCGGGCGGTG	59660
Qy	24748	-----	24747
Db	59661	ACGGCAGCGGACAGCAGCTCAACCCCAATCGCTGACGGCGGCCACGAGCAGAAATCT	59720

Qy	24748	-----	24747
Db	59721	TCGACCTCATCGACCGGAAGTTTCGGGCGCTGACCGCGCTTCTCTCGCCTCAGCTCCCGCTG	59780
Qy	24748	-----CCGCAAGTG	24756
Db	59781	ATTACTGSAACGGGTATTTTCGATGGCCAATGAAGAAAGCTCCGCGAGTACCTCNAACG	59840
Qy	24757	GCCCATCGCGCTAC-----CGTCGAGCA	24779
Db	59841	TGTGCTGCTCAACTGMAAGGGCGCAGAACGCTGCAACAGTTGGAGCCCAAGAGCA	59900
Qy	24780	CGAACCGATCCCATCATCGGTATGGCATGTTCCTTCCCGGGCGGTACGTTCTTGCCGA	24839
Db	59901	CGACCCCATCGCATCGTGTGATGGATGTTCGTTATCCCGGTGGCGCTCTCCACTCCGGA	59960
Qy	24840	CGACTGTGGGAATTCGCTTCGGGTAGGACGCTATCGCGGCTCTTCCCGACGACCG	24899
Db	59961	GGAGCTGTGGCGACTGTGTCTCGACGAGGAGACGCGATCGCAACTTTCGCCGAAGACCG	60020
Qy	24900	CGGCTGGGACCTGACACGCTCTACGACCCCGACCCCGACACCCCGGACCTCTGATAC	24959
Db	60021	TGGCTGGAATCTGACAGAGCTTTCGATCTCTGATCCCGGCGGACCGCGGACCTCTACGT	60080
Qy	24960	CCGAAACGGCGGATTCCTCTACGCGCGAGGCGCACTTCGACCGCGAAATTTCTTCGGCATCAG	25019
Db	60081	CCGCGAGGTGGTTTCTCGCGCGGGTTCGGGACTTCGATGCGCGGCTCTTCGGGATCAG	60140
Qy	25020	CCCCCGGAAGCCCTCGCATGGAACCCCGACGAAAGAACTCTCTCTCGAAGCCGCTGGGA	25079
Db	60141	TCCGCGGAGGACACAGCGCATGGAACCCCGCAACAGCGGTGTCTGTGGAGATCTCGTGGGA	60200
Qy	25080	AACCATCGAACACACCGGCATCAACCCCAACCCCTCCACGACACCCCGGAGGCTTT	25139
Db	60201	GGTGTTCGAGCGCGCGCATTTGACCCGTTTCTTTCGGGGGTACCAAGACCGGTGTGT	60260
Qy	25140	CGCGGAATCAACGCTCAAGACCAACCGCGCATATCCGCCAAAGCGGTGATGAGAGAC	25199
Db	60261	CGCGGCGCTGATCTACACAGCTACGCGTTCGGGTTCGCAAGACCCCGCGGAG-----	60315
Qy	25200	CATCGAGGCTACGCCCTGACCGGAGTTTGGGAAGTGTGGCGTTCGGCGCGGGTGGCTA	25259
Db	60316	-TTCCAGGGTTACTTTCGCCACCGGCAACGGGGCAGCGTTCGATCCGCGCGGGTGGCTTA	60374
Qy	25260	CACCTCGGCTCAAGGCGCGCGGTTCGCTGATACGCGGTTCGCTGCTGCTGCT	25319
Db	60375	CACCTTCGGGTTAGAGGGCGCGGCTCACCGTGGACACCGCTGCTGCTGCTGCT	60434
Qy	25320	GGCGTTGATTCGGCGCGGCGGCTTCGCTGCGGTGAGTGTTCGATGGCGCTTGC	25379
Db	60435	GGCGTGCACCTGGCTGCCAGTCCCTGCGGCTGGGCGAATGCGACCTTGGCCCTTGGCGG	60494
Qy	25380	GGGTGTCAGGTGATGCTCTCCGGTACGTTTGTGGAGTTTTCAGCTCAGCGGGTCT	25439
Db	60495	TGGATTTTCGGTATGATGCCACGCGCGGAGCTTCGTCGAGTTTTCAGCGCGGCAACCGCACT	60554
Qy	25440	GGCGCGGACGCGGCGTCAAGGCTTATTCCGGGCTGCTGACGCTACCGGCTGGGCGGA	25499
Db	60555	GGCTTCGGATGGCGCGGTGCAAGCGCTTTCGCGGATTCGCCCGACCGGCAACCGCTGGGCGA	60614
Qy	25500	GGGTGTGGGATGCTGCTGTTGGAGCGGCTCTCCGACGCGCGCTCGCAACGCTACCGTGT	25559
Db	60615	GGGCGCGGAATGCTGCTGTGTAACGCTGTTCGAGCGCAGCAGCAAAACGCGCACCGGCT	60674
Qy	25560	CTGCGCGTGTGCTGGCGAGTGGGTCAACACGAGACGGTTCGAGCAACCGTCTTGACCGC	25619
Db	60675	GCTGGCGGCTGTGCTGCTTCCGCGATCAACACGAGACGGGACGCTTCAACGCGCTGACCGC	60734
Qy	25620	GCCCAACGGGCGCTTCCGAGCAGGCTGTCTCCGTACGGGCTTGGCCAAATGGGGACTGAC	25679
Db	60735	GCCAGCGGTCCGCGACAGCAGCAGTGTATCCGCCAAGCGCTTGGCGAAGCGCGGTGTTC	60794

Qy	25680	CCCGCCGAGTGT	CGACGCACTGGAGGCCACGCGACCCGGGACCACTCTGGGGGACCCGAT	25737
Db	60795	GCCCGCGAGGT	CGATGTGTGTCGAGCGCGACGCGCACGGCTTTGGGCGACCCGAT	60854
Qy	25740	CGAGGCCAGGCA	CTCTGGCGCGCTTACGGACAAACACCGCCCGCACCGCCCTTTGTG	25799
Db	60855	CGAGGCGCAGCCCT	GATCGCCACTACGGGGCGAAACCGGTGGCGGATCATCGCCTGCT	60914
Qy	25800	GCTGGGATCCT	CAAACTCAACATCGGGCAGCAGGCGCGCGGGCGTGGCGGAGT	25859
Db	60915	GCTGGGTTCT	CAATGTGAAATCGGCACACCCAGGCTGCGCGTGTGGCGGGGT	60974
Qy	25860	CATCAAGATG	TGATGGCCCTGGCGAAACCGGTGTGCGACAGACCCCTCACAGTGGACGA	25919
Db	60975	GATCAAGTCGT	CTCTGSCCATCAGGCACCGGAGATGCCCGCAGCCTGCAATCGACCA	61034
Qy	25920	GCCACACCCCG	AGGTGATCTGTGTCCACGCGCAGGTACAATCTCTTGAACAACCGGTGCC	25979
Db	61035	GCCATCGACGA	CGTGGACTGTGTGGCGGCGCGGTGCGGCTGCTCACGGAACAGCGTTGA	61094
Qy	25980	CTGGCCCGCGA	CCCGCGCGCGCGCACGCCACGCGCGGTGTATCATTCGGCGTCAAG	26039
Db	61095	CTGGCCGG-----	ATCTCGCGAGCGCGCCGAGCAGGGGTGTCTCTGTTGGCATGAG	61148
Qy	26040	CGGCACCAAC	CGCCACATCATCTCGAAGACACCCACTCCCGACGACGATACCGA	26099
Db	61149	CGGTACCAAC	CGCACACCTGATCGTGGAGAGTATCCGACGAGCGGTCTCGGGCAGTAC	61208
Qy	26100	CGACGAACCG	CTGCGCAACGCGCTGCGCAACGCGCTGCCCCATCCCTCTTCCTCGGTGCGGT	26159
Db	61209	CGA-----	GCAGACCGGGCGCATTTCCCTGGCCGCT	61238
Qy	26160	GTGGCGAGGT	CTGAGCGCGGTTCGGGCGCAGGCACAGGCGTTGCGCAGTACGTGCG	26219
Db	61239	GTCCGGCAAC	AGCAGACGGCAATTGCGGAGCGGCTGCGGAGTGTCTCTCGTASTGAC	61298
Qy	26220	AGCCCGCCCGA	CATGTGCACTCGACATTTGTGGGGTCTGGCCGCGCGCGCGCGCT	26279
Db	61299	CGAGCACCCG	GAGCGGACTGGGGACGTGCGGTACTCGCTGGCCACCGGTGCGCTGC	61358
Qy	26280	ACTGGAAACA	CGCGCGCTGATCTCTGGCGCGGACCGCAGGAACTGGCGCAGCACTGAC	26339
Db	61359	GATGGACACA	CGGGCTCTCTGTGTGTCGACGATCGGGACTCTTTCTGTCGCGCGACTGAC	61418
Qy	26340	AGCCCTGSCA	GCGGGGAAACCCACCCACATCACAGGCGCACCCCGGGCGGTGA	26399
Db	61419	GGCGTTGGCT	GCGGCGTTCCGGCAGCCAACTG-----GGTGCAGGGCGCGCGCACTG	61472
Qy	26400	CCGCGGCGGT	CTCTCTTCTTCCCGGACAGGCGCGCAGTGGCGCGGATGGGCT	26459
Db	61473	CAAGGAAAGT	CGCGTTCTGTGTTCCCGCGCAGGGCTCGCATTTGCGAGGGATGGCAG	61532
Qy	26460	GACCTGTGCA	CTCTCTCAACCGTGTTCGCGGAAACATCGACGACATGCGAGAAAGCCCT	26519
Db	61533	GGAACTGTCC	GAATCTCTCGCAATCTCTCGCGGTGTTCCCGCGGGAAGCTGGCGGATGCGCGCGGCTAC	61592
Qy	26520	CACCCCTGGT	GCGCTGTGCTCGACCGACATCTTGCAACCGGACCCCGACGACCCCGC	26579
Db	61593	GGCCCCCTTA	CGTGGACTGTGTCTGTCTGCGGCTCTCTGCGGTGATGCCGATGCAACCGC	61652
Qy	26580	ATGCCAACAA	CGCCAGTCGATGCTCCAGCCGTCTTTCAGCATCATGGTCTCCCTCGCGCG	26639
Db	61653	GCTGGATCG	CGACAGCTGATTCAGCTCGCGCTTTCGCAATGATGTGTCTGCTGGCGA	61712
Qy	26640	CTGTGGGCTC	TACCGGCAACCGCAGCGGCTCTCGGCCCATCTCCACGGAGAAAT	26699
Db	61713	ACTGTGGCG	TTCTGTGCGGATGAGCCCGCGCGGTGCTCGGTCTATTCACAGGGGAGAT	61772
Qy	26700	GCGCGCGCCA	CATCTGCGGCGCATCTACGCTTGAAAGCGCCGCCAAACCTGTGCACT	26759
Db	61773	GCGCGCGCCCA	TGTGCGAGGCGCTTTGCTCTTGACTGATGCGGTGCGCATCATCGCTGC	61832
Qy	26760	GCGCAGCGCG	CGCATCTGGCCGCGGTACGAGCGCGGGGCGGCATGGGCTCATCTGCCCTGCC	26819

D	b	61833	CGCCTCGCATGCGGTGTGGCGCTGAACCGGAAGGAGGCATGTCGCGATTGCTTGCC	61892
Q	y	26820	CGCCAGGACGTGCAGCACTCATTTTCGAAACGCTGGGAAGCGCATTTTGGGTGGCAGC	26879
D	b	61893	GGAACGGCGGTGGTAACGCAATCGCAGGCTGCCGG-----AGCTGACCGTTGCGGC	61946
Q	y	26880	CCTCAAACGGCCCCCATCTCACACCGTCTTCGGCGACAACGAAGCGGTGGATAGGTTGCT	26939
D	b	61947	GGTCAACGACACCGGCTCCACTGTGTTTTTCGGCGAACCGTCCGCTCTGGAGCGCTGCA	62006
Q	y	26940	GGGCGAATGCAACGACACCGGCTTAGGGCCAAAACGCAATCCCCTGCACTAGCCTCCCA	26999
D	b	62007	GACCGAACTGACCGCGGAAAAAGTGCAGCCCGCGGGTGGGAAATGATTACGCTCGCA	62066
Q	y	27000	CTGCCCCACGTCACACCTCCACGACGAACCTCTGCATCTGTCTGGGAGACATCACCCC	27059
D	b	62067	TTCGCGCAGATCGCCAGGTCGAGGCGGGTTCTGGACCGBCTGGCGAAGTCGGTCTC	62126
Q	y	27060	CCAGCGCTCCACCGTSCGTTTCTTCTCCACCGTGAAGGCACCTGGCTGGACACCAAC	27119
D	b	62127	CGAACCTGCTGAGATCGCTTTTCTACTCGACGGTTCACCGCGAGCGACCGGCGC	62186
Q	y	27120	CCTGGACGCGGCTACTGTGTAACGCAACTCTCACACGACCGTTCGCTTCAGCCAGCCAT	27179
D	b	62187	ACTCGACGCGCATACTGTGTAACGAACCTTCGGCAGCCCGTCCGCTTCCAGCAGACCGT	62246
Q	y	27180	CCAGACCTTGACCGACGCGACACCGCGCTTTCAGAAATCAAGCCCCACCCACCCCT	27239
D	b	62247	CGCCGGATGGCAGATCAGGGCTATCGGTTCTTCTGTGAGGTGAGCCCGCACCGCTGCT	62306
Q	y	27240	CGTCCCGCCCATCGAAGAACCACCGAANAACAACCCGAAACATCACCGCGACCGGCAG	27299
D	b	62307	CACGCGCGNAATCCAGNAACGCTGGAAGCGCGGACGCGGCGGGGTGGTCCGTTTC	62366
Q	y	27300	CCTCGCGCGGCGGACAACGACACCCAACCGCTTCTCAACCGCCCTCGCGCCACACCCAC	27359
D	b	62367	GCTCGCGGTGGCGAGGGGGGTCTCCGGCGCTGGGTGACTTCGCTGGCGCGAGTGCAGGT	62426
Q	y	27360	CACGGCATCGGCACACCCACCACTTGGCACCACTACACCCAAACCCACCCCCACCC	27419
D	b	62427	GGCGGATGCGGGTGAATTGGGAACAGTATTCTCTAACACCGGAGCCCGACGGTGCC	62486
Q	y	27420	CAACCCCCACACCACTCGACCTGCCCCACTACCCCTTCCAACACCGACACTACTGGCT	27479
D	b	62487	-----GCTGCGGACCTACCGTTTCCAGCGGACGCGTACTGGTT	62525
Q	y	27480	CCAAACACCC---ACCAACAACCGACTCAACACACCGGCTTCAACCCCAACCCCA	27536
D	b	62526	GGAGTCCGCGGAGTACGACGCGGGCGATCTCGGTTTGGTGGGCTTGTCTTCGCGGAGCA	62585
Q	y	27537	CCGCTCTTCAACGCGCACACTCACCTCGCGCACAAACAACAACAATACTACCGCGCG	27596
D	b	62586	TCCCTCTGCTCGGGCTGCGGTGACGCTGGCCGATGGGGCGGGTTCCTGTGACCGGCAA	62645
Q	y	27597	CCTCTCCCTACGCAACCAACCTCTGGTCAACCGACCAACCGTTCGCGGCGATGCTCTCT	27656
D	b	62646	GCTGTGGTCAAGACCAAGCCTGGTTGGCCGACACGCTGGTTCGGGGGGATCCTGCT	62705
Q	y	27657	GCGGGCAACGCGCTCTCTGAACACTCGCCCTTCAACGCGGCGAAACGGGTGGAATGCGCTCG	27716
D	b	62706	GCCCGCACCGCTTCTGTGSAATGTGATAGCGCGCGGACCAAGTTCGGGTGGGATCT	62765
Q	y	27717	GGTGGGGAATCAACCTTGCACGCAACCGTTGGTGTATCCCGCAACCGAGGACGTACGCTT	27776
D	b	62766	GATCGAGGATTTGTCCTCTGACGATCCCGTGGTTTTTCCCGCGACCGGTGCGTACAGGT	62825
Q	y	27777	GCAGGTCAACCGTTTCGGGCAACCGATGAGAGTGGCCCATCGCGCCCTCGCGATCCATCGTA	27836
D	b	62826	GCAGATCGGGTTGGCGGTTCGGAACGAGCGCGGGCGCGCTCGGTCCGCTGCAATTCCTG	62885
Q	y	27837	CTCGGCACCGCTGCTGCGCGGACCGGGAGTGGACCCGTTCAACGCCACCGGCTCTCTCAC	27896







15892 GGGTTCTCGGACAGCGGCTGACCGGCAACCGGCTCGGGGTGAGGGGTGTCGGAATGCTGCTGTG 15951  
15232 GCGTTCTCGCGGAAGCCGACGGTTGCGGTGCGGAGGCGCGGGATGCTCTCTGCTC 15291  
15952 GAGCGGCTGTCGAGCGCGGGCGGCTCGGTACCGAATCTCTCGCGGTGCTGGCAGT 16011  
15292 GAGCGGCTCTCGATGCGGTCAAAACGGGTCAATCCCGTCTCGCGGTCTCTCGAGGCTCC 15351  
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15412 CCGGTATCCGCAAGCGCTCGACAGCGCGGCTCACTCCAAAGGACGTGACGTGCTC 15471  
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15532 ACCTATGGGAGGCCATTTCCAAAGACAGACCCCTCTGGCTTGGAGCCTCAAGTCCAAC 15591  
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16432 CTGCGCGGGGAGGAGTGTATCTGTTGGCGGTGAGCGGCACCAACGCCCACTCATCTCTC 16491  
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17152 GCGCTCTTTCGCTTCAGGTGCGCTCTCAACCGCTCTCTCAGCAGGCTTCAACATCACC 17211  
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16594 CCGTGGGCGAGCGCTCTCATCGCGCGCTCAACAGCGGCGGCGGCGGCTCGTATCC 16653  
17452 GCGACCCCGCACACCGCTCCAAACATCAACACCTCTCTGCAACCAAGGATCAAAAC 17511  
16654 GCGAGCGCGCGGCTCGAGCGCTGATCGACTGCTCAACGCGAGCGAGTCTTCGCG 16713  
17512 AAAACCTCTCCCAACAAAACGCTTCACTCCCGGCAACAAACCGCTCTCTCAACCA 17571  
16714 GGAAGAGTCCGCGTCACTAGCGCTCCCACTCAGCCAGATGAGCGCGCTCCAGACGAG 16773  
17572 CTC-----CAGCAGCACACCAACCTCACTACCAACCAACCGGCTCTCTTTATTCGACC 17622  
16774 CTCGCGGAGGTAGCCAACTCGCTCTCGAGGTGCGAGTCTCTTTATTCGACC 16833  
17623 ATACCGGCAACACCCACCGGACCAACTCTCTACCGCGGCTCTACTGAGCAACCAAGCC 17682  
16834 GTACCGGACACGCTCGAGCTCGAGCTCGAGGCGGTACTGATGGAACCTC 16893  
17683 CGCAACCGTCTGACTAGCGCACCAACCAACCGCTTCAACCAACCGGCTTCAACCG 17742  
16894 CGGCAACCGTCTCTCTCGAGCGGACCGAGCGGCTCTCGAGATGGGATCGCTTC 16953  
17743 TACATGNACTCGGACCGGACCAACCTCTAC-----CAGCTTCAACCAACCACTCTCC 17799  
16954 TTGCTGAGGTGAGCGCTCATCCGCTGCTCACTCGCTGCTCTCGGAGACCTTGGAGCGC 17013  
17800 AACACCCCAACCAACCGCTTCAACCAACCGGCTTCAACCAACCGGCTTCAACCG 17859  
17014 TCACGCTGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17073  
17860 CTCACCACTCTGCAACCAACCAACCACTTGGCAACCGGCTTCAACCAACCGGCTTCAAC 17919  
17074 CTCTTGTCTCTTGGGCGGAGCTTATGGCGGCGCTTCAACCGGCTTGGAGGCGCTTC 17133  
17920 AACCAACCAACCAACCGCTTCAACCGGCTTCAACCGGCTTCAACCGGCTTCAACCG 17979  
17134 TTGCGCGCTTCTGCTTCCCGGAGGCTCTCACTTCCCGCTTCCAGCGGAGGCT 17193  
17980 TACTGGCTCGAAGACACACCGGCTGCGGATTCGCTTGGGTTTCGGGTTTCGGGCGG 18039  
17194 TTCTGGCTCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 17244  
18040 GCAGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18099



QY 20227 GCCGAATTTCTGGGATCAGCCCGCGAAGCCCTCGCATAGAACCCCGCAGCAAGCTC 20286  
Db 19441 CTTGCTTTCTTGGCATCAGCCCTCGCGAGGCAAAATACCTCGACCCCGCAGCCGCTG 19500  
QY 20287 CTCTTCGAACCGCCCTGGGAACCATCAACACGCGCGGATCAACCCCGCAGCCCTCCAC 20346  
Db 19501 CTCTTCGAATCTGCTGCTGGCCCTCAGGAGCGCGGATCGTCTCCCTCCACCCCTCAAG 19560  
QY 20347 GGCACCCCGACCGAGTCTTACCGCGCACCAACGAGCAGGACCGCGGCACACATCGT 20406  
Db 19561 GATTCTCCACCGGCTCTTGTGGCATCGGCGCAGGAATACGACTGGAAAC--- 19617  
QY 20407 CAGGCCCGAGCGGTACCGAGGATTCGTCTGACCGGGGAGCCACAGCATCGCCTCC 20466  
Db 19618 ACGAGCTCCGAAGAGTCCGAAGCGTATGCCCTCCAAAGCACCGCGGCTCTTTGCGCG 19677  
QY 20467 GGCAGATCTCTATACCTCTGGGTGGAAGGGCTGCGGTACCCCTCGACACAGCGTGT 20526  
Db 19678 GGGCGCTTGGGCTTACACGCTCGGCTGCAAGGGCCCGGCTCTCGGTGACACCGCCTGC 19737  
QY 20527 TCCTCTCGCTGCTGCCCTGCACCTCGCCTGCCAGTCCCTCAGTCCGGTGAATGCACC 20586  
Db 19738 TCCTCTCGCTGCTGCCCTCCACCTCGCTGCGAAGCCCTCCGACAGGGCGAGTGCAAC 19797  
QY 20587 ATGGCTTTGGCGCGGGGCCACGGTCATGACACCCCGATCACCTTACCGAATTCGCC 20646  
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QY 20647 CGCCAAACCGGACTCGCCCGGACGGGCTTGAAGGGGTTCGAGGGGTCTCGGCGGCGGTGACGGT 20706  
Db 19858 GGCATGCGTGTCTTGGCGCCGATGGCGGCTCCAAAGCTTCTCGACCAACGCGCGACGGC 19917  
QY 20707 ACCGCTGGGTGAGGTGTGGGATGCTGTGTGGAGCGGCTCTCGAGCGCCGCGCG 20766  
Db 19918 TAGGACCGGAGAGGGGTGTGTCTTGTGCTTGGCTTGAAGGGCTCGGCGAGCCCTCGCC 19977  
QY 20767 AACGTCAACGTGCTTGGCGGTGTGTGTGGAGTGGCGTCAACAGGAGCGGTGCGAGC 20826  
Db 19978 CGAGGACACCGCTCTCGGCTCTGCGCGCACCGCATGACCATGACGGCGGCTG 20037  
QY 20827 AACGTGTAGCGGCGCCCAACGGGCGCTCCAGAGCGCGTCAACGAGCGGCGCTCGCC 20886  
Db 20038 AGCGGCATCAGCGGCGCCCAATGGCACCTCCACACAGAAAGTCTCCGCGCGCGCTCCAC 20097  
QY 20887 AACGGGACCTGACCCCGCGAGCTGATCGGTGGAGGCGCCACGCGCACCGGACCACT 20946  
Db 20098 GACGCCATATCGGCGCTTGCAGCTGATCGATGCGATGCGATGCGATGCGATGCGATGCG 20157  
QY 20947 TTGGCGACCCGATCAGGCGCCAGGCCATCTTCGCGACCTACGGACAGGACCGTCCCGGC 21006  
Db 20158 TTGGGAGACCCATCGAGGTGCAAGCCCTGCGCGCGCTTACGCGATGGCAGACCCGCT 20217  
QY 21007 AACGGGCGTGTGGCTGGCTCGTCAAGTCAAGCTGAGACACACAGCGCGCGCG 21066  
Db 20218 GAAAGCCCTCTCTTCTCGGGGCACTCAAGACCAACATTTGGCCATCTCGAGCGCGCTCC 20277  
QY 21067 GCGTGGCGGAGTGATCAAGATGTGATGCGCTCCGCGACCGGACACTCCACCGACT 21126  
Db 20278 GGCCTCGGGGCTCGCCAGATCGCTGCTCCCTCCGCGCATGACGCGCTGCGCGCCAC 20337  
QY 21127 CTCACCGGATGAGCCGTGCGCGCATGTGACTGCTCGGCGGTGCGGTGCGATGCTGT 21186  
Db 20338 CTCACACGACCCCGCGCAATCCCTGATCGATGCGATGCGCTGCGCATGACGCTGCTC 20397  
QY 21187 ACGGAGACGTGCTTGGCGCG---CGGGAGGGGGCGCGCGCGGCGAGGTGTCA 21243  
Db 20398 GATGACACAGGGGCTGGGCGCGCACGAAGATGGCAGTCCCGCGCGCGGCGCTTCC 20457  
QY 21244 TCATTGGCGGTGAGCGGACCAACGCGCCACGTCATCTCGAAGAGACCGCGCGAGC 21303  
Db 20458 GCCTTCGGAATCTCGGCGCACCAAGCCCGCTTATCTCTCGAAGAGGCTCCCG-----C 20510

QY 21304 GTTCCGGGGGACCAACCCGCGCAGCAGGATGCGGTAGTGGCGAGGAGGTGCTTCCGCGC 21363  
Db 20511 GATCCCGCAGGCGCAGGCCACCGCGGCACAGC-----TCGCTCGAGCGCTTCCGCG 20564  
QY 21364 AGTCTGGGTGTGGCGTGGCTGGTGGCCAAAGTGGAGCGCGGCTTGGCGCGCCAG 21423  
Db 20565 AGCC-----TGCCCGGTGCTCTGTGGCGCAGGAGCGCGGCGTGGCGCGCCAG 20616  
QY 21424 GCCCAGGCGCTGACGACGCCACCTCAGCGACCAACCCCGGCTTGCACCTTCGCGCAGTTCGGA 21483  
Db 20617 GCCCAGAGGCTCCGCGACACCTCTCGCCACGACGACCTCGCCTTGGCGGATGTAGCC 20676  
QY 21484 TACACCTTCGCGCACGCGCGCGGTGTTCGACCAACGCGGCCACCTCATTCGCGCGCAC 21543  
Db 20677 TACTCGCTCGCCACACCGCGGTACCTTTCGAGACCGTGGCGCTCTCTGTTGTCACGAC 20736  
QY 21544 CGGACACCTTCTTCGAAGCATCTCAGGCACTGCGCGCAGGGAACCCACCGCGCGTTC 21603  
Db 20737 CGCGAAGAGTCTCTTCGCGCTCGATTTCGCTCCCGCAGGGAAGCGCCCGCGAGCAC 20796  
QY 21604 ATCCACAGCAGCGCCCGCAGCGGACCGGGACCGGGAGGCGCGCAAAAGACCGCATTC 21663  
Db 20797 GTCGTGCAACGAAGGGAG-----CCACGGCAAGTGTCTTTC 20835  
QY 21664 ATCTGCTCGGACAGGGAACCCAAAGCCCGCGCATGCGCCACGCGCTTCAACACCCAC 21723  
Db 20836 GTCTTCTGCGCAAGGCTCGCAGTGGGAAGGATGCGCTCTCTGCTGCTGATACCTCG 20895  
QY 21724 CCGTCTTTCGCGCGGCACTCAAGCATCTGACACCACTTCGACCCCGCCTCGACCC 21783  
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QY 21784 CCCCTCTCCCGCTCTCACCCAAACGACAAACGACAAACGAGGACCGCGCGCA 21843  
Db 20956 TCGTGTCTGCGGTGCT-----CCGCGCGAGGAGGGCGCGCC 20994  
QY 21844 CTGCTTCAGCAGACCCCGTACGCCAGCCCGCTTTCGCGCTTTCAGGTCGCGCTCATC 21903  
Db 20995 CCGCTCAGCGGTGCGAGTGTTCAGCGCGCTTTCGATGATGCTGCTGCT---G 21051  
QY 21904 CGCTCTTACCGAGGCTACCATCACCCCGCTTCTACGCGCGGACACTCTCTCGGC 21963  
Db 21052 GCOCGCTGTGGGCTCCATGGGCGTGGAGCGCGCTGCTGGCGCATAGCGAGGC 21111  
QY 21964 GAAATACCGCGCGCCACCTCGCGCGCATCTCACCTCACCGACGCGCACCCCTCATC 22023  
Db 21112 GAGATCGCGCGGCTGTGTGGCGGCGGTGTGCTGAGGAGCTGCGACAGCTGGTG 21171  
QY 22024 ACCCAACGCGC---ACCCTCATGCAAAACATGCCCCCGCGCACCATGACACCCCTCCAC 22080  
Db 21172 GCGTTCGCGAGCGTGGCTCGTGGAGCTCGCGCGCAGGGGCGCATGGCGCGTGGAG 21231  
QY 22081 ACNACCCACACACATCACCCACCATCACCGCCACGAAAGACCTTGCCTATGCC 22140  
Db 21232 CTGCGGAGGCGAGGTGCGACGCGCTTCAGCGCTATGGCGATGCGGCTCTCCATCGGG 21291  
QY 22141 GCATCAACACCCCGCTCTCTGTCATGAGGCGACCCCGCACACGCTCCACACATC 22200  
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QY 22201 ACCACCTCTGCGCAACAAAGGATCAAAACCAAAACCTTCCCGCACCAACAGCGCTTC 22260  
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QY 22261 CATTCGCCCGACACCAACCCCATCTCAACCAATCCACGAGCACACCCAAACCTTACC 22320  
Db 21412 CACTTCGCGAGGTGCGATTCGCGAGAGCTCTTCGATCTCTGCTGTGCTGCTCGAG 21471  
QY 22321 TACCACCCCGCACACCCCTTCTCATCGCGCAACACCCCGCACCGCAACTC----- 22374  
Db 21472 CCGCGCTCGAGGGGCTTCCGTTTCTACTCCAGGTTAGCGGCGCGCGATCGACGGGAGC 21531  
QY 22375 ---CTCACCCCGCACTACTGGACCCCAAGCCCGCAACACCGTTCGACTACGCCACCAACC 22431

Db 21532 GAGCTCGAGCGCGCTACTGTTACCGGAACCTTCGGGAGCGGTCCGTTCTCGCAGAGCT 21591  
Qy 22432 ACCGAAACCTCCACCAACAGCGGTACAGCTTACATCGAACTCGGACCGACAAACACC 22491  
Db 21592 GTGCAAGGCT---CCTTTCGCGGGAACATCGCTTCTTTCGTTGGAGGTGAGCCCAAGTCT 21648  
Qy 22492 CTCACACCTTCACCCACCAACCTCCCAACACCCCAACCCCAACCCCTCACCTCACC 22551  
Db 21649 GTGCTGACTTGGCTTTCGACAGAGCTCTCGAAGGCTCGGAGGCTCGGCGGCGGTGTC 21708  
Qy 22552 CACCCCAACCAACCAACCCCAACCTCTCTACCAACCTTCGCGGAGGTCTCGGAGGCT 21768  
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Qy 22612 TGGCAACCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCTCGAC 22671  
Db 21769 TACGTCACAGGCTTCGCGCTGATTTGGAGCAGATCTTGCCTCCCGGGAAGCGGTGCG 21828  
Qy 22672 CTCCCACTACCTTCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 22731  
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Qy 22732 AGCCCGGTCAAAAGCGTTCCTCGCGCTCGGTCCAGACACCGCGAGTCTGGAAGTTCTGG 22791  
Db 21889 GCGGCGTCAACCACTTGTCTCGCTCGAGGGC-----GGTCTGCGAGGCGCATCGAG 21942  
Qy 22792 GACGGGTGAAGGAGAGAGCTTCAGAGCTTCGCGAAGCTTCGCGAAGCTTCGAGCTCT 22851  
Db 21943 AGCGGGAATATCGACGCTCAGCGCTCAGCGCGAGCTTCCACGTGGAGCGGCGAGCGCGCC 22002  
Qy 22852 GCTCTGAGACGGTGGTGGCGGCACTCTCGCTGGACCGGCAACCAACCAACCAACCAAC 22911  
Db 22003 GCGCTTGCCTCTCTCTTCCCACTCTCGGAGCTTTCGCGAGCTTTCGCGAGCGCAAGAGCGGGC 22062  
Qy 22912 GCGATCAACACTGAGCACTTACAGGAACCTTGAACACCTTCACTCCCAACCAACCAAC 22971  
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Qy 22972 CAACCCCA---CAAACTGGTCTATGCGCATTCGCGAATTCGCGAATTCGCGAATTCGCG 23028  
Db 22123 GCGCACTTGGCGGCGGCACTGCTCTCTGCTGCGCGGCTCTGAGACGAGCGCGCTC 22182  
Qy 23029 ATCAACCACTCTCAACCACTTCCACCAACCAACCAACCAACCAACCAACCAACCTC 23088  
Db 22183 CCCTCGCGCTTACGAGGCGCTCCCGCGGCGGCGGCGGTCTCTCGCGTGGCGCTG 22242  
Qy 23089 AACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 23148  
Db 22243 AGCCAGGCGCACTTGAACCGGAGCTCTCGCGAGCACTTGGCGGCTTGGCGGCTTGG 22295  
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Qy 23209 ACACCCACCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCTCCC 23268  
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Qy 23269 CAACCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 23328  
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Db 22588 ATCGACGAGCGCGCTGCGGCTTCTGCTCCGCTCTCGCTTCTGCGCAACGATGAGAC 22647  
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Db 22768 GGGCGCTTCGCTCAGCTCGCGGATGCT---CGCTCGAGAGGCGGAGACCACTC 22824  
Qy 23689 CTCTCACAGCGGCAACCGGCGGCGGCAACCGGCGGCGGCAACCAACCAACCAACCAAC 23748  
Db 22825 GTCTCTATCAGCGCGCGGAGGCGGCGGAGGCGGCTTCGAGCTTCACGCGGAGCTC 22884  
Qy 23749 CAACAAAAGGCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 23808  
Db 22885 ACGGCGCTTGGCGCGGCTTCACTTTCGCGGCTGCTGATGCTGCGCGAGAGGCTGTC 22944  
Qy 23809 CAACAACTCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 23865  
Db 22945 GCGACGCTTCTCGAGCAGCTCGACGCGGAGGCTCGAGGCTCGCGGCGGCTTCAACG 23004  
Qy 23866 GCGGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 23925  
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Qy 23926 ACGGACGAGGCAACCGGCGGCGGCTTCTGATGATGCTTCTTCTTCTTCTTCTTCTT 23985  
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Qy 23986 CTTGAACACTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 24045  
Db 23122 CTGAGCGCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 23181  
Qy 24046 GCATCTCGGCGGCAACGATACCTGGAACGCTTGGGCGGCGGCTTGGGCGGCGGAACT 24105  
Db 23182 GGATACCGCGGAAACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 23241  
Qy 24106 CTTCCCGGCGCATCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 24165  
Db 23242 CAGCGGACAGCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 23301  
Qy 24166 GCGGCTCATGTTTACCTTGAAGGCGGCTTCTGCGGATTCGAGGCGGCGGCTTCTG 24225  
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Qy 24226 GCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 24285  
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Qy 24346 ATTCCGAGGTTTGGCAAGCGGCTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGG 24405  
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Qy 24406 ACCACACTCAGCGATTCGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 24465  
Db 23539 CCGGCG-----ACCTTCTGCAAGCTTCGAGGCGGCTTCGAGGCTTCGAGG 23580  
Qy 24466 AAGCAGAACCAAGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 24525  
Db 23581 GAGCAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 23640  
Qy 24526 CGTAATTCGGAAGGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTTTCG 24585  
Db 23641 GAAGGCGGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTTTCGAGGCTT 23700



QY	24586	ACGTGGGTCAAGTTGAGCAAGAACTCGCCAAAGSAAACGGGACTGCCACTCCCCCGCTCC	24645	QY	25666	AATCGGGAATGACCCCGGCGCATGTGACGACGTGAGGGGCCACGGCACCGGGACCACT	25725
Db	23701	ATGACCGTGAAGTTCTGTCGGCGCTTGCAACAGGCGACCGGCATCAAGCTCCCGGCCACC	23760	Db	24760	GACGCCCGCATCAACCCCGCGAGTGTGACCTGTCGAGTGCATGCGACCGGACCTCG	24819
QY	24646	CTGGTCTTCGACTATCCACCCCGCAGGAGTGTGCTGCCATCTCTGGCACACACTGCTC	24705	QY	25726	CTGGGGACCGGATCGAGGCGCCAGGCATCTCTGGCGCGCTACGGACACACCGGCCCCAC	25785
Db	23761	CTCGGCTTCGACATCCCTCTCTCTCATCGCTGCGCTCTTCATCGCGACTCGTCTGCC	23820	Db	24820	CTGGGAGACCCCATCGAGGTCAAGCCCTTGCGCGCGCTTACGCCGAGCGGACAGCCGCT	24879
QY	24706	GACCTAGACGACGAAGAGGACCGCGCACTGTGCAATGTCTCTCCCGCAAGTGGCCCATCGG	24765	QY	25786	CACGCCCTTGTGCTGGGATCCCTCAAAATCCAACTCGGGCCACGACAGCGCGCCGCG	25845
Db	23821	CACGCCCTCGGACGAGGCTCTCCGCGAGGGA-----CGCGCGCGCTCCGCGC	23871	Db	24880	GAAAAGCTCTCTTCTCGGCGCGCTCAAGACCAACATCGGCCATCTCGAGGCGCGCTCC	24939
QY	24766	CGTACCGTGGAGACGAACCGATCGCCATCATCGGTATGGCATGTCTCTCCCGCGCGC	24825	QY	25846	GGCTGGGCGAGTATCAAGATGGTATGCGCTCTCGGCAACAGGCGCTCTGCGCACAGACC	25905
Db	23872	CGCGCTCGAGCGACGAGCCCATCGCATCGTGGCATGGCTTCCACCAAGGGCGGCGGTGAGGCC	23931	Db	24940	GGCTTCGGGCGTTCGCAAGATGGTCTGCTCGCTCGGCAACGCGCTCTGCGGCCAC	24999
QY	24826	GTACGTTCTCGCGACGACTGTGGGATTTGCTCGCTTGGGTAAAGACGCTATCGGCTC	24885	QY	25906	CTCCACGTGGACGAGCCACCCCGCAGGTGTGACTGGTCCACAGGCGGAGTACAACTCTCTG	25965
Db	23932	GTGCGGATGTGACGCTCTTTGGAGTTCTTCCACCAAGGGCGGCGGTGAGGCC	23991	Db	25000	CTCCACGCGACCCACGCAATCCCTCATCGATGGGAGGCGCTCGCCATCGAGTCTGTC	25059
QY	24886	TTCGCCGACGCGCGGTGGACCTGGACAGCTTACGACCGCTTACGACCCGACCCGACACCC	24945	QY	25966	ACACAACCGGTGCTGCGCGCGACCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	26025
Db	23992	ATTCAC---AGAGCGCTGGGACCGCGGTGCGCTTACGACCCCGACCCCGACCGCGAC	24048	Db	25060	GATACCCCGAGGCTTGGCCCGCGCACGAAGATGGCAGTCCCGCGCGCGCGCATCTCC	25119
QY	24946	GGCACTTCTACACCCGAACCGCGGATTTCTTACGGCGGACGGCCACTTTCGACCGCGAA	25005	QY	26026	TCATTGCGGTGACGCGGACCAACGCGCACATCATCTCTGAAGAGAACCCACTTCCCGAG	26085
Db	24049	GCCAAAGAGTACGTCCGGCATCGCGCATGCTCGACACAGATCGACTCTTTCGACCCCTGCC	24108	Db	25120	GCCTTCGATTTCTCGGCGACCAACGCGCACGTCATCTCTGAAAGAGGTCTCCCGCGCGCTG	25179
QY	25006	TCTTTCGATCAGCCCGCGGAAAGCCCTCGGCATGAGACCCCGACGAGACTCTCTCTC	25065	QY	26086	GACAGCATACCGAGGACCGCGCTGCGCAACGACCGAGCGCTGCGCCATCTCCCTCCCT	26145
Db	24109	TCTTTCGATCAGCCCGCGGAGGCAACACCTCGACCCCGACCGCGCTGCTCTCTC	24168	Db	25180	CCGCGCGAGCCCGCACCTTACAGCGCGCGGTGCGAAGCGCG-----TCCCGCGCGC	25230
QY	25066	GAACCGCTGGGAAACCATCAACAGCGCGCATCAACCCCGACACCCCTCGACGCGACC	25125	QY	26146	CTTCCGTCGCGGTGTCGGCGAGTCTGAGCGCGGTGTCGGGCGGAGGACAGCGGTG	26205
Db	24169	GNATCTGCTGCTGCTCTGAGACCGCGCATGCTCCCGACCTCTCTCAAGACTCC	24228	Db	25231	TGGCCGCTGCTCTGTCGGCCGAGGAGCGCGCGCTCGCGCGCGAGCGGAGGCTC	25290
QY	25126	CCACCGAGTCTCCCGGAAATCAAGCTCAAGACCAACCGCGCGCATATCGCCAAAGC	25185	QY	26206	CGCAGTACGTGGCAGCGCGCGCGCATGTCTCTGCGGACATGTGTGCGGGTCTGCGC	26265
Db	24229	CTCACCGCGCTTCTCGTGGCATCTGCGCGCGGAATACGGATG-----CAAGAG	24279	Db	25291	CGCAGCACCTCTGCGCCACGACGACCTCACCTCGCGGATGTGGCTATTCTGCTGCGC	25350
QY	25186	CGTATGTGAGACCATCAGGGCTACGCGCTGACCGCGAGTTCGGGAGGTGCGGCTCC	25245	QY	26266	CGCGCGCGCGGTACTTGGAAACCGCGCGCTCTCTGCGCGGAGGACCGCGAGGAACTG	26325
Db	24280	CGAGCTCGGAAGGTTTCGAGGTTTACTTTCATCAAGGACATTCGCGCGCTCTTGGCGG	24339	Db	25351	ACCAACCGCGCGCTTTCGAGCACCGCGCGCTCTCTGAGCCCAACCCCGCGAGGCTC	25410
QY	25246	GGCGGGTGGCTACACGCTCGGGCTCGAAGCGCGCGGTGCTGCTGGATACGGCGGT	25305	QY	26326	CGCAGGCACTGACAGCCCTGCGACCGCGGAAACCCACACCCCATCACACAGGCGCAC	26385
Db	24340	GGGGCTTGGCTATACGCTCGGGCTTCAGGGGCGCGATCTTCGGTTCGACCCGCGCTGC	24399	Db	25411	CTCTCGCGCTGACTGCTCGCCGAGGACGAGCGCGCGCGCGCGCGCGCGCGCGCG	25464
QY	25306	TGCTGCTGTGGTGGCTTGCAATTGGGCGGCGAGGGGTTGCTGCGGGTGAAGTGTTCG	25365	QY	26386	ACCGGGCGGTGACCGCGCGCGCTGCTCTTCTGCTTCTTCCCGAGACGGCGCGCGAGTGG	26445
Db	24400	TCCTCTGCTGCTCTCCCTCACCTCGCTCGCTGCGCAAGCCCTCGACAGGGCGAGTCAAC	24459	Db	25465	GGACGGAGCGGAAGCCACGCGCAAGCTGCTCTTCTGCTTCTTTCGCGCAAGGCTCGCAGTGG	25524
QY	25366	ATGGCGCTTGGCGGGGTGACGCTGATGCTCTCGGGTACGTTTGTGGAGTCTTCA	25425	QY	26446	CGCGGATGGCGCTGACCTGCTCACCTCTCACCGCTGTTGCGGAGACACATCGACGCA	26505
Db	24460	CTCGGCTCGCGCGGGGTGCTGCTCATGCTCTCCCCCGACACCTTCTGTCATCTCTTCC	24519	Db	25525	GAAAGGATGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	25584
QY	25426	CGTACGCGGGTCTGCGCGGACGGCGGTGCAAGGCTATTTCGGCGGCTGCTGACGCT	25485	QY	26506	TGCGAGAAAGCCCTCACCCCTGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	26565
Db	24520	CGTCTGCGCGCTTGGCGCGGACCGCGCTCCAAGACCTTCTCGGACAAACCGCGACGCG	24579	Db	25585	TGCGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	25644
QY	25486	ACCGGCTGGCGGAGGTGTGGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	25545	QY	26566	CCCGACACCCCGCATGGCAACAGCGGACGCTGGTCCAGCGCGCTCTTTCAGCATCATG	26625
Db	24580	TACGGACGGGAGAGGCGTCTGCTGCTTGGCTCGAGCGGATCGGCGACGCTCTCGCC	24639	Db	25645	GAGGCGCGCTCTCTCGACCGCGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	25704
QY	25546	AACGCTACCGTGTCTGCGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	25605	QY	26626	GTCTCTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	26685
Db	24640	CGGACACCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	24699	Db	25705	GTCTCTCTGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	25764
QY	25606	ACCGTCTGACCGCGGCAACGGGCGCTCCCGAGCGGTGCTCATCTGCTCAGGCGCTGCGC	25665	QY	26686	TCCAGGAGAAATCGCGCGCGCGCATCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	26745
Db	24700	ACCGGTATACCGCGCGCAACGGGCGCTCCAGAGAGGCTCTCTCTGCTGAGGACGCGCGC	24759	Db	25765	AGTCAGGCGGAGATCGCGCGCGCTTCTGCTGCGAGGCGCTCTCTCTCTGAGGACGCGCGC	25824
				QY	26746	AAAACCGTTGCACTGCGCAGCGCGGCACTGCGCGCGCTGCTGCGAGCGCGGCGCGCATGCGC	26805



Qy 28962 GGGCTGGTGGCTTCGGGCGAGTCCGAGCACCCGAGACCGCATCAGCTGCTGGACTTGA 29021  
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Qy 27831 GGGTCTCGCTCGCTCCGCGCAGAGCAGCACCAGAGCGCCCTCTCGTCTCGACCT 27890  
Db |||||  
Qy 29022 CGGGGACACAGAGCGGAGCCGGTCACTGCGCAGCGGCGGTGAACCTCGGGGAGCGGCA 29081  
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Qy 27891 CGACACAGCAGAGGCTCCACACACGCTCTGCTCGGCGCTTCGACGCAAGAGAGCCAGA 27950  
Db |||||  
Qy 29082 GCTTGGCTCGGCGCGGAGGCTGTTCAACGACGCGTGTGCGCGCGCCACGTCGTGCGC 29141  
Db |||||  
Qy 27951 GATCGCCCTCGCAAGCGCAACCCCTGTTTCAAGGCTCTCACGCCCTGCC----- 28001  
Db |||||  
Qy 29142 CGACGCCCTACCCCGCGTACCCGCGTGGCCGTACCGTCAGCGGTCACGACGCGTACC 29201  
Db |||||  
Qy 28002 -----CCAGGCGCCACGGA 28016  
Db |||||  
Qy 29202 GGCAGCGGTCCTTCCTTCGGGCGGAACCGTGTGATCACCAGCGGAACCGGTGCTCT 29261  
Db |||||  
Qy 28017 CACAGCGTCCCGCAGGCTCGGAGGACCGTCTCTATCAGGAGGACCGGACGCT 28076  
Db |||||  
Qy 29262 GGGCGGCTCGTGGCGCGGCATCTGTCGAGCGCACGCGTACGSCATCTGTTGCTGGC 29321  
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Qy 28077 CGGCGCCTGTCGGCGCGCGCTCGTCTGTAACACACGCGCAAGCACCTGCTCTCAC 28136  
Db |||||  
Qy 29322 GGGTGGCGCGACCGGACCGGAGGTCGCGCGAGTTGGGGCGGAGCTCGGTGGCT 29381  
Db |||||  
Qy 28137 CTCGCGCAGGCGGAGCGCTCCGGGTGCTGATGTTTCGAGCGAGCTCGAAGCTCT 28196  
Db |||||  
Qy 29382 CGGCGCAGCGTGGAGTGTGTCGCTCGACGCGCGGACCGGACGAGCTGGCGGACCT 29441  
Db |||||  
Qy 28197 GGGGCTTTGCTACCTTCGCGCGTGGAGCGTGGCCGATCACCGCTCTAAAGGACCT 28256  
Db |||||  
Qy 29442 GCTGACCGGATCCCGACGATCGGCGCTGACCGGTGCTGTCGACAGTGGGATCCT 29501  
Db |||||  
Qy 28257 TCTGATTAACATTCGAGCGCTACCCGGTCCGCGCGCTGTCGATCGCGCAGGCTCT 28316  
Db |||||  
Qy 29502 GGACGACCGGTGATCAGTGTGCTCGCGGAGCGGCTCGGGGCGCTCTCCCGGCGCA 29561  
Db |||||  
Qy 28317 CGACGGCATCTGCTCGCGCGCATGAGCCTCGAGCGGATCGACCGGCTTCGCCGCCA 28376  
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Qy 29562 GCGGACCGCTGGCTGCTTCGACGAGTGAAGCGCGCGGCGGAGCTGTGCGCTTCGT 29621  
Db |||||  
Qy 28377 GATGATCCCGCTGGCATCTTCATCAGTCACTCACCAGATAAGCCCTTCGCGCTTCAT 28436  
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Qy 29622 CATGTTCTCTCGGCTCGGCGTGGTGGTTCGCGCGGAGTGAAGCGGCGGAGCTGCTG 29681  
Db |||||  
Qy 28437 CCTTCTCGTCCGTCGCGCGGCTCCTCGGAGCTCAGTCACTCAACTACGCGGCTGC 28496  
Db |||||  
Qy 29682 CAACGCGCTCTCGACTTCTTGTCTCATCGCGCGCGGAGGCTGCGCGCTCTC 29741  
Db |||||  
Qy 28497 GAGCGCTTCTCGATGCGCTTCGCGCACACCGCGCGCGGCAAGGCTCCCTGCTCATC 28556  
Db |||||  
Qy 29742 TCTGCTGGGCGCTGTGGAGAGGCGCACAGGATGACGGGCCACCTCGACGTCGACGA 29801  
Db |||||  
Qy 28557 GCTCGGTGAGCCACTGGGCGGAGCGGCAATGACAGACGACGTCAGCGCGCGCG 28616  
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Qy 29802 CCATGCGGATCAGCGCGGGAATGCGGCGCTGCGGCTGCGGAGGCTCTGGGCT 29861  
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Qy 28617 GCGCCCTCGATGAGCGCGCGG---CCTTCTCTCGACCTCTGAGGAGAGGCTCGCCCT 28673  
Db |||||  
Qy 29862 GTTCGACGCGGCTTGGCGGAGCGGCTGCTGATGCGGCTCGGCTCGACCTCAC 29921  
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Qy 28674 CTTCGATGCGGCTTCTTCGNAACGAGACCGGCTGTTCGCGCGCTTCGACTTGAG 28733  
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Qy 29922 GCGGTAGCGTGTGTCGCGCTGCGCACCGGTGCGCGCTGTGTCGAAGTGTGCTTCA 29981  
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Qy 28734 GCGGTACGGGCGAAGCGCGGAGC-----GTCCCCCGTGTGTTCCAAAGTCTCGTCCG 28787  
Db |||||  
Qy 29982 GCTGCTCGTTCGCTCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30022  
Db |||||  
Qy 28788 CGCTGCGACCATGACGAAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 28828  
Db |||||

RESULT 5  
US-08-456-837-6  
; Sequence 6, Application US/08456837  
; Patent No. 5643774  
; GENERAL INFORMATION:  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James M.  
; APPLICANT: Beck, James Joseph  
; APPLICANT: Hill, Dwight Steven  
; APPLICANT: Ryals, John Andrew  
; APPLICANT: Gaffney, Thomas Deane  
; APPLICANT: Lam, Stephen Ting  
; APPLICANT: Hammer, Phillip E.  
; APPLICANT: Uknes, Scott Joseph  
; TITLE OF INVENTION: Genes for the synthesis of  
; antipathogenic substances  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ciba-Geigy Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/456.837  
; FILING DATE: 01-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/457,205  
; FILING DATE: 01-JUN-1995  
; APPLICATION NUMBER: 08/258,261  
; FILING DATE: 08-Jun-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8614  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28958 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-456-837-6

Query Match 10.2%; Score 3140.6; DB 1; Length 28958;  
Best Local Similarity 54.1%; Pred. No. 0;  
Matches 8239; Conservative 0; Mismatches 6284; Indels 698; Gaps 63;  
Qy 14872 ACAGACCCCATCAACCCCGCTCGGTGATGTCCTCGTGGCAAGTCTCGCAGGAGCGAGAC 14931  
Db 14236 ACTGCCCTCGCTCGTTCGCTTGCAGAGACCTCTCCCTCCCGCGCGCGAGCGAG 14295  
Qy 14932 GAAGAGCTGTTCGCGCTGGTTCGACCCATCGCGCCGCTGTGCTGGGCGCATGCCACTCCC 14991  
Db 14296 CGCGTCTCTCGATCTCGTCCGACCGACCGACCGCTCCGCTCGCTCGCTCGCTTC 14355  
Qy 14992 GAAGTATGCTTCGGAACAGGCGCTTCAAGAGCTGGGTTTGTATTTCTCTCGCGCAATT 15051  
Db 14356 GAATCGCTCGATCCCATCGCCCTCTCAAGAGCTCGGCTCGATTCCTCATGGCCCTC 14415

Qy	15052	CAGCTTCGTAATCGACTGCTGTCTGTGACGTTTGACCTCGCGGCTTCGGGCGCACGCTGATCTTC	15111
Db	14416	GAGTTCGGAATCGACTCGCGCGCGCGCGCGGCTCGGCTCGAGCTACTCTCCTCTTC	14475
Qy	15112	GATTACCCCACTCCGATGGCGCTTTGCCAGTTTCCTCCGGGCGCGATCGTCGGAGCGGAC	15171
Db	14476	GACTATCAACCCCGCATCGCGCTCTCAGCTTTTTTTCACGACGATCTCTTCGG---GGGA	14532
Qy	15172	ACAGGCACGACCACTCGTCTCTGCGCTAACTGCGGTTCCCGCGCGACGAGCCGATCCCAATC	15231
Db	14533	ACCACCACCGCCCCGCGTACCGCTCACCCCGGGGGGAGCGAGACCTATCCCAATC	14592
Qy	15232	GTCCGCATGCGCTGTTCGGTACCCCGGTGATGTACGACCGGTTCATGATCTCTGGCAGGTG	15291
Db	14593	GTGCGATGAGTTCGCGCTTCCCGGCGACGTGCGACGCCGAGGATCTCTGGAAGCTC	14652
Qy	15292	GTCAGTGGTGGCCATGACGGATGCGGCGATTTCCGACAAACCGTGGGTGGACCTCCGAC	15351
Db	14653	TTGCTGACCGGACAAGATGCATCTCCGCTTTTCCCAAAATCGCGGCTGGAGTCTCGAT	14711
Qy	15352	ACGCTGTAAACCGGACCCGACCAACCGAAACGAGCTACACCGGAGCGCGGATTC	15411
Db	14713	CGGCT-----CGAGCGCCCGTCTCCAGTCCGGAGGGGGCTTC	14757
Qy	15412	CTTTACGACGACGCAATTTTCGATCCCGACTTCTTCGGTATCAGTCCGCGTAGGCACTG	15471
Db	14758	GTCTACGACGACAGCGCTTCGATCCGGCTTCTTCGGGATCAGTCCACGTAAGCGCTC	14817
Qy	15472	GCGATGACCCGACGACGCGCTGCTCTGGAACAGCGTGGGAGGACATCGAACACGCC	15531
Db	14818	GCGGTGATCCCAACAGCGCATTTTGTCTCGAGATCACATGGGAAGCCTTCGAGCGTCA	14877
Qy	15532	TGCAATCAACCCCGACAGCCTCGTGGCACACCAACCGCGCTTTCGCGGGCTGCCTAC	15591
Db	14878	GCGATGACCCGCGCTCCCTCAAGAGACCAAGCGGGTCTTCGTTGGCGTATGGCAG	14937
Qy	15592	CAGCACTACGCGCGCTTTTCCACAGCTCCGGCAGGGTTTCGAGGGGTATCTCGGGCAC	15651
Db	14938	AGCGACTACCAATGCATCGCTGTGTGAACGCGACTGGCGGAATACAAGGACTCGTTGCCACC	14997
Qy	15652	GGAAGCCAGGCAGTATCGCTCGGTGTGTGTGCTACGCTCTCGGCTCGGAAGGTCCG	15711
Db	14998	GGTAGCGCAGCGGT---CCGTCCGGCCGAATCGCATACACGTTTCGAGCTTCAAGGGGCC	15054
Qy	15712	GCCCTCAGCTGCACACTGCTGCTCTTCGTCCTCGTCTGCACCTGCGCCGTGTCCAG	15771
Db	15055	GCCATCAGCGTGGAGACGGGTG---AGCTTCTCGTCCGGTTACCTCGCTCGCCAG	15111
Qy	15772	GCGTCCGGTCCGCGAGTGTTCATGCGCCCTCGCGGTTGGCGTCACGGTGATGTCACCC	15831
Db	15112	GCCCCCCCCACGCGCAATACTCCCTGGCGCTCGCTGGCGGGTGACCATCATGGCCACG	15171
Qy	15832	CCGGCCGGGTTCGTGGAGTTTTCGGCGCAGCGGGGCTCGCGTGGACGGGCGGTGCAAG	15891
Db	15172	CCAGCCATATTCATTCGCGTTTCGACTCCGAGAGCGCGGTTGCCCGCGAGGTCTCGCAAG	15231
Qy	15892	GCGTTCTCGCAGCGGTGACGCAACCGGCTGGGGTGGGGTGTTCGGAATGCTGCTGGTG	15951
Db	15232	GCCTTCTCGCGGAGCGCGAGGTTCGCGCTGGCGCGAAGCGCGCGGATGCTCTGCTC	15291
Qy	15952	GAGCGGTTCGACGCGCGCGGCTCGGTACCGCAATCTTCGCGGTGGTGGCTGGCAGT	16011
Db	15292	GAGCGCTCTCGATGCGGTCCAAACGGTTCATCCGCTCTCGCGTCTCTCGAGGCTCC	15351
Qy	16012	GCGGTCAATCAGGACGTTGCGACGACGCGCTGACGGCGCCCAACGGGCGTTCGACGAG	16071
Db	15352	GCGGTCAACAGGACGCGCGAGCCGAAGGCTTCACGCGGCCCAATGGCGCTCCGCCAGAG	15411
Qy	16072	CGTGTCACTCGCTGGCCCTGGCCAAACGGGACCTTCACCCCGCGAGTTCGATCGGTG	16131
Db	15412	CGCGTCACTCGGCAGCGCTTGACGACGCGCGGCTCACTCCAAAGGACGTGCACTGTGTC	15471
Qy	16132	GAGGCCACCGGCACCACTTTTGGGCGACCCGATCGAGGCGCCAGGCTCTCTCGCC	16191

[illegible]

Db 16414 CCCGCGCGCTCGTCGGGCACACAGCGGCGAGATAGCGCGCGCTTCGTGCGAGCGCT 16473  
Qy 17272 CTCACCTCACGAGCGGCACACCTCATCACCAAGCGGCACCTCATGCAAAACATG 17331  
Db 16474 CTCCTCTCGAGGACGCGCGCGCATCGCGCGCTTCGGAGCAAGCGTCACACCGTCG 16533  
Qy 17332 CCCCGGGGACCATGACCAACCTCTCACACCAACCCCGCCACCATCACCAACCTCATC 17391  
Db 16534 CCGGCAACGGGCAATGGCGCGCTCGAGCTCGCGCGCTTCGACCTCCAGACCTACCTCGCT 16593  
Qy 17392 GCCACGAAAGACCTCGGCATCGCGCATCAACACCCCACTCCCTCGTCATCAGC 17451  
Db 16594 CCCTGGGGGACAGGCTCTCCATCGCGCGCTCAACAGCGCCGAGCAAGCTCGATACC 16653  
Qy 17452 GGCACCCCGCACACGCTGCAACACATCACACCTCTCGCAACCAAGGATCAAAACC 17511  
Db 16654 GCGAGCGCGCGCTCGAGCGCTGATCGACTCGCTCACCGAGCGAGTCTTCGCC 16713  
Qy 17512 AAACCTCTCCCAACAAAGCGCTTCACCTCCCGCCACCAACACCCCATCTCAACCA 17571  
Db 16714 CGAAGAGTCGCGCTGAGCTAGCGCTCCCACTCAGCGCCAGATGGAGCGCGTCCAAGACG 16773  
Qy 17572 CTC-----CACCAGACACCAACCTCCTACCTACCAACCAACCAACCCCTC 17622  
Db 16774 TCGCGCGAGGTCTAGCCAAACATTCGCTCTCGAGCTGCGAGCTCCCTCTTTATTCGACC 16833  
Qy 17623 ATACCGCGCAACACCCCGACCAACTCTCACCCCGCACTACTGACACCAACAGCC 17682  
Db 16834 GTACCGGACCAAGCTCGAGCTCGAGCTCGAGGCGGTACTGTATGGAACCTC 16893  
Qy 17683 CGCAACACGCTGACTAGCGCAACACCAACCTCCCAACACCGGCTCACAC 17742  
Db 16894 CGGCAACCGCTCTTCTCGAGCGGACCGAGCGGCTCTCGAGATGGGATCGCTTC 16953  
Qy 17743 TACATCGAATCGGACCGACCAACACCTCAGC---CAGCTCACCCACCAACCTCCC 17799  
Db 16954 TTCTGCGAGGTGAGCGCTCTATCCCGTCTAGCTCGCTCGCGGAGACCTGGAGCGC 17013  
Qy 17800 AACACCCCGCACACACCTCACCTCACCAACCCCGCACCAACCCCAACACCTC 17859  
Db 17014 TCACCGCTCGATCCGTCGTGCTGCTCATTCAGCGGAGGAGGCACTCCCGCT 17073  
Qy 17860 CTCACCACTCGCCAAACCAACCACTGAGACCTGAGACCCCGCACTACCAACCAAC 17919  
Db 17074 CTCTTGTCTCTTGGCGGAGCTCTATGGCGGCGCTCACGCCGAGTGGAGGCTTC 17133  
Qy 17920 AACCAACCCACACCAACCTCACCTCGACCTCCCGCACTACCTTCGAACACGAC 17979  
Db 17134 TTGCGCGCTTCTGCTCCCGCAAGGTCTCACTCCCGCACTAGCGCTTCAGCGGAGCGT 17193  
Qy 17980 TACTGGCTCGAAAGCACACAGCGGCTCGGATCGGTTCCGGTTCCGGGCGG 18039  
Db 17194 TTCTGGCTCGAGCGCCCAACGACACCCGNA-----GGGCTCGCTCCCGCTCG 17244  
Qy 18040 GAGGAGCTCGGGGGGACGCGAGAGTGGAGTTCGGGTTCTGGGACCGGTTGGCGCGC 18099  
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Qy 18100 CAGGACCTGGAAACGCTCGGACCACTCGCGCTCGCGCTCGCGCTCGGACG 18159  
Db 17305 CAGCTCC-----ACCGGACGCGGACGAGCGCGCGCTTCGCGCTG 17349  
Qy 18160 GTGGTGGCGGACCTCTCGCTCGGACCGCGCAACCAACAGCAAGCGCGATCAACAC 18219  
Db 17350 CTCCTCCACCTCTGAGCTTTTACCACAGCGCCGAAGAGAGAGACCGGTTCGACAC 17409  
Qy 18220 TGGACCTTACGAGAAACCTGGAACCTCTCACCTCCCGCAACCA-----CCCAACCAAC 18276  
Db 17410 TGGCGCTACCGATCACGTGGAGGCTCTGACCAACCGCGGCAACCGCGGACCTCGCC 17469  
Qy 18277 CAACCTTGGCTATCGGCTATCCCGAAACCGAGACCAACCGCGGATCAACCAATC 18336  
Db 17470 GGCACCTGGCTCTGCTGCTCGCTCGCGCTCGCGGACGAGCGGCTCTCTGCGCAACGCTC 17529

Qy 18337 CTCACCAACCTTCACACCAACCGCATCACCCCATCCCTTCCCTTCAACCAACCAACCCAC 18396  
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Qy 18397 ACCAAACCCCAACACTTCCACCAACCGGACAAAGCCCAAAACCAACCAACCGGACCC 18456  
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Qy 18457 ATACCGGCTGCTCTCCCTCTCGCTCGCTGAGCAAAACACCCACCCCGCCACCCAC 18516  
Db 17647 ATTGCGGCGTGTCTCTCTCTCTCGCTGAGCGCGCCCTCTCGGAGCACTGCGGCC 17706  
Qy 18517 ACACCAACCGGACCTCTCTCAACCTCACCTCACCAACCAACCAACCAACCAACCCCA 18576  
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Qy 18637 ACACACCCCAACGAGCCCAACCTGCGGACTCGCGGACCAACCTCTCTCTCTCTCTCTCT 18696  
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Qy 18757 CTCAACCAACCTCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCGGC 18816  
Db 17947 TTGCTCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18006  
Qy 18817 ACCACACCGCGGCTCTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCC 18876  
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Qy 18937 CACCACTCTACCAACCAACCAACCAACCAACCAACCTCTCTCTCTCTCTCTCTCTCTCTCT 18996  
Db 18127 CGATGGCT---CGCTCGAAAGGCGCTGAGCACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18183  
Qy 18997 CACACCCCGCACGACCAACCTCACCAACCAACCTCAACCAAAAGGATCCACTCACC 19056  
Db 18184 CAGCGCGAAGCGCGCTGAGCTCACGCGAGCTCACCGCGCTCTCTCTCTCTCTCTCTCTCTCT 18243  
Qy 19057 ATACCACTCTCGACACCAACCAACCAACCAACCTCTCAACCAACCTCTCTCTCTCTCTCT 19116  
Db 18244 TTGCGCGGCTGATGTCTCGGACGAGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18303  
Qy 19117 CCACAAACCCCG---TCACCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19173  
Db 18304 GCGGAGGCGCACAGGTGAGCGCGCTTTCACGCGGCGGCACTCGAGCGCCACCGCTCTCTCT 18363  
Qy 19174 CTACCAACCTCACCCCGCAACCAACCTCAACCAACCTCTCTCTCTCTCTCTCTCTCTCTCT 19233  
Db 18364 CTGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18423  
Qy 19234 CACCTCTCTCAACCAACCTCAACCAACCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19293  
Db 18424 AGACACCTCTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18483  
Qy 19294 GCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19353  
Db 18484 GCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18543  
Qy 19354 GAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19413  
Db 18544 GATGCGCTGCGGAGCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18603



QY 19414 ACCTGGCAAGGAAACGGACTGGCGACTGGTCAAGTCAGCGAACATCTCCGCGCGCGGG 19473  
DB 18604 GTGTGGGCGGGGGGATGGCTACCGGGCTCTGGCAGCCAGCTAGAGCAACGGGT 18663  
QY 19474 ATGTTTGGCATTGCGCCCGAGTTGGCGGTCAAGCTTTGACGGCGGATCGCGAGCGGG 19533  
DB 18664 CTGTGGCGATGGCCCGCTCGTGGCCGTGGCGAGCTCGGCGTGGCGCTGGAGCAGAC 18723  
QY 19534 CGCCGAGTCTCTCGTGGCGGATATCGACTGGAGAAATTTGGGACCGGTTCTCCAGC 19593  
DB 18724 GAGACACCCCTACCGTGGCGGACATCGATGGGCGCGCTTTGGCGCTTCGTTAGCGCC 18783  
QY 19594 AAGTCGTGGTCTTCTCGAG---GACCTTCCAGGACACAGGAACTGAGAGGCGCGC 19650  
DB 18784 GCTCGCTCCCGCGCTCTCGCGGATTTGCCGAGGCGGAGCGGCTCTCGAAGCCAGC 18843  
QY 19651 AG-----TACGTTGAGCAGCAGGAGAGCAAACTCTCGGCACTCTCATGGGTGG 19704  
DB 18844 GCCGATGGTCTCTCGAGCAAGACGGGCGCCACAGGCTCTCTCGAAGCTCCGAAACCGC 18903  
QY 19705 TCAGTTCCGAGCAGGAGAGAGTGTCTAGCTCGTCTCGCATCCACTCCGCGCGAGTG 19764  
DB 18904 TCGGAGCGAGCAGATCCACTGTCTCTCTCGTGGTGGCGCCACGAGCGGCGCTCGTC 18963  
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QY 19825 GACTCGTTGGCGGGTGGAGTTTCGCAACCACTCTCGCAGCAGCAGAGCTGGTCTG 19884  
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QY 19987 CGACCCCGGCGAGAGCTCGATGAGCGATCGCCATCGTTGGATGGCTGTGCTTCCCC 20046  
DB 19204 GCGTCTCTCGGCGAGCGAGCGCCATCGCCATCGTGGCATGGCCCTCGCTTGGCG 19263  
QY 20047 GCGGAGTGACTCGGCGGAGCTTCTGGGATCTGATCTCTCTCGAGCAGCGCGATC 20106  
DB 19264 GCGGCGATCGGCGATGTCGAGCTCTTTGGGAGTTCTCGCCCAAGACGCGACGCGCTC 19323  
QY 20107 GCGGATTTCCCAACCGACCGGCTGGGACCTGGACAGCTCTACGACCCCGACCCCGAC 20166  
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QY 20167 CACCCCGGCACTGTCTACCCGAAACGGCGGATTTCTTACGACGAGGCGCATTTGAC 20226  
DB 19381 GCCAAGGCCAAGAGCTACGTCCGCGATCGCCGCATGCTCGACCGAGTGCATCTTCGAT 19440  
QY 20227 GCGGATTTCTGGCATCAGCCCGCGGAGCCCTCGCCATGGACCCCGACGAGCTC 20286  
DB 19441 CCGTCTTTTGGCATCAGCCCTCGAGGCGGCAAAATACCTCGACCCCGACGACCGGCTG 19500  
QY 20287 CTCCTCGAAACCGCTCGGAAACCATCGAAACGCGCGCATCAACCCCGACACCTCCAC 20346  
DB 19501 CTCCTGATCTGCTGTGGCTCTGAGGAGCGCGCATCGTCCCTCACCTCTAAG 19560  
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DB 19738 TCCTCTCGTCTGTCGCGCTCGACCTCGCTGCGAAGCCCTTCGACCAACCGCGAGTGAAC 19797  
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Qy 27703 GTGACTGCGCTCGGGTGGAGAACTGACCTGACGCGACCGTGTGTGATCCCGCACACC 27762  
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Qy 27763 GAGGACGTGACGTTGCAAGTCACTCGGCGAGCGGATGAGGTGGCCATCGCGCGCTC 27822  
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Qy 27823 GCGATTCACCTGTAATCTCGGCAACCGCTGCTGCGGCGACCGGAGTGGACCGCTCACGCG 27882  
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Db 26985 -----CGGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 27036  
Qy 28003 GGTGATAGGCGGCGGACTCGGACATCGCTTACGCGCGCGCTTTCGAGGGGCTGC-AGC 28061  
Db 27037 GCAGCGCTCGAGAG---CGCTGGGCTTGTCTTATGGCGCGAGTTCCAGGGGCTTCGCGCG 27093  
Qy 28062 CGCTGAGGTTTCGCGGACGATGTCTTGGCGGAGGTGGGTGCGGCGGAGGCTCTCGG 28121  
Db 27094 CGTCTAAGCGCGCGGACGAGCTCTTTCGCGGAGCAAGCTTCCCGGACGCGCG----- 27147









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Db 17827 GCCATCCACCAAGCCCATGATCTGGGGCTTGGGCGGCTCGTGGCTCGAGCACCC 17886  
Qy 18697 ACCCAACGCGCGGAATATGACCTTCCCAACACCCCAACCCCAACCTTCAACAC 18756  
Db 17887 GAGCGGTGGGCGGCTCGTGACCTCGCGCAGCGCTCGACGCGAGCGCGCAGCGCGC 17946  
Qy 18757 CTCACCCAAACCTCACCCAAACCCCAACCAACCAACCAACCAACCAACCAACCAAC 18816  
Db 17947 TTGCTCCCGGCGCTCGCCAGCGCCACGACGAAGACCAAGCTCGCGTGGCGCGCGCGC 18006  
Qy 18817 ACCCAACGCGCGCTCACCCCAACCAACCTCACCCCAACCAACCAACCAACCAACCC 18876  
Db 18007 CTCTAGCAGCGGCTTGTGCGGCGCGCTCGGGATGCGCTGCGGCTCGCGGCTTC 18066  
Qy 18877 ACCCCCAAGGAACCAACCTTATCACCGCGGAACCGCGCGCTCGCCACCAACCTCAC 18936  
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Qy 19354 GAGCGCTCGCCACACCGCCACACCAACCTTCCCGCCACCAACCTTCCCGCGGCG 19413  
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Qy 19414 ACTTGGCAAGGAAGGAGCTGGGCTGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 19473  
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Db 17014 TCACCGCTCGATCCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 17073  
Qy 17860 CTCACCAACCTTCGCCAAACACACACACCTTCGACACCCCAACCTTCGACACCCAC 17919  
Db 17074 CTCCTTGCTCTCTTGGCGGAGCTCTATGGCGGCGCTTCAGCCCGAGTGGAAGGCTTC 17133  
Qy 17920 AACCAACCCCAACACACACCTTCGACCTTCGACCTTCGACCTTCGACCTTCGACCTTC 17979  
Db 17134 TTGGCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 17193  
Qy 17980 TACTGGCTCGAAGACACACACCGGGTTCGATCCGCTTCGCTTCGCTTCGCTTCGCTTC 18039  
Db 17194 TTCTGGCTCGAGCCGCCCAACGACACACCCCGAA-----GGCGTCTCTCCGCTCGC 17244  
Qy 18040 GAGGGAATGGGGGGGAGCGACGAGGTGGAGTGGCGTTCGCGGAGCGCGTGGCGCGC 18099  
Db 17245 CGATCGATGGCGGTTTTTGGCAAGCAATCGAACGCGGGGACCTCGACGCGCTCAGCGGC 17304  
Qy 18100 CAGACCTTGAACAGGTTCGCGACACGTTCGCGTTCGCGTTCGCGTTCGCGTTCGCGTTC 18159  
Db 17305 CAGCTCC-----ACGCGACGCGGACGAGCAGCGCGCGCGCTCGCCCTG 17349  
Qy 18160 GTGGTGGCGGACTCTCGCTGGGACCGGACCGGACCGGACCGGACCGGACCGGACCGG 18219  
Db 17350 CTCCTTCGACCTCTCGAGCTTTTACCACGAGCGGCGGCGGCGGCGGCGGCGGCGGCG 17409  
Qy 18220 TGGACCTTACGAGAACTTGAACCCCTTACCTTCCCGACCA-----CCACCAACCCAC 18276  
Db 17410 TGGCGCTACCGATCAGCTGGAGGCTCTGACACCGCGCGGCGGCGGCGGCGGCGGCGG 17469  
Qy 18277 CAAACCTGGCTATCGCATCCCGGAAACCCAGACCCACCCCGGACCATCACAACATC 18336  
Db 17470 GSCACTGGCTCTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 17529  
Qy 18337 CTCACCAACCTTCACACACCGGATACCGGCTACCGGCTACCGGCTACCGGCTACCGG 18396  
Db 17530 ACCGATGGCTTACCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17589  
Qy 18397 ACCAACCCCAACACTCTCACACACCGGACCAACGAGCGGCGGCGGCGGCGGCGGCGG 18456  
Db 17590 ATAGCGCGGCGGCTCTACCGAGACCTGCGGAGGCTGTTGCGGAGCTGCTGCTGCT 17646  
Qy 18457 ATCAGCGGCTGCTCTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 18516  
Db 17647 ATTGCGGCGTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 17706  
Qy 18517 ACACCCACCGGACCTCTCTAACTCTACCTCTACCTCTACCTCTACCTCTACCTCTACCT 18576  
Db 17707 CTGCGCGGCGGCTTGGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 17766  
Qy 18577 CCAACCCCTCTGCTAGCGACCAACCAACCGGACCAACCGGACCAACCGGACCAACCGG 18636  
Db 17767 GAGGCTCTCTGCTGCTCTTACGCGGCGGCGGCTCTGCTGCTGCTGCTGCTGCTGCT 17826  
Qy 18637 ACACACCCCAACCAACCGGACCAACCGGACCAACCGGACCAACCGGACCAACCGGAC 18696  
Db 17827 GCCATCCACCAACCGGACCAACCGGACCAACCGGACCAACCGGACCAACCGGACCA 17886  
Qy 18697 ACCACACCGGCGGATCATGACCTCTCCACCAACCGGACCAACCGGACCAACCGGACCA 18756  
Db 17887 GAGCGGTGGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17946  
Qy 18757 CTCACCAACCGGCTCACCAACCGGACCAACCGGACCAACCGGACCAACCGGACCAAC 18816  
Db 17947 TTGCTCCCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 18006  
Qy 18817 ACCACACCGGCGGCTCACCGGACCAACCGGACCAACCGGACCAACCGGACCAACCGG 18876  
Db 18007 CTCTACGACCGGCTTCTGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 18066

Qy 18877 ACCCCACGAAACCACTCATCAGCGGGAACCGGCGCTTCGCGACCCACCTCAC 18936  
Db 18067 ATGCCCCGAGCACCATCTCATCAGCGTGGTATCAGCGGCGCATTTGGGCTCACGTCGC 18126  
Qy 18937 CACCACTTACCAACCAACCAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18996  
Db 18127 CGATGGCT---CGCTCGAAAGGCGTGAGCACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18183  
Qy 18997 CACACCCCGGACGACCAACCTCACCACTCAACCACTCAACCACTCAACCACTCAACCT 19056  
Db 18184 CAGCCGAAGCGCGGTGGAGCTCACGCGAGCTCACGCGGCGGCGGCGGCGGCGGCGGCGG 18243  
Qy 19057 ATCAACCACTTGGACACCAACCAACCACTCAACCACTCAACCACTCAACCACTCAAC 19116  
Db 18244 TTGCGCGGTGGATGTGCGGACGAGGCGCTTCTGCGAGCTTCTGCGAGCTCTGAC 18303  
Qy 19117 CCACAAACCC---TCACCACTCATCCACCGGACCTCTCTCTCTCTCTCTCTCTCTCT 19173  
Db 18304 GCGGAGGCGCACAGGTGAGCGGCTTCCACGCGGCGGCGCATCGAGCCCAACGCTCCG 18363  
Qy 19174 CTACCAACCTCACCCCGGACCACTCAACCACTCAACCACTCAACCACTCAACCACTCA 19233  
Db 18364 CTGCGCGCACTCTCATGAGGATCTGCGGAGGTCTCTCGGCAAGGTACAAGGTGCA 18423  
Qy 19234 CACCTCTTCCACCACTCACCAACCAACCACTCAACCACTCAACCACTCAACCACTCA 19293  
Db 18424 AGACACTTCCAGACTTCTGCGCTCTGAGCCCTCGAGGCTTGTCTCTCTCTCTCTCTCT 18483  
Qy 19294 GCGCGCGCACTTTGCGGCGACCGGCGCAAGCCAACTACGCGGAGCAACGCTTACCTC 19353  
Db 18484 GCGCGGTCTGCGGCGGCGGCGGCAACAGGCGCTATGCGCTGCGCAACGCTTCTCTC 18543  
Qy 19354 GAGCGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19413  
Db 18544 GATGCGTGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18603  
Qy 19414 ACCTGGAAGAAACGAGCTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19473  
Db 18604 GTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18663  
Qy 19474 ATGTTCCGATGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19533  
Db 18664 CTGTGCGGATGCGCGCGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18723  
Qy 19534 GCGCGGAGTCTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19593  
Db 18724 GAGACCACTTACCGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18783  
Qy 19594 AAGTCTGCGGCTTGTCTGCGG---GACCTTCCCGGCGGCGGCGGCGGCGGCGGCGG 19650  
Db 18784 GCTGCTTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18843  
Qy 19651 AG-----TACGTTGAGCAGACGAGGAGCAAACTTCGCGGCAACTCTCATGGTGG 19704  
Db 18844 GCGGATGCTCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 18903  
Qy 19705 TCAGTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 19764  
Db 18904 TCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 18963  
Qy 19765 CTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 19824  
Db 18964 CTGGGCGATACCGAGGCTCCAGGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19023  
Qy 19825 GACTGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19884  
Db 19024 GATTGCTCATGACCGTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19083  
Qy 19885 CCGAGGAGTCTGCTTCTGATACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19944  
Db 19084 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 19143



Qy	19945	GAGATCGGAGTTTCAGCCCGACA-----ACTCAACTCCGTTCCG	19989
Db	19144	TCGTCGCCCAACGCGCTTCGCGCGAGGCTCTCGTCGAGCGGACGCGCGCGCTCCG	19203
Qy	19987	CGACCCCGGACAGAGCTCGATGAGCCGATCGCCATCGTTGGCATGGCCTGTGCTTCGCC	20046
Db	19204	GCGGTTGCTTCGGGAGCAGAGCCCATCGCCATCGTCGGCATGGCCCTTCGCGTTGGCG	19263
Qy	20047	GGCGGAGTGACCTCGCGGACGACTTCTGGGATTCGATCTCTCTCGGAGCAGGACCGGATC	20106
Db	19264	GSCGGCATCGCGATGTCGACGCTCTTTGGGAGTTCTTCGCCCAAGGACGCGACGCGTC	19323
Qy	20107	GGCGGATTCGCCACCGACCGCGGCTGGACCTTGGACACGCTCTAGACCCCGACCCCGAC	20166
Db	19324	GAGCCCATTTCCCATGCCCC--GATGGGATGCGCGTGCCTCTAGGACCCCGACCCCGAC	19380
Qy	20167	CACCCGGCACCTGTCTACACCCGAAAGCGGATTCCTCTAGGACGAGGACACTTCGAC	20226
Db	19381	GCCAGGCCAAGAGCTACGTTCGGCATGCCGCATCTCTGACGAGGTGACCTCTTCGAT	19440
Qy	20227	GCCGAATTTCTTGGGCATCAGCCCCCGCGAAGCCCTCGCCATCGCATCGACCCCGACGACTC	20286
Db	19441	CCTGCCCTCTTTGGCATCAGCCCTCGGGAGGCCAATACTCTGACCCCGACGACGCGCTG	19500
Qy	20287	CTCTCTGAACCCGCTTGGAAACCATCGAACACGCGGATCAACCCCGACACCTTCAC	20346
Db	19501	CTCTCGAATCTGCTTGGCTTGGCCCTCGAGGACGCGGATCGTCCCTCCACCCCTCAAG	19560
Qy	20347	GGCACCCCGACCGAGTCTTACCGGACCAACGAGCAGGACACGCGGCACACATCCGT	20406
Db	19561	GATTTCTCCACCGCGCTTCTGTGCGCATCGCGCCAGCGAATACGCACTGCGAAGC---	19617
Qy	20407	CAGGCCCCGAGCGGTACCGAGGATTCGTCTTGACCGGGGAGCCACAGCATCGCCTCC	20466
Db	19618	ACGAGCTCCGAAAGGTTCGAGGATATGCCCTCAAGGACACCGCGGGTCTTTTGC	19677
Qy	20467	GGCCGAATCTCTACATCTCTCGGTTTGAAGGCGCTGCGGTCAACCTCGACACGCGTGT	20526
Db	19678	GGCGGCTTGGCTTACACGCTCGGCTGCAAGGCGCGCGCTCTCGTTCGACACGCGCTGC	19737
Qy	20527	TCTCTCTCGTCTGTCGCTTGCACCTTCGCTGCGAGTCCCTCAGTCTCGGTGATGCAAC	20586
Db	19738	TCTCTCTCGTCTGTCGCTTCCACCTCGCTGCCAAGCCCTCCGACAGGCGAGTGCAAC	19797
Qy	20587	ATGCGCTTGGCCGGGCGGACGCTCATGACACCGCCGATCACCTTCACCGAATTCGCC	20646
Db	19798	CTGCGCTTCGCGGGGCGTCTCCGTATGGCTCTCCCGGGCTCTTGCTGCTCTTTCC	19857
Qy	20647	CGCAACGCGGACTCGCCCCCGACGGCGTTGCAAGGCGTTCTCGCGCGCGGCTGACGGT	20706
Db	19858	CGCATGCTGCTTTGGCGCCGATGCGCGCTCCAAGACCTTCTCGACCAACGCGGACGCG	19917
Qy	20707	ACGGCTGGGGTGAGGGTGTGGGATGCTGTGTGTGAGCGGCTCTCGACGCGCGCGCG	20766
Db	19918	TACGGAACGCGGAGAGGGCGTCTGCTCTTGGCCCTCGAGCGGCTCGGGACGCGCTCGCC	19977
Qy	20767	AACGGTCACCGTCTCTGGCGGTGGTGGCGAGTGGCGTCAACAGGACGGTGCAGC	20826
Db	19978	CGAGGACACCGCGTCTCTGCCCTCTGTTCGCGGACCGCCATGAACATAGAGGCGCGTGC	20037
Qy	20827	AACGGTCTGACCGCGCCCAACGGGCGCTCCCGACGCGGTATCCGCGACGCGCTTCGCC	20886
Db	20038	AGCGCATACCGCCCCCAATGSGACCTTCCACACGAGGTTCTTCGCGCGCGGCTCCAC	20097
Qy	20887	AACGGGACCTGACCCCGCGACGTGTGATGCGGTGGAGGCCCAACGCGACCGGACCACT	20946
Db	20098	GAGCGCCATATCGGCGCTTGCAGACGTTCGACGTCTGCAATGCAATGCGACCGGACCTCC	20157
Qy	20947	TTGGGCGACCCGATTCGAGGCCACAGGCCATCTCTCGGACCTACGGACAGGACCGTCCGCG	21006
Db	20158	TTGGGAGACCCCATCAGAGGTGAAGCCCTTGGCGCGCGTCTACGCGATGGGAGACCCGCT	20217
Qy	21007	AACGGGCGGTGTGGCTGGGCTCCGTCAAGTCCAACTCGGACACACAGCGCGCGGCG	21066

Db	20218	GA	AAGCCTCTCCTTCTCGGCGCACTCAAGACAACATTTGGCCATCTCTCGAGGCGCGCTTCC	20277
Qy	21067	GG	CTGGCCGGAGTGATCAAGATGTGTGATGGCCCTCCGCCACCGGACACTTCCACCCGACT	21126
Db	20278	GG	CTCGGGGCGTCCCAAGATCGTCGCTCCCTCGGCCATGACGCCCTGCCCCCACC	20337
Qy	21127	CT	CACGCGGATGAGCCGTGCGCGCATGTGGACTGTGTCGGGGTGCGGGTGACGTGCTG	21186
Db	20338	CT	CACACGACCCCGCGCAATCCCTGTATCGATGGGATGCGCTCGCCATCGACGTGCTG	20397
Qy	21187	AC	GGAGACGTGCCCTTGGGCCCG--CGGGAGGGGGCGCGCGGGGGGAGGAGTGCA	21243
Db	20398	GAT	GCACGAGGGCGTGGGGCCGCCACGAAGATGGGAGTCCCGCGCGCGCGCTCTTCC	20457
Qy	21244	TC	ATTGGCGCTAGCGGCACCAACGCCCACTCATCTCTCGAAGAAGCAACCGCGCCGAC	21303
Db	20458	GC	CTTCGGACTCTCCGGCACCAACGCCCACTTATCTCGAAGAGGCTCCCG-----C	20510
Qy	21304	GT	TCGGGGGACCAACCCGCCGACGAGGATGCGGTAGTGTGGCGAGGAGGCTGCTGCGGC	21363
Db	20511	GAT	CCCGCAGGCGAGCCACCGCGCACAGC-----TCGCGTCGCAGCGCTTCCCGC	20564
Qy	21364	AG	TCTGGGTGTGGCCGTGGCTGTGTGGCCAAAGTGCACGCGCGGCCCTTCGGGCCAG	21423
Db	20565	AG	GC-----TGGGCCGTGTCTGTTCGGCCAGGAGCGCGCGCTGCGGCCAG	20616
Qy	21424	GCC	AGGCCCTGCAGCGCCACCTCACCGACACCCCGCCTCGACTCGCCGACGTGGGA	21483
Db	20617	GCC	CAGGCTCGGACACACTCTTCGCCCAAGACACTCGCCCTGCGCGATGTAGCC	20676
Qy	21484	TAC	ACCTTCGCCACGCCCGCGCGTGTTCGACCAACCGCGCACCTCATCGCGCGAC	21543
Db	20677	TAC	TCGCTGCCACACCCCGGCTACCTTCGAGCACCGTTCGCGCTCTCGTGTCCACGAC	20736
Qy	21544	CG	GACACTTCTCGAAGCACTTCAGGCACTTCGGCGCAGGGGAACCCCAACCCGCGCTC	21603
Db	20737	CG	GAAGAGTCTCTTCGCGCTCGATTGCTTCGCCACGGAAGCGCCGCCCGGAGCACC	20796
Qy	21604	AT	CACAGCAGCGCCCAAGCGGGACCGGGACCGGGAGCGCGAGGAAGACCGCATTC	21663
Db	20797	GT	CGTGAACGAAGCGGAAG-----CCACGGCAAGTGTCTTTC	20835
Qy	21664	AT	TGCTTCGGACAGGGCACCAACGCCCGCATGGCCAGGGCTCTACCAACCCAC	21723
Db	20836	GT	CTTCTGGCAAGCTCGCAGTGGGAAGGATGGCCCTCTCCCTGCTCGATACCTCG	20895
Qy	21724	CC	GTTCGCGCGCACTCAACGACATCTGCACCCACTTCGACCCCACTCGACCA	21783
Db	20896	CC	GTCTTCGGGCAAGCTCGAAGCGTTCGAGCGCGCCCTCGCGCCCACTGTGACTGG	20955
Qy	21784	CC	CTCTCTCCCTCTCACCAACACACACGACACGACACGAGGACCGCGCGCA	21843
Db	20956	TC	GCTGCTCGGTGTCT-----CCGCGGAGGAGGGCGCGGCC	20994
Qy	21844	CT	GCTCAGCAGACCCCGTACGCCCAGCGCCCTCTTCGCGCTTCAGGTCGCCCTTCCAC	21903
Db	20995	CC	GCTCGACGGGTGCAGCTGGTTCAGCCCGGCTGTCTCGATGATGCTCTCGCT---G	21051
Qy	21904	CG	CTCTCACGACGGCTACACATACCCCCCACTACTACGCGGACACTTCCCTCGGC	21963
Db	21052	GCG	CGCTGTGGCGCTCCATGGCGCTCGAGCCCGACGCGGTGGTTCGGCCATAGCAGGCG	21111
Qy	21964	GA	ATACCGCGCCCACTTCGCGGCATCTCACCTTCACGAGCGCACCACTCATC	22023
Db	21112	GAG	ATCGCGCGCTGTGTGGCGGCGCTGTCTCGCTCGAGGACGCTGCGCAAGCTGTG	21171
Qy	22024	ACC	CAACGGCC---ACCTCATGCAACCATGCCCCCGCACCATGACCACTCCAC	22080
Db	21172	GCG	CTGGCAGCGCTGTGTGAGCTCGCGGCGCAGGGGGCCATGGCCGCGGTGGAG	21231
Qy	22081	ACC	ACCCCAACCATCACCACTCACCGCCCAACGAACGACTCTGCCCATCGCC	22140

Db 21232 CTGCGGAGGCGGAGGTGCGACGGCGCTTCAGCGCTATGCGATCGGCTCTCCATCGG 21291  
Qy 22141 GCATCAACACCCCACTCCCTCTGATCAGCGGACCCCGCACACCGTTCACACATC 22200  
Db 21292 GCGATCAACAGCCCTCGTTTACGACGATCTCCGCGAGCCCGCTGCGCGCCCTG 21351  
Qy 22201 ACCACCTCTGCAACAAACAGGCAATCAAAACCAAAACCCCTCCACCAACACGACCTTC 22260  
Db 21352 CTCGCGATCTGAGTCTGAGGGGCTCTTCGCGCTCAAGCTGAGTTAGACTTGCCTCC 21411  
Qy 22261 CACTCCCCCAACCAACCCCACTCCCTCAACCACTCCACGACACACCAACCCCTCACC 22320  
Db 21412 CACTCCGCGAGGTGAGTCTGATTCGCGAGAGCTCTCTGATCTCTCTGCTGCTGCTGAG 21471  
Qy 22321 TACCAACCAACCCCAACCCCTCTATCAGCGCAACACCCCAACCCGACCAACTC----- 22374  
Db 21472 CCGCGCTCGACGGCGGTCCGCTTCTACTCCAGGTGAGCGCGCGCGATCGACGGGAGC 21531  
Qy 22375 ---CTCACCCCACTACTGACCCCAACAAAGCCCGCAACACCGTCTGACTAGCCACCAACC 22431  
Db 21532 GAGCTCGACCGCGCTACTGTTACCGGAACCTTCGCGAGCGGTCCGCTTTCGAGACGCT 21591  
Qy 22432 ACCCAACCCCTCCACCAACAGCGGTCTCAACCTACATCGAACTCGGACCCGACCAACACC 22491  
Db 21592 GTGCAAGGCT---CCTTGCGGGAACATCGCTTCTTCGTGAGGTGAGCCCAAGTCT 21648  
Qy 22492 CTCACACGCTCACCAACCAACCTCCCAACACCCCAACCAACCAACCTCACCCTCACC 22551  
Db 21649 GTGCTGACTTGGCCCTTGACAGCTCTCGAAGCGTCTCGAGCGCTCGGCGCGGTGGTC 21708  
Qy 22552 CACCCCAACCAACCCCAACCCCACTCTCACCAACCTCGCCCAAAACCAACCAACCAACC 22611  
Db 21709 GGCTCTCTGTGAGGCGAGAGGGGATCTACGGCGCTCTCTGCTCTGCTCTTCGAGGTC 21768  
Qy 22612 TGGCAACCCCACTACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCTCGAC 22671  
Db 21769 TAGCTCAAGGCTTCGCCCTGATTTGAGAGAGATCTCTGCCCGCGGAGCGGTGCG 21828  
Qy 22672 CTCGCCACTAGCCCTTCGACACCAACCACTACTGCTCGAATCTACCACTACCGGCCCAACC 22731  
Db 21829 CTGCCCACTACTCCCTTCAGCGAGCGCTTCGTGCTCGAGCGCTCTCACGCGACCCGCC 21888  
Qy 22732 AGCCCGGTCAAAAGGCTTCTCGCGCTCGGCTCCAGACACCGCGAGTCTCGAGTCTCG 22791  
Db 21889 GCCGGGTCAACCACTTGCTCGCTCGAGGGC-----GTTCTGCGAGCCATCGAG 21942  
Qy 22792 GACCGGTGAACAGGAAGACCTCAGAGCTTCGCCGAACCTCGAATCGAGCGCTCT 22851  
Db 21943 AGCGGGAATATCGACGGCTCAGCGCGCAGCTCCACGTGGAAGCGGCGAGCGCGGCC 22002  
Qy 22852 GCTCTGGAACGGTGGTGGCGCACTCTCCGCTGGCAGCGCCCAACCAACCAACCAAGCC 22911  
Db 22003 GCGCTTGCCTGCTCTTCCCACTCCGAGCTTTCGCCAGCGAGCGCAAGAGCAGGCG 22062  
Qy 22912 CGCATCAACCTGAGCTTACAGGAACCTCGGAACCCCTCACCTCCCGACCAACCCAC 22971  
Db 22063 ACGTCTGAGCTGCGCTTACCGATACGTGGAAGCTCTGACCAACCGCACACGCGCC 22122  
Qy 22972 CAAACCCCA---CAAACCTGGCTCTACGCACTCCCGGAACCCAGACCAACCAACCCCAAC 23028  
Db 22123 GCCGACCTTGGCGGCACTTGGCTCTCTGCTGCTGCGCGCGCTCTGGAAGAGCGCGCTC 22182  
Qy 23029 ATCAACCAATCTCACCACCTCCACCAACGCGCATCACCCCATCCCTCTACTGTC 23088  
Db 22183 CCTCTCGGCTCACCAGCGCTCGCCCGCGCGCGCGCGCTCTCGCGTGGCGCTG 22242  
Qy 23089 AACCAACCAACCAACCCCAACCTTCACCAACACCTCCACCAACCCCTCCACCAACCGCAACAA 23148  
Db 22243 AGCGAGGCCACTTGAACCGGAGGCTCTGCGCGAGGCTCTGCGCGAGCTTGGCGAGCTTG----- 22295  
Qy 23149 GCCCAAAACCAACCAACCGGACCCATCAGCGGCTGCTCTGCTCTCTGCGCTCGACGAA 23208  
Db 22296 -----CGCGGAGACGGCGCGCTCGCGCGTGTCTGCTCTCTGCGCTCGACGAA 22347

Qy 23209 ACACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCTCTCAACCTCACCTCTCCCC 23268  
Db 23248 AGTCCCTCGCGGACCATGCGCGTCCGCGGAGCTCGCTTCTCGCTCACCTCGTC 22407  
Qy 23269 CAAACCCCAACCCCAACCCCAACCCCAACCCCTCTGTTGATGCGCACCAACCAACCGCCACC 23328  
Db 22408 CAAGCCCTCGGCGACATCGCCCTCGACGCGCTTGTGGCTCTTACCCGCGGCGCGTC 22467  
Qy 23329 ACACCCCAACCCCAACCCCTCACAACCCCAACCCCAACCCCAACCCCTGCGGAGCTCGCC 23388  
Db 22468 TCCGTCGAGCACTCCGACCCCATCGCCATCGCAGCGAGCGATGACCTGCGGCGCTGGGC 22527  
Qy 23389 CGCACCACTCTCTCGAAGACCCCAACCCCAACCCCGCGAATCATCGACTCTCCACCAACC 23448  
Db 22528 CGGTCTGGCTCTGAGACCCCGAGGCTGCGGAGGCTCTGCGAGTCTGCGGCGAGCG 22587  
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Qy 23509 CAATCGGCTCTCGACACGCGCACCAACCCCGCGCTCACCCCAACCAACCTCACCCTCACC 23568  
Db 22648 CAGCTCGCTCTCCCGCGCGGCTTCTAGCTCGCGCGCTCTCGCGCTCTCGCTCGGC 22707  
Qy 23569 CCACACCAACCAACCCCAACCCCAACCCCGCGAACCCTCATCACCGCGGAGCC 23628  
Db 22708 GACGCGCGCGCGCATCTTCAAGCCCGAGGACCTCTCTCATCACCGGAGGAC 22767  
Qy 23629 GCGCGCTCTCGCACCCCTCACCTCACCAACCCCAACCCCAACCAACCAACCAACCTC 23688  
Db 22768 GCGCGCTCTCGCTCAGCTCGCGCGATGGCT---CGTCGAGAGGCGGAGAGCACCTC 22824  
Qy 23689 CTCCTACAGCGGAAACCGCGCCCAACCCCGCGCACCAACCAACCTCACCAACCAACCTC 23748  
Db 22825 GTCTCTATCAGCGCGCGGAGGCGCGAGGCGCTCGAGCTCTCACCGCGAGCTC 22884  
Qy 23749 CAACAAAGGATCTCACCTCACCTCACCAACCTCGGACACCAACCAACCAACCAACCTC 23808  
Db 22885 ACGCGCTTGGCGCGCGCTCAGCTTTCGCGCTGTGATGTGCGCGAGAGGCGCTGTC 22944  
Qy 23809 CAACAACTCTCAACCACTCCCGCCCAACCAACCC---TCACCAACCTCATCACCAACC 23865  
Db 22945 GCCACGCTCTCGAGAGCTCGACGCGGAGGCTCGAGGCTCGCGCGCTCTCACCGC 23004  
Qy 23866 GACGCGTCACTCTTTCGCGCGCGTCTCGGAACCGATGCGGAATCTCTCTCTCTCGGT 23925  
Db 23005 GCGCGCATCGGCGCGCACTCGCTCGCGCCACCTCTCTCATGAGCTCGCGAGCT 23064  
Qy 23926 ACGCGAGGAGCAACCGCGCGCGCTCTCATGATGTTGCTGCGGACCATGAACG 23985  
Db 23065 GTCTCTGCAAGTCTTAGCGGAGGAACTCACAAG---CTGCTCGTCTCTCGACCC 23121  
Qy 23986 CTTGAACACTTCTCTCTCTCTCGCGCGCGCGCTTGGGCGAGCGGAATCAGTGC 24045  
Db 23122 CTGACGCTTCTGCTCTTCTCTGTCATCGACGCGCTCTGCGCGCGGAGCAACAGCC 23181  
Qy 24046 GCATCTCGCGCGCAACGCTACCTGAGCGGCTCGGAGCGATCTGACACACATGGA 24105  
Db 23182 GGATACGCGCGGAAACGCTTCTCGACGCGCTTGGCGCGAGCGCGAGCTCTTGA 23241  
Qy 24106 CTTCCGCGGATCATGCTGCGCGCGCTTGGCGCGGAAAGGCGATGTCGCGCGGTGAT 24165  
Db 23242 CAGCGGAGACGTCGCTGCTGCTGCGCGCTGCGGCGCGCGCTGCTGATATTACGCGG 23301  
Qy 24166 GCGGCTCATGTTACTGGAAGCGCGCATCTGCGGATGGAAGCAACGATGCGCTC 24225  
Db 23302 CCCCTGGCAGCCAGCTGGAGCAACGCTCTGTCGCGGATGCGCGCTCTGCTGCGCGCTG 23361  
Qy 24226 GCGGATTCATCTGCGCGCGCGAGGCGGCAATTCACACTGATCATCGCGGACATC 24285  
Db 23362 GCGCGCTCGCGAAGCGCTGAGCAAGAGAG---CCACGCTACCGCTCGCGACATC 23418

QY	24286	GA	CTGGAGCGCTTCGTCCCGCTTACCGCTCGACGCCACAGCCCGCTCATCGAGGAC	24345	Db	24460	CT	CGCCCTCGCGCGGGCGTGTGCTCATGTGTCTCCCGCCAGACCTTGTTCATCTCTTCC	24519
Db	23419	GA	CTGGCGCGCTTTGCGCTTTCGATCAGCGTCGTCTCGCTCCCGCGCTCTCTGCGACT	23478	QY	25426	CG	TACAGCGGGGTCTGGCGCGGACGGGGGTGCAAGGGCTATTCTGGCGGCTGCTCAGCGT	25485
QY	24346	AT	TCGGAGTTTCGCAAGCGCTCAGGAGCTGGAAGAGCTGCGTTCGACGGCAAGAGC	24405	Db	24520	CG	TTCGCGGCTTGGCGCGCCGACGGCGCTTCAAGACCTTCTCGGACAAACGCGACGGC	24579
Db	23479	TG	CCGAGCGCGCCCTCGAAGACAGAAAGGCGCTCTCTCTCGAGCACGGCCCGG	23538	QY	25486	AC	CGCTGGGCGCGAGGGTGTGGGATGCTGTGTGGAGCGGCTCTCCGACGCCCGCTCGC	25545
QY	24406	ACC	CACAGCTCAGCCGATTCGCGAGCTCTCTCCGTGAGCGATTGGCCCGCATGACGTCCTCA	24465	Db	24580	TAC	GAGCGCGAGAAGGGCTGTGTCTTTCCTTCGAGCGGATCGGCGACGCCCTCGCC	24639
Db	23539	CCCC	CCG-----ACCTCTCGACAAGCTCCGGAGCGCTCGGAGC	23580	QY	25546	AAC	GGTACCGTGTCTTGGCGCGTGTGTGGAGTGGGTCAACACGAGACGGTGGAGC	25605
QY	24466	AAG	CAGAACAGGTGTGTCTGGCTGTGATTCGGAACAGGATCTGACACGTTCTCGGCTT	24525	Db	24640	CG	GACACCGCGCTCTGTCTCGCGCGTGTGTGGAGCGGCGCATCAACACGACGGCGCGT	24699
Db	23581	GAG	AGCTCTGCTGTCTCGCGCGTGTGTGCGAGACGAGCGGCTCTGTCTCTCGGCCAC	23640	QY	25606	AAC	GGTGTGACCGCGCCCAACGGGCGCTTCCAGACAGCGTGTCTCCGTCAAGCGGCTCGC	25665
QY	24526	CG	TAAATCGGAAGGATCGAGGACCAACGAGCTTCCGCGACTCCGGCTTCGACTCGCTG	24585	Db	24700	AG	GGTATACCGCGCCCAACGCGACCTCCAGACGAAGGTCTCTCGGGCGCGCTCCAC	24759
Db	23641	GA	AGCGCGTTCAGAGCTCGACCCCGACAGGCTTCTTCGACTCGGTCTCGATTCTGATC	23700	QY	25666	AAT	CGGAGCTGACCCCGCGCGATGTGACGAGTGGAGGGCCACCGGACCGGGACCACT	25725
QY	24586	AC	GTGGGTCTAGTTCAGCAAGAACTCGCCAAAGAAACCGGACTGCACTCCCGCCCGTCC	24645	Db	24760	GAC	CGCGCATCACCCCGCGCGAGCTGACGCTGTGTGAGTGGCATGGCACCGGACCTCG	24819
Db	23701	AT	GACGCTCGAGCTTCGTGGCGCTTGCAACAGGCCACCGGCATCAAGCTCCCGGCCAC	23760	QY	25726	CT	GGGAGCCGATGAGGCCCAGGCATCTCTGGCGGCTAGGAGCAACACCGCCCCCAGC	25785
QY	24646	CT	GGTCTTGGACTATCCACCCCGCAGGAATGTGTGCCATCTGTGGACACAACTGTCT	24705	Db	24820	CT	GGAGACCCCATCGAGGTGCAAGCCCTGGCGCGCTTACGCGACGGCAGACCCGCT	24879
Db	23761	CT	CGCTTCGACCATCTCTCTCTCATCGCGTGGGCTCTTCATGCGGACTCGCTCGCC	23820	QY	25786	CAC	CGCCCTTGTGGCTGGGATCCCTCAATCCAAATCCGAGATCGGCGACGACAGCGCGCG	25845
QY	24706	GAC	CTAGACGAGAGAGCGGCACTGTGCAATGTCTCTCCGCAAGTGCCCATCGG	24765	Db	24880	GA	AAAGCTCTCTCTTCTCGCGCGCTCAAGACCAACATCGGCGATCTCGAGGCGCGCTCC	24939
Db	23821	CAC	GGCTCGGACGAGGCTCTCCCGGAGGCGA-----CGCGCGCGCTCCGCG	23871	QY	25846	GG	CGTGGCGGAGTCAATCAAGATGTGATGCTCTCGCAACCGGCTCTCTGCAACAGACC	25905
QY	24766	CG	TACCGTCGAGAGCAACCGATCGCCATCATCGGTATGGCATGTCTCTCCCGCGCGC	24825	Db	24940	GG	CTCGGGGGTGTGCCAAGATGGTCCCTCGCTCCGCGACGAGCGCTTGCCTCCAC	24999
Db	23872	CG	CGCTCGAGGAGAGGCCATCGCCATCTGTGGCATGGCCCTGGCTTCCCGGGCGC	23931	QY	25906	CT	CACTGTGGAGAGCCCAACCCCGAGGTCTGCTGTGTCCAGGCGCAGTACAACTCTG	25965
QY	24826	GT	ACGTTCTGCGAGCACTGTGGAAATGTCTGCTTGGGTGAGGAGCTATCGGCGTC	24885	Db	25000	CT	CAAGCGACCCCAACGCAATCCCTCATCGAGTGGAGGGCGCTCGCCATCGACGTCTG	25059
Db	23932	GT	CGCGATGTGAGGCTCTTTGGGAGTTCTTCCACCAAGAGCGCGAGCGCGTCTGAGCC	23991	QY	25966	AC	CAACCGGTGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	26025
QY	24886	TT	CCGACCGGCGGCTGGGACTGTGACAGCTCTAGACCCCGACCCCGACCAACCC	24945	Db	25060	GAT	ACCGCGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	25119
Db	23992	AT	TCAC---AGAGCGGTGGAGACCGCGTGCCTCTACGACCCCGACCCCGACCCGAC	24048	QY	26026	TC	ATTGGCGGTGAGCGGACCAACCCCGACATCATCTCTGAAAGAGCACCACTCCCGAG	26085
QY	24946	GG	CACCTGTACACCCGAAACCGCGGATTCCTCTACGGCGGAGGCACTTTCAGCCGAA	25005	Db	25120	GC	TTTGGATTCTCGGGACCAACGCCCACTCATCTCTGAAAGAGCTTCCCGCGCGCTG	25179
Db	24049	GCC	AGAGTACGTTCGGGATCCCGGATGTCTGACCAAGTCACTCTTTCAGCCCTGCC	24108	QY	26086	GAC	AGCGATACCGAGCAACCGCTGTCCAAACGCAACCGAGCGCTTCCCGCTTCCCT	26145
QY	25006	TT	CTTTCGATCAGCCCGCGAAGCCTTCGCCATGGACCCCGACCAAGCACTCTCTCTC	25065	Db	25180	CC	GGCGAGCGCGCACCTCACAGCGCGGTGCAAGCGCG-----TCCCGCGCGC	25230
Db	24109	TT	CTTTCGATCAGCCCGCGGAGGCAACACCTCGACCCCGACGACCGCGCTGTCTCTC	24168	QY	26146	CT	TCCGCTGCGGTGTGGCGGAGTCTGAGCGCGGTGTGGCGCGGCGGCGGCGGCTG	26205
QY	25066	GA	AAACCGCTGGAAACCATCGAACCGCGGATCAACCCCGACCAACCTTCACGGGAC	25125	Db	25231	TG	GGCGGCTCTCTTGGCGCGGAGGAGCGCGCGCTTCCCGCGCGGCGGCGGCTC	25280
Db	24169	GA	ATGTGCTGTGGCTTCGAGAGCGCGGATCGTCCCGACCTCTCTCTCAAGGACTCC	24228	QY	26206	CG	CAGTACGTGGGAGCGCGCGCGGACATGCTCTGCGGACATGTGTGCGGCTCTGCG	26265
QY	25126	CC	ACCGGAGTCTTCGCGGATCAAGCTCAAGACCAACCGCGCGGATTCGCGCAAGC	25185	Db	25291	CG	CAACCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	25350
Db	24229	CT	CACCGGCTCTTCTGCGGATCTGCGCGCGGAGTACCGGATG-----CAAGAG	24279	QY	26266	CG	CGCGCGGCGGCTACTGGAACACCGCGCGGCTCATCTCTGGCGGCGGAGCGCGGAGAACTG	26325
QY	25186	CG	TGATGTGAGACCATCAGGGCTACGCTTACCGCGGAGTTCGCGGAGTGTGGCGTCC	25245	Db	25351	ACC	ACCGCGCGGCTTTCGAGCAACCGCGCGCTCTCTGAGCGGCGGCGGCGGCGGCGG	25410
Db	24280	GCG	AGCTCGAAGGTTTCAGGTTTACCTTCATCAAGGACATTCGCGGCTCTTTGGCGG	24339	QY	26326	GCG	CAGGACATGACAGCCCTGGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	26385
QY	25246	GG	CGGCTGGCTACAGCTCGGCTCGAAGCGCGCGGCTGTGGTGGATACGGCGGT	25305	Db	25411	CT	CTCGCGGCTCGACTGTCTCGCGCGGAGCAAGCGCGCGCGCGCGCGCGCGCGCG	25464
Db	24340	GG	GGCTTGGCTTATACGCTCGGCTTCAGAGCGCGGCTCATCTTCGCTCGACACCGCTGC	24399	QY	26386	ACC	CGGCGGCTGACCGCGGCGGCGGCTGTCTTCTGCTTCCCGGAGCGGCGGCGGCGGCTG	26445
QY	25306	TG	CTGTGTGGTGTGATTTGGGCGGCGGAGGCTTTCGCTGCGGCTGAGGTTCG	25365	Db	25465	GG	AGCGGAGGAGCGGCAAGCTGTCTTCTGCTTCTTCTGCGGAGGCTTCGCGGCTG	25524
Db	24400	TC	CTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	24459	QY	26446	GCG	GGGATGGGCGGCTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	26505
QY	25366	AT	GGCGCTTGGCGGCGGCTGACGCTGTCTCTCGGGTACGTTTGTGGAGTCTCTCA	25425					



QY 28662 TGCTCCGCGCGCGTGTGCTGGTGTAGGTGGTGTGCGCCACACCGAAGCCCGGAGTA 28721  
Db 27612 CGCTTCGCTCCAAAGCCTCGTATCGCCCTTTCATCGCTCTGCGCGAA----- 27660  
QY 28722 TTCCGCCGAAGCCCCCGGAGCGCGGACCGAGGCGCTGCGAGGCCCGCGGACGTGCT 28781  
Db 27661 ----- 27660  
QY 28782 GCACGTGGCGGTGTCACACGCGTCCGCTGACGCGGTGCGCGGAGATGTTGCCAG 28841  
Db 27661 -----GCGGACCTCATCGCGAGCGCGCGAGACCAACCGCGGCGCTCGCCCT 27710  
QY 28842 GCTCAGGCTGGCTGGGAGGAGCGGCTTCCACAGACGCGGCTGCTGCTTCTGACGTG 28901  
Db 27711 CTTGAAAGCTGGCTCGCGAGGAGCGGCTTCCGCGGCTTCCGCGGCTGCGCTGCTCACCG 27770  
QY 28902 CGGCGCGTGGCGCGCTCGCGGACGATGCGAGGACCTGCGCGGCGCGGCTG 28961  
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Db 27831 GGGTCTGCTGCTCCGCGAGGAGGACCCAGAGCGCTTCTGCTCTGTCGACCT 27890  
QY 29022 GCGGCGACAGAGGCGAGCGGCTGCTGCTGCGAGCGGCTGAACTCGGCGGAGCGGCA 29081  
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QY 29142 CGACGCGGTACCGCGCTACCGCGCTGCGCGCTGCGCGGCTCACGCGGCTGCGGCTAC 29201  
Db 28002 -----CCAGGCGCCACGGA 28016  
QY 29202 GCGAGCGGTCTCTTCTTCGCGCGGAAAGCTGTGATACCGCGGAAACGCTGCT 29261  
Db 28017 CACAGCTCCCGCGAGGCTCGAGGACCGCTCTCTCATACGCGGAGGACCGCGGACGCT 28076  
QY 29262 GGGCGGCTGCGGCGGCTGCTGCGGAGGCGGCGGCTGCGGCTGCGGCTGCTGCTG 29321  
Db 28077 CGGCGCTGCTGCGGCGGCTGCTGCGGAGGCGGCGGCTGCGGCTGCGGCTGCTGCT 28136  
QY 29322 GGGTGGGCGGACCGGAGCGGCTGCGGCGGAGTTCGCGGCGGAGCTGCGGCTG 29381  
Db 28137 CTCGCGCAGGCGGAGGCTCGGCTGCTGATGCTTTCGAGGAGCTCGAAGCTCT 28196  
QY 29382 CGGCGGACGCTGAGGCTGCTGCTGCGAGCGGCGGAGCGGAGCTGCGGAGCT 29441  
Db 28197 GGGGCTTTCGCTCACCTCGCGGCTGCGAGCTGCGGCTGCGGCTTAAAGGAGCT 28256  
QY 29442 GCTGACGCGATCCCGGAGGATGCGGCGGCTGAGCGGCTGCTGCTGCTGCGGAGCT 29501  
Db 28257 TCTGATTAACATTCGAGGCTCACCGGCTGCGGCGGCTGCTGCTGCTGCGGAGCT 28316  
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Db 28317 CGAGCGGCTGCTGCGGCGGCTGAGCTGAGGCGGATGAGCGGCTTTCGCGGCGG 28376  
QY 29562 GCGGAGCGGCTGCTGCTTTCGAGGCTGAGCGGCGGCGGAGCTGCTGCGGCTTCTG 29621  
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QY 29622 CATGTTCTTCTCGGCTGCGGCTGCTGCGGCGGAGGAGGCTGAGCGGCGGCT 29681  
Db 28437 CCTTCTTCTGCTGCGGCTTCTGCGGAGCTCAGGCTTCAACCAAGGAGGCTTCTG 28496  
QY 29682 CAAAGCGGCTTCTGCTTCTTCTGCTCATCGCGGCGGCGGAGGCTGCGGCGGCT 29741  
Db 28497 GAGCGCTTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 28556  
QY 29742 TCTCGCTGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 29801

Db 28557 GCTCGCTGGAGCACCTGGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 28616  
QY 29802 CCATGCGGAGTACAGCGCGGAGAAATGCGCGGCTGCGGAGCTGCGGAGGCTTGGCGCT 29861  
Db 28617 CGCCCTCGCATGAGCGGCGG---CCTTCCCTCGACCTTGNAGGAGGCTGCGCT 28673  
QY 29862 GTTCGAGCGGCTTGGCGGAGCGGAGCGGCTTCTGATGCGGCTGCGGCTGCGCTCAC 29921  
Db 28674 CTTGATGCGGCGCTTTCGAAACGAGACCGGCTGCTGCGGCGGCTTTCGACTTGA 28733  
QY 29922 GCGCGTACGCTGCTGCGGCGGCTGCGGAGCGGCTGCTGCGGAGGCTTCTGCTCA 29981  
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QY 29982 GCTGCTGCTGCTGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30022  
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## RESULT 8

US-08-458-076A-6  
; Sequence 6, Application US/08458076A  
; Patent No. 5698425  
; GENERAL INFORMATION:  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James M.  
; APPLICANT: Beck, James Joseph  
; APPLICANT: Hill, Dwight Steven  
; APPLICANT: Ryals, John Andrew  
; APPLICANT: Gaffney, Thomas Deane  
; APPLICANT: Lam, Stephen Ting  
; APPLICANT: Hammer, Phillip E.  
; APPLICANT: Ukner, Scott Joseph  
; TITLE OF INVENTION: Genes for the synthesis of  
; NUMBER OF SEQUENCES: antipathogenic substances  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ciba-Geigy Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,076A  
; FILING DATE: 01-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/457,205  
; FILING DATE: 01-JUN-1995  
; APPLICATION NUMBER: 08/258,261  
; FILING DATE: 08-Jun-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8614  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28958 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO



ANTI-SENSE: NO  
US-08-458-076A-6

Query Match 10.2%; Score 3140.6; DB 1; Length 28958;

Best Local Similarity 54.1%; Pred. No. 0;

Matches 8239; Conservative 0; Mismatches 6284; Indels 698; Gaps 63;

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QY 14932 GAAGAGCTGTTGCGCTGCTGGTGGCAACCATGCGCGCTGTGCTGGGCAATGCCACTCCC 14991
DB 14296 CGCGTCTCTCGATCTGCTCGGCAACCGAAGCGCTCTCGTCTCGGCTCGCTCGTTC 14355
QY 14992 GAAGTGTATGCTCCGAAACAGGCTTCAAGAGCTGGGTTTGATTTCTCTCGCGCAATT 15051
DB 14356 GAATCGCTCGATCCCCCATCGCCCTTACAAGAGCTCGGCTCGATTTCTCATGGCCCTC 14415
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DB 14416 GAGCTCCGAAATCGACTCGCGCGCGCGCGGCTGCGGCTCCAGGCTACTCTCTCTTTC 14475
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DB 14593 GTGCGATGAGTGTGCGCTTCCGCGCGAGTGCGCAACCGCGAGGANTCTCTGAGGCTC 14652
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QY 15412 CTTTACGAGCGAGCAATTTGATCCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15471
DB 14758 GTCTACGAGCGAGCGCTTCTGATCCGCTTCTTCTGCGATGCTGCTGCTGCTGCTGCTGCT 14817
QY 15472 GCGATGAGCGGAGCGGCTGCTGTGAAACAGCGTGGGAGGATCGAAGACGCC 15531
DB 14818 GCGGTGATCCCAACAGCGGATTTGCTCGAGATCATGGAAGCCTTCGAGCGTGCA 14877
QY 15532 TGATCAACCCGAGCGCTCGTGGGACCAACCGCGCTTTCGCGGCTGACCTAC 15591
DB 14878 GGCATCGACCGGCTGCTTCAAGGAAGCCAAAGCGGCTTCTGCTGCGGCTATGGCAG 14937
QY 15592 CACGACTACGCGCGCTTCCACAGCTCGCGGAGGTTTCGAGGGGTATCTCGGGCAC 15651
DB 14938 ACCGACTACCATGATGCTGCTGTAACCGGATCGCGCAATACAGGACTGTTGCCACC 14997
QY 15652 GGAAGCGAGGAGTATCGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15711
DB 14998 GGTAGCGCAGCGCT---CCGTCCGCGCGAATCGCATACAGTTTCGAGCTTCAAGGGCCC 15054
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DB 15055 GCGATCGAGTGGAGACCGCGTGC---AGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15111
QY 15772 GCGCTGCGCTCGCGGAGTGTTCATGCGCTTCCGCGGCTGCGCTGCTGCTGCTGCTGCTGCT 15831
DB 15112 GCGCGCGCGCGGAGTACTCTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15171
QY 15832 CCGCGCGGCTGCTGGAATTTTCGCGGAGCGGCGCTGCGCGGCTGCGCGGCTGCGCGGCTGCG 15891
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DB 15172 CCAGCCATATTATCGGCTTCGATCCGAGAGCGGGTGCCTCCCGAGCGGTGCTGCTGCAAG 15231
QY 15892 GCGTTCCTCGGAGCGGCTGAGCGCACCGGCTGGGGTGGAGGTGTCGAATCTCTGCTGTG 15951
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DB 15292 GAGCGGCTTCTCGATGCGCTCAAAACCGTTCATCCGCTCTCTCGCGTCTCTTCGAGGCTCC 15351
QY 16012 GCGGTCAATACGAGCGGCTGAGCAACCGGCTGACGCGGCTCAACCGGCGCTGCTGAGAG 16071
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DB 15472 GAGGCTCAGGCGACGCGGCAACCGCTCGAGGACCGGCTGCGGCTGCGGCTGCGGCTGCGG 15531
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DB 15532 ACCTATGCGGAGCGGCTTCCAAAGACAGACCGCTGCGGCTGCGGCTGCGGCTGCGGCT 15591
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DB 15712 TCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15768
QY 16432 CTGCGGCGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16491
DB 15769 CTTGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15828
QY 16492 GAAGAACACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16551
DB 15829 GAGAGGCTCCCGCGGCA----- 15847
QY 16552 GAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16611
DB 15848 -----CGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15902
QY 16612 GCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16671
DB 15903 GCGCGTGTCT-----TGTGCGGCGAGGAGC 15927
QY 16672 CAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16731
DB 15928 GAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 15987
QY 16732 CTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16791
DB 15988 CTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16047
QY 16792 GCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16851
DB 16048 GCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16107
QY 16852 GCGGAAACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16911
DB 16108 GAGAGCGCGCACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16148
QY 16912 GCGCGAGGAAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16971
DB 16149 --CCACGCGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16206
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QY	15972	CAGGGCTCTACACACACCACCCCGTCTTGGCGGCGGCACTCAACGACATCTGCACCAC	17031
DB	16207	CTCTCCCTGTCTGACATCTCTCGCCCGGTCTTCGCACACACAGCTCGAAGCATCGAGCGCGG	16266
QY	17032	CTCGACCCCCACCTCGACACACCCCTCTCTCCCTCTCTCACCACGAGCCCAACACCCAG	17091
DB	16267	CTCGGTCTCTCAGCTCGAGTGGAGCTGTCTCGCGTCTCTGCGCGCGACGAGGGGCGCCCC	16326
QY	17092	GACACACACCTCTGAAGAAGCGCGGCACCTGTCTCCAGCAGACCCCGTACGCCGAGCCC	17151
DB	16327	TCCCTCGACCGCGTGCACGTCGTG-----CAGCGCGCCTCTTT	16365
QY	17152	GGCCTCTTGGCTTCCAGGTTCGCCCTCCACCGCTCTCTCACGAGCGGCTACCAATCACC	17211
DB	16366	GGCGTCAATGGTCTCCCTGCGCGCCCTCTGGCGCTCGCTCGGCGTCTGA-----G	16413
QY	17212	CCGCACCTACTTACGCCCGGACATCCCTCTGGCGGAATCACCGCGCGCCACCTCGCGCGCATC	17271
DB	16414	CCCGCGCGCTGTCTCGGCACACGACGAGCGGAGATAGCGCGCTTGTTCGAGGCGCT	16473
QY	17272	CTCACCTCTACCGACGCGACACCTCTATCAACCAAGCGGCACCCCTCATGCAACCATG	17331
DB	16474	CTCTCCCTCGAGACGCGCGCGCATCGCGCGCTCTGCGCAGCAAAAGCGTCAACACCGTCG	16533
QY	17332	CCCCCGGACCATGACACCTCTCCACACACCCGCCACCATCACCCACCACTCACC	17391
DB	16534	CCGGCAACGGGCATGGCGCGCTCGAGCTCGGCGCTCCGACCTCGAGACCTTACCTCGCT	16593
QY	17392	GGCCAGCAAAACGACCTCGCCATCGCGCGCATCAACACACCCCCACCTCTCGTCTATCAGC	17451
DB	16594	CCCTGGGGCGACAGGCTCTCCATCGCGCGGTCAACAGCCCCAGGGGCACGCTCGTATCC	16653
QY	17452	GGCACCCCCACACCGTCCAAACATCAACACCTCTGCCAAACAAGGATCAAAACC	17511
DB	16654	GGCGAGCCCGCGCGCTCGACGCGCTGTATCGACTGTCTCACCGCAGCGAGGTCTTTCGCC	16713
QY	17512	AAAACTCTCCACCAAAAGCGCTTCCACTCCCCCAACCAACCCCATCTCTCAACCAA	17571
DB	16714	CGAAGAGTCGCGTGTGACTACGCTCTCCACTGAGCCCATGGAAGCGCGTCCAGACGAG	16773
QY	17572	CTC-----CACCAGCACACCAAAACCTCTCACCTACCAACCCACCCACACCCCGCTC	17622
DB	16774	CTCGCGCAGGTCTAGCCAACATCGTCTCTGGAGTGTGGAGTCCCTCTTTATTTCGACC	16833
QY	17623	ATCAGCGCCAAACCCCAACCGACCAACTCTCAACCCCGCACTACTGAGACCCAAACAGCC	17682
DB	16834	GTACCGGCAACCAAGGCTCGACGCGCTCCGAGCTCGACGGCGGTACTGTGTATCGAAACCTC	16893
QY	17683	CGCAACACGTCGACTAGCGCACACACCCAAACCTCCACCAACGCGGTCAACACC	17742
DB	16894	CGGCAAACCGTCTGTCTTGAGCGGACGAGAGGGCTCTCGAGCATGGGCATCGCTTTC	16953
QY	17743	TACATCGAATCTGGAGCCCGCAACACCTCTCAC---CACCTCTCACCCACCAACCTCCCC	17799
DB	16954	TTCGTGGAGTTCAGCCCTCATCCCGTGTCTCAGCTCGCCCTCCGGAGACCTTCGAGCGC	17013
QY	17800	AACACCCCGACACACCTCTACCCCTACCCACCCCGCACCAACCCCGCAACCCACCTC	17859
DB	17014	TCACCGCTCATCCCGTCTGTCTGGCTGCATTTGACGCGAGGAAGGCCACCTCCCGCGT	17073
QY	17860	CTACCAACCTTCGCCAAAACCAACCACTCTGCGACCCCGCACCTTACACCCACCAACC	17919
DB	17074	CTCTTGTCTCTTTGGGCGAGTCTATGGCGGGGCTTACGCCCGAGTGGAGGGCCTTTC	17133
QY	17920	AACCAACCCCAACCAACCTCTCGACTCTCCACCTCCCGACCTTCCCAACCAACGACAC	17979
DB	17134	TTTCGGCCCTTCTCTCCCGCAAGGTCTCACTCCCGCACCTACGCTTCCAGCGGAGCGT	17193
QY	17980	TACTGGCTCAAAAGCAACAGCGCGGTGCGGATTCGGTTTCGGTTTCGGGGCGG	18039
DB	17194	TTTCGGCTCGAGCCCGCCCAACGACACCCCGAA-----GGGTGTGCTCTCCGCTCGC	17244

Qy	18040	CGAGGGACTGCGGGCGGACGCGACAGGTGGAGTTCGCGTTCTGAGACGGGTGGCCCGC	18099
Db	17245	CCGATCGATGGCGGCTTTTGGCAAGCCATCGAAACGCGGGGACCTCGACGCGCTCAGCGGC	17304
Qy	18100	CAGGACCTTGGAAACGGTCCGCGACCAACGGTTCGCGCTGCCCGCTCCCGCGCTCGGACACG	18159
Db	17305	CAGCTCC-----ACGGGACGGCGACGACGAGCGCGCCCTCGCCCTG	17349
Qy	18160	GTGFTGCCGACTCTCGCTTGGCAGCGGCACCCAAACGACGACGAGCGCGCATCAACACC	18219
Db	17350	CTCCTTCCACCCCTCTCGAGCTTTTCAACACCAAGCGCAAGAGCAGAGCAGCGTTCGACACC	17409
Qy	18220	TGGACCTTACGAGGAACCTGGNAACCCCTCAACCTCCCTCCCAACA-----CCACCAACCCAC	18276
Db	17410	TGGCGCTTACCGCATCAGCTGGAGGCTCTGACCAACGCGCGCACGCGCGCGACCTCGCC	17469
Qy	18277	CAAACTTGGCTCATCGCCATCCCGAAACCCAGACCCACACCCCGCCACATCAACAACATC	18336
Db	17470	GGACCTTGGCTCTCTGTGTGCTCGCGCTCGGGCTCGGGACGACGGCTCTCCTTGCACGGCTC	17529
Qy	18337	CTCACCAACTTCACCAACGAGCATCAACCCCATCCCTTCACTCTCAACCAACACCCAC	18396
Db	17530	ACCGATGGCTTACCAGCGCGCGCGGTGTCTCTCGCTGCGCTGAGCCAGCTGAGTGTTCAC	17589
Qy	18397	ACCAACCCCAACACTTCCACACACACCGACAACAGCCCAAAACACACACACCGGACCC	18456
Db	17590	ATAGCCCGCGCGCTCTCACCGAGACCTGCGCGAGGCTGTGTCCGAGACTGCCC--CCG	17646
Qy	18457	ATCACCGGCTGTCTCTCTCTCTCGCTCGCTTCGACGAAACACCCACCCCGCCACACCCCGAC	18516
Db	17647	ATTGCGGCGTGTCTCTCTCTCTCGCTTCGACGAGCGCGCTCGGGNCCATGCGGCC	17706
Qy	18517	ACACCCACGGCACCTCTCAACTCACTCACCCCTCACCCAAACCCACACCCCAACCCCA	18576
Db	17707	CTGCCCGCGGCTTTGCCCTCTCTCGCTCGCTTCGCTCGCAAGCCTTCGGGACCTCGCCCTC	17766
Qy	18577	CCAACCCCTCTGTGTGACGACACACAAAGGCAACACACACCAACCCCAACGACCCCGCTC	18636
Db	17767	GAGGCTCCCTTTGTGCTCTTTCACGGCGCGGCGCTCTCGATTGGACACTCCGACCCCACTC	17826
Qy	18637	ACACACCCACCCAGCCCAACCTTGGGACTCGCCCGACACACCTCTCTCGAACACCCC	18696
Db	17827	GCCCATCCACCCAGCCATGATCTTGGGCTTTGGGCGCGTGTGTGGCTTCGAGCACCCC	17886
Qy	18697	ACCACACCGCGGAATCATCGACTTCCCAACACCCCGCCACCCCGCCACACCTCTCCACAC	18756
Db	17887	GAGCGTGGGCGGCTCGTCGACCTCGCGCGAGCGCTCGACGAGCGCGCGAGGCGCG	17946
Qy	18757	CTACCCCAAACTCTACCGAACCCCAACACCAAAACCCAACTCGCCATTCGACACACCGGC	18816
Db	17947	TTGTCTCCGGGCTTCGCGCAGCGCAACGACGAGACCACTCGCTGCGCTGCGCCGCGCGGC	18006
Qy	18817	ACCACACCGCGGCTCACCCCGACACCTTACCCCGCCCGCCACACCAACCCCGCCCGCC	18876
Db	18007	CTCTACGACGCGCTTGTTCGCGCGCCCGCTCGGGATGTGGCTGTGGCTGTGGGCTTC	18066
Qy	18877	ACCCCGCCAGAACCACTCTATCAACGCGCGGAACCGGCGCCCTCGCCACCCACCTCAC	18936
Db	18067	ATGCCCGGAGCACCATCTCTATACCGGTGTGACGGCGCCATTGGCGCTTCAGTCGCC	18126
Qy	18937	CACCACTTCACACCAACCAACCCCAACCACTCTCTCTCAACGACGAAACGGGCGCC	18996
Db	18127	CGATGGCT---CGCTCGAAAGCGCTGAGCACCTCGTCTCATAGCCGACGAGGGGCG	18183
Qy	18997	CACACCCCGCAGCAACACTTCAACCCCACTTCAACAAAAGGCATCCACCTCAC	19056
Db	18184	CAGGCGGAAGCGCGTGGAGCTTCAACGCGGAGCTCACCGCCCTCGCGCGCGCGTCA	18243
Qy	19057	ATCACCACTGGGACACGACAAACCCAGACCAACTTCAACAACTCTCTCAACACCATCCCC	19116
Db	18244	TTGCGCGGTGGATGTGCCGACAGGACGGCTGTGTGCCACGCTTCTCGAGGAGCTCGAC	18303
Qy	19117	CCACAACACCCCC---TCACCAACCGTCACTTCAACCGCAGGCACTCTCGACGACGCCAC	19173

Db 18304 GCCGAGGGCCACAGGTAGCGCCGCTGTTCCACGCGGGCGCATCGAGGCCACAGCTCG 18363  
Qy 19174 CTCACCAACTCACCCACCCAACTCAACAGCTCTCCGCGGCCAAAGGCCACAGCGCC 19233  
Db 18364 CTCGCGGCGACCTCATGAGGATCTCGCGAGGTGTCTCCGCGAAGGTACAAGGTGCA 18423  
Qy 19234 CACCTCTCTCACCAACTCACCAACACACACCCCTCAACGCTTCTGCTCTACTCTCTCC 19293  
Db 18424 AGACACTTCCAGACTGCTGGCTCTCGACCCCTCGAGCCCTTGTTCTCTCTCTGTC 18483  
Qy 19294 GCCGCGCCACCTTCGCGGCACCCCGCCAAAGCAACTACGCGGCAGCAACGCTTACTCTC 19353  
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Qy 19354 GACGCGCTCGCCACACCGGCACACCCACACCTCCCGCCACACAGCATGCTTGGGGC 19413  
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Qy 19414 ACCTGGCAAGAAACGGACTGGCGACTGCTCAAGTCACGCAACATCTCCGCGCGCGGG 19473  
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Qy 19534 GCGCGAGTCTCTGTCGCGATATCACTTGAAGAAATTTGGACCGGTTCTCTCAGC 19593  
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Db 18904 TCGGAGACGAGCAGATCCACTGCTCTCTCGCTGCTGCGCCACGAGCGGCTCTGTC 18963  
Qy 19765 CTGGGCGGAGACTCCGAGGCCATCCGCGCGCTGGCTGTTCAAGGATCTAGGGTTC 19824  
Db 18964 CTGGGCGATACGAGCGCTCCAGGTGACCCCGCAGGGCTTCATGAGACTCGGCTC 19023  
Qy 19825 GACTGCTTGGGGGTGGAGTTTCGCAACCACTTCGAGCAGCAGAGAGCTGGCTTG 19884  
Db 19024 GATTGCTCATGACCGTTCGAGCTTCTGCGCGCTTTCGAGCGGCCACCGGCATCAAGCTC 19083  
Qy 19885 CCGAGACTCTGCTTTCGATTACCCAGCGCCACAGCTCGCCCAATTTCTGCTCTCC 19944  
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Qy 19945 GAGATCGGGAGTTCCAGCCCGACA-----ACTCACTCCGCTTCG 19986  
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Qy 20107 GCGGATTTCCCAACCGAGCGGCTGGGACTGACAGCTCTACAGCTTACAGCCCGACCCCGAC 20166  
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Qy 20167 CACCCGCGCATCTGCTTACACCCGAAACCGCGGATTCCTCTACGACGAGGCGCACTTCGAC 20226

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Db 19441 CTTGCCCTTCTTGGCATAGCCCTTCGAGGCGCAATACCTTCGACCCCGACGCGCTG 19500  
Qy 20287 CTCCTCGAAACCGCTTCGGGAAACCATGAAACACGCCCGGCATCAACCCCGCACCTCTCAC 20346  
Db 19501 CTCCTCGAATCTGCTGGCTGGCCCTCGAGGAGCGCGGCATCGTCCCTCCACCTCAAG 19560  
Qy 20347 GGCACCCCGACCGGAGTCTTCAACGCGCAACCAACGAGCAGCAGCGGCGACATCGGT 20406  
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Qy 20407 CAGGCGCGAGCGGTACGAGGAGTTGCTCTGACCGGGGAGCGACCGAGCATGCTCTCC 20466  
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Qy 20467 GCGCGAATCTCTACATCTTCGGTTGGAAGGGCTCGGGTCACTCTCGACACAGCGGTG 20526  
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23269 CAAACCCCAACCCCAACCCCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 23338  
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Db 23302 CCGTGGCAGCCAGCTGAGCAAGCTGCTGTGCGCGGATGGCGCGCTTCTGCGCG 23361  
Qy 24226 GCGGATTTCCATGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24285  
Db 23362 GCGGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23418  
Qy 24286 GACTGGGAGCGCTTGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24345  
Db 23419 GACTGGGCGCGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23478  
Qy 24346 ATTCGGAGGTTTCGCAAGCGGCTCAGGAGCTGGAAGCAGCTGCGTGCAGCGCAAGAC 24405  
Db 23479 TGCCCGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23538  
Qy 24406 ACCAGCTCAGCGGATTCGACGCTCTCTCGTGTAGCGATTTGGCGCGCTCTCA 24465  
Db 23539 CCCCCG-----ACCTCTCGACAAAGCTCCCGAGCGCTCGGAGAGC 23580  
Qy 24466 AAGCAGACACAGGCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24525  
Db 23581 GAGCAGCTTCTGCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 23640  
Qy 24526 CGTAATCGGAAGGATCGAGGACCAACGAGCGCTTTCGCGCGCGCTTCGACTCGCTG 24585

Db 23641 GAAGGCGCTTCCAGCTCGACCCCGACAAGGCTTCTTCGACCTCGCTCTCGATTGATC 23700  
Qy 24586 ACCTCGGCTCAGTTCAGCAAGGACTCGCAAGAAACCGGACTGCCACTCCCGCGTCC 24645  
Db 23701 ATGACCGCTCAGGCTTCGTGCGCGCTTGCACAGCGCACCGGCACTCAAGCTCCCG 23760  
Qy 24646 CTGCTCTTTCAGCTATCCACCCCGCAGGAATGTGTGCCCATCTGCGCACACAACTCGTC 24705  
Db 23761 CTGCGCTTCAGACCATCTCTCTCATCGGCTCTTCATGCGGACTCGTCTGCC 23820  
Qy 24706 GACTAGACGACGAGGAGGACGCGGCACTGTGCAATGCTCTCCGCAAGTGCGCCATCG 24765  
Db 23821 CAGCGCTTCGCGACGAGGCTCTCGCGCAGGCGA-----CGCGCGCGCTCCGGC 23871  
Qy 24766 GGTACCGTTCAGGACGAAACGATCGCCCATCATCGGTATGCGATGTCTCTCCCGCGG 24825  
Db 23872 CGCGCTTCGAGCGACGAGCCCATCGCCATCGTGGCATGCGCTCTGCGCGCTTCGCG 23931  
Qy 24826 GTACGTTCTGCGCAGCAGCTGTGGGAATGTCTGCTTCGGGTAAAGACGCTATCGCGTC 24885  
Db 23932 GTCGCGATGTTCAGCGCTCTTTGGAGTTCTTCCACCAAGGCGGAGCGGTTCGAGCC 23991  
Qy 24886 TTCCCGACGACCGCGCTCGGACCTGAGACGCTCTTACGACCCCGACCCCGACCC 24945  
Db 23992 ATTCCAC---AGAGCGCTGGACCGCGTGCCTCTACGACCCCGACCCCGACCGGAC 24048  
Qy 24946 GGCACCTGTACACCCCGAAAGCGCGGATTCCTCTACGCGCGAGGCCACTTCGACCGGAA 25005  
Db 24049 GCCAAGAGCTACGTCGCGCATGCGCGATGCTGACACAGATCGACCTTCGACCCCTGCC 24108  
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Db 24109 TTCTTCGCGCATCAGCCCGCGGAGGCAACACCTCGACCCCGACCGCTCTCTCTC 24168  
Qy 25066 GAAACCGCTTCGGAAACCATTCGAAACCGCGGATCAACCCCGACACCCCTCCACCGGAC 25125  
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Qy 25126 CCCACCGGAGTCTTCGCGGGAATCAAGCTCAAGACCGCGCGCATATCCGCGCAAGC 25185  
Db 24229 CTACCGCGCTTCGTCGCGCATCTGCGCGGGAATACGCGATG-----CAAGAG 24279  
Qy 25186 CGTGATGTGAGACCATTCGAGGCTACGCGCTGACCGCGAGTTTCGGGAAGTGTGCGCTC 25245  
Db 24280 GCGAGCTCGAAGGTTCCGAGGTTACTTTCATCCAAGGACTTCGCGCTCTTTGGCGG 24339  
Qy 25246 GCGCGGTGCGCTACAGCTCGGCTCGAAGGCGCGCGGTGTGCTGAGTACGCGGTGT 25305  
Db 24340 GGGGCTTGGCTATACGCTCGGCTCCAGGGCGCGGATCTTCGCTCGACACCGCTCGC 24399  
Qy 25306 TCGTCTGCTTGTGGGCTTGCATTGGGCGCGGAGGCTTCGTCGCGGTGAGTGTTCG 25365  
Db 24400 TCCTCTCGCTGCTCTCCCTCCACCTCGCTGCGCAAGCCCTCGACAGGCGAGTCAAC 24459  
Qy 25366 ATGCGCTTCGCGGGGTGTGACGCTGCTCTCCGGTACGTTTGTGGAGTTCTCA 25425  
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Qy 25426 CGTCAGCGGGTTCGCGCGGACGCGGTGTGAAGGCTTATTCGCGGCTGTCTGACGCT 25485  
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Qy 25486 ACGGCTTGGCGCGGAGGCTGTGGGATGCTGCTGTGTGAGCGGCTTCGACCGCGCTCG 25545  
Db 24580 TAGGACGCGGAGGAGGCTGCTGCTCTTCGCTTCGCGGAGTTCGCGGAGCTTCGCC 24639  
Qy 25546 AACGCTCACCGTCTCTGCGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 25605  
Db 24640 CGGAGACACCGCTCTCTGCTCTCTGCTCGCGGACCGCTTCAACACGAGCGCGCTG 24699  
Qy 25606 AAGGCTTCAGCGCGCGCAACGCGGCTTCCAGAGCGGTGTCTATCTGCTGAGGCTCTG 25665  
Db 24700 AGCGGTATACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCAC 24759



QY 25666 AATGCGGAGTGAACCCCGCCGATGTGACGAGTGGAGGGCCACGGCAACCGGGACCACT 25725  
Db 24760 GAGCCCGCATCACCCCGCGAGCTCGAGGTCGTGAGTGCAATGGCAACCGGACCTCG 24819  
QY 25726 CTGGGGGACCGATCGAGCCCGAGCACTCTGGCGCGCTACGGACACACCGCCCGCAC 25785  
Db 24820 CTGGGAGACCCCATCGAGGTGAAGCCCTGGCGCGCTTACGGCCGAGAGACCGCT 24879  
QY 25786 CACCCCCTTGTGGCTGGATCCCTCAAAATCAACATCGGCGACGACAGCGCCCGCG 25845  
Db 24880 GAAAGCCTCTCTTCTCGGCGGCTCAAGACCAACATCGGCCATCTCGAGGCGCGCTCC 24939  
QY 25846 GCGTGGGCGGAGTCAATCAAGATGTGATGGCCCTCGCGAAGCGGCTCTGCGACAGACC 25905  
Db 24940 GGCCTCGGGCGCTCGCGAAGATGTCGCTCGCTCCGCGACAGCGCTGCCCCCGCAC 24999  
QY 25906 CTCCACGTGGAGAGCCACCCCGCCAGTTCGACTGGTTCACAGGCGCGATACACTCTG 25965  
Db 25000 CTCCACGGACCCCGCAATCCCTCATCGAGTGGAGGCGCTCGCCATCGACGTGTC 25059  
QY 25966 ACACAAACCGGTGCGTGGCCCGCGACCGCGCGCGCGCACGCGCGGTGTCA 26025  
Db 25060 GATACCCCGAGGCTTGGCCCGCGCACGAAGATGGAGTCCCGCGCGCGCGCATCTCC 25119  
QY 26026 TCATTGCGGCTCAGCGGACCAACGCCCGCACATCATCTCGAAGAAAGCACCACTCCCCAG 26085  
Db 25120 GCTTCGGATTCTCGGGCACCAAGCCCGACAGTTCATCTCGAAGAGCTCCCGCGCGCTG 25179  
QY 26086 GACAGGATACGACGAGAACCGCTGCGAAGCGCACAGCCCTGCCCATCTCCCTCCCT 26145  
Db 25180 CGGCGGAGCGCGCACCTCAAGCGCGCTCGAAGCGC-----TCCCGCGCG 25230  
QY 26146 CTTCCTGCGGTGCGGAGGTCGAGGCGGCTGCGGCGCGGCGGCGGCGGCGGCTTG 26205  
Db 25231 TGGCCCGTCTCTGCGGCGAGGAGGCGCGCTCGCGCGCGCGCGCGGCGGCGGCTC 25290  
QY 26206 CGCCAGTACGTGGGACCGCGCGGACATGTCACTGCGGACATTTGGTGGGCTTGCGCC 26265  
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QY 26266 CGCGCGCGGCTACTGGAACACCGCGCGCTCATCTGGCGCGGCGGCGGAGAACTG 26325  
Db 25351 ACCACCGCGCCACTTCGAGCACCGCGCGCTCTCGTAGCCCAACACGCGGACGAGTC 25410  
QY 26326 GCGGAGGCACTGACAGCCTGCGAGCGCGGAAACCCACCCACATCACACAGGCGCAC 26385  
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QY 26446 GCGGGATGGGCTGACCTGCTGCTACCTCTCACCGGTGTCGCGGAAACATACGACGCA 26505  
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QY 26566 CCCGACGACCCCGGATGGCAACAGCGGAGTGGTCCAGCCCGTCTCTTTCAGCATCATG 26625  
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QY 26626 GTCTCCCTCGCGCGCTGCGGCTCTCTACGCGATCGAACCGGACGCGGCTCTCGGCGAC 26685  
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QY 26686 TCCAGGAGAAATCGCGCGCCACATCTCGCGGCGACTCAGGCTGAAAGACGCGCC 26745  
Db 25765 AGTCAGGCGGAGATCGCGCGCGCTTCTGTCGAGGCGGCTCTCTCTCGAGGACGCGCC 25824

QY 26746 AAAACCGTTGCACTGCGCAGCCGCGCACTGCGCCCGTACGAGCCGCGGCGCCATGCGC 26805  
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QY 26806 TCACTGCGGCTGCGCGCGCGCAGGAGTGCAGCAGCTCATTTCCGAACGGTGGGAAGGGCAG 26865  
Db 25885 GCGCTCGAGCTCGCGCGCTCGGACCTCGAGACCTTACCT---CGTCTCCCTGGGCGGACAGG 25941  
QY 26866 TTGTGGGTGGCAGCGCCCTCAACGGCGCCCACTCCACACCGCTCTCGGCGGACACCAAGGCG 26925  
Db 25942 CTCTCCATCGCGCGCTCGACAGCCCGCGGCGAGCTCGTGTTCGCGGAGCGCCCGCGCC 26001  
QY 26926 GTGATAGGTGTGTGGCGCACTGACCGACACCGCGCTTACGGGCGAAGCATCTCCGCTC 26985  
Db 26002 ATCGACGCGCTGATCGACTCGCTCACGCGAGCGAGGTCTTCGCGCGGCAAAAGTCCGCGTC 26061  
QY 26986 GACTACGCTCCCACTGCGCCCGCGCTCCAGCCCTCCAGCAGCAACTCTCGACCTGCTG 27045  
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QY 27046 GGAGACATCAACCCCGCGCTGCCAGCGTCTTCTCCACCGTGGAAAGGCACTCGG 27105  
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QY 27166 TTGAGCCACGCGATTCAGACCTGACCGACGACGACCGCGCTTCATCGAAATCAGC 27225  
Db 26242 TTCTCGAGCGCGACCGAGCGCTCTCGACGATGGGCTTCTTCTGTCGAGGTTCAGC 26301  
QY 27226 CCCACACCCCTCGTCCCGCATCGAGACACACCGAAACACACCGAAACATC 27285  
Db 26302 CCCATCCGCTCTACGCTCGCTTCGCGAGCTTCGCGAGCGCTCACCGCTCGATCCC 26361  
QY 27286 ACCGCGACCGGAGCTTCGCGCGGCGACAAACACACCGCTTCCTCACCGCGCTC 27345  
Db 26362 GTCTGCTGCGCTTCAATTCGACGCGGAGAGGCGCACCTCGCGCGCTCTCTCTCTCG 26421  
QY 27346 GCCACACACACACCGGCGATCGGACACACCGACCGCTGGCACCACTACACCA 27405  
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QY 27406 ACCACACCCACACCCCGCACACCTCGACCTGCGCACCTACCCCTTCCAAACAC 27465  
Db 26461 GCCTTCTGGGCGCTTGGCTCCCGGCAAGGTCTCCCTCCACCTACCCCTTCGACGC 26520  
QY 27466 CAGCACTAGTGGTCCAAACCAACCAACCAACAA---CAACCGACCTCACCAACCGGCTC 27522  
Db 26521 GAGCGCTTCTGGCTCGAGCGCTCCACGCGGCAAGCTGCGGAGCTCGCTCGCAGGCTG 26580  
QY 27523 ACCCGCACACCGCGCTCTTCCCTACGCGCACCTACCTTCGCGGACAAACACACAA 27582  
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QY 27583 CTACTCAACCGCGCTCTTCCCTACGACCAACCGCTGCGCTACCGACCAACCGCTGCGC 27642  
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QY 27643 GGCAATGCTCTCTGCGCGGCGACCGCTCTCGAACTCGCCCTCCAAAGCGCGGAAACGG 27702  
Db 26701 GGCAATGCTCTGCGAGCGCGCTCTCTCGAGCTCGCGCTCGCTGCTGCTGCTGCTGCT 26760  
QY 27703 GTGAGTGGCTCGGCTGGAGGAACTGACCTGCGACCGCATCGGACCGTGGTGGATCCCGCACAC 27762  
Db 26761 GTGCGCTCGACACCGCTCGAAGAGCTCACTGCTGCGCGCGCGCTGCTGCTGCTGCTGCT 26820  
QY 27763 GAGGACGTGAGTGGAGTTCACCGTTCGCGGCGCGCTGAGAGTGGGCTGCGGCTGCGGCTC 27822  
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QY 27823 GCGATCCACTCGTACTCGCGGACCGCGCTGCTGCGGCGGAGTGGAGTGGACCGCTCACGCGC 27882

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Qy 27883 ACGGCTCTCTACACACACGCCGACACCGATACCGTGCCGACACGCCACACGACGCC 27942  
Db 26938 ACGGCTCTCTCGCGCAAGCTAGCCCGCTCCATTCCTTCCATGCTC----- 26984  
Qy 27943 TGCCCTTGGCGGAGCTGCGCCCGCCCGCGCGACCCATCGAACTGGGCGACGCTTAC 28002  
Db 26985 -----CGGAATGGCCCCCTTCGGCGCCACCCAGGTGGACACCAAGGTTTCTAC 27036  
Qy 28003 GGTCTATGGCGGCGACTCGGACATCGCTACGGGCGCGCTTTCAGGGGCTGC-ACGC 28061  
Db 27037 GCAGCCCTCGAGAG--CGCTGGGCTTGTATTATGCCCCCGAGTTCCAGGGCTTCGCCGC 27093  
Qy 28062 GCGCTGGAGGTTGGCGGACGATGCTCTGGCGGAGGTGCGTCTGCGGAGAGGCTCTCG 28121  
Db 27094 GGTCTACAGCGCGCGAGAGCTTTCGCGGAGCAAGCTTCGCGGACGCCG----- 27147  
Qy 28122 CGATCTCCGGCGGCGCTTCGGGTTCACCCGCGCTTGTTCGACGCGGCCCTGCACGC 28181  
Db 27148 CGAAGAGACGCGCTGTTTTGCCCTCCACCCGCGCTGCTCGACAGCGCTTGCAGGC 27207  
Qy 28182 CACGGCGCTCACCCCCAGAACGGGACGGCTCGACGGAGAACGTCGCCACGAGAGCAT 28241  
Db 27208 GCTGCGCTTTGTAGACGACAGGCAAGGCGCTTCA----- 27242  
Qy 28242 GCGTACCGCGAGCCACAGCGCGAGCTGCGGTTACGCTTGAGCGCGCTGCTCGCA 28301  
Db 27243 -----GGATGCGCTTCTCGTGGAGCGGAGTATCGCTGC 27276  
Qy 28302 CACGCGCGGAGTTCCGTTGCGGTACGCTGCGCGAGTCCGACGACGATATGC 28361  
Db 27277 CTC--CGGTGAGACCAACCTCGCGGTGCTTCCACCGCTCTGAGGCGGAATCCTC 27334  
Qy 28362 GGTGCGCTTCCCGCGCGCGACGAGACGGTGGCGGTGAGTTCGAGTGGCTCGC 28421  
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Qy 28662 TGCTCCGCGCGCGGTGCTGCTGCTAGTGGTGTGCCCCACACCGAAGCCCGGAGTA 28721  
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Qy 28722 TTCCGCGGAAGCCCCCGGGAGCGCGGACCGAGCGCTGCGAGGCGCGCGGACGCTG 28781  
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Db 27951 GATCGCTTCGCAACGCGCAACCCCTGTTTCAAGGCTCTACGCGCTGCG----- 28001  
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Db 28002 -----CCAGGCGCCACCGGA 28016  
Qy 29202 GGCAGCGGCTCCCTTCTCCGGCGGAACGGTCTGATCACCGCGGAAACCGGTGCTCT 29261  
Db 28017 CACAGCGTCCCGCGAGGCTTCGAGGACACGCTCTCATCACGGAGGACCCGACGCT 28076  
Qy 29262 GGGCGGCTCGTGGCGCGCATCTGTGGAGGCGCACGGGTACGGCATCTGTTGCTGGC 29321  
Db 28077 CGGCGCTGCTGGCGCGCGCTCGTCTGTAACACCAACGACGCAACCTGCTCTCAC 28136  
Qy 29322 GGGTGGCGGACCGGACCGCGGAGGTGCGCGGAGTTCGGGCGGAGCTCGGTGGCT 29381  
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Qy 29382 CGGCGCACGCTGGAGTCTGCTCGCTCGACGCGGCGGACCGGCGAGCTGGCGGACCT 29441  
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Db 28317 CGACGGCGATCTGCTGGCGCATGAGCTTCGAGCGGATCGACGCGCTTTCGCGCCCAA 28376  
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Db 28617 CGCCCTTCGATGAGCGCGCGG-----CCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 28673  
Qy 29862 GTTTCGAGCGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 29921  
Db 28674 CTTTCGATGCGCGCTTCTTCGAAACCGAGACCGCGCTTGGTCCCGCGCGCTTTCGACTTGA 28733  
Qy 29922 GGGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 29981  
Db 28734 CGGCTCAGGGCGGAAACCGCGCGGAG-----GTCCCGCGCGCTGCTGCTGCTGCTGCT 28787  
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Db 28788 CGCTCGACCGCTACGGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 28828

## RESULT 9

US-08-764-233A-4  
Sequence 4, Application US/08764233A  
Patent No. 5716849  
GENERAL INFORMATION:  
APPLICANT: Ligon, James M.  
APPLICANT: Schupp, Thomas  
APPLICANT: Beck, James J.  
APPLICANT: Hill, Dwight S.  
APPLICANT: Neff, Snezana  
APPLICANT: Ryals, John A.  
TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Ciba-Geigy Corporation  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,233A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/729,214  
FILING DATE: 09-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/258,261  
FILING DATE: 08-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: 1506/CIP6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28958 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Sorangium cellulosum  
IMMEDIATE SOURCE:  
CLONE: p98/1  
US-08-764-233A-4

Query Match 10.2%; Score 3140.6; DB 1; Length 28958;  
Best Local Similarity 54.1%; Pred. No. 0;  
Matches 8239; Conservative 0; Mismatches 6284; Indels 698; Gaps 63;  
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DB 14236 ACTGCCCTCGCTGCTGCTTGCAGAGCACCTCTCTCCCTCCCGCCCGGAAAGCGAG 14295  
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QY 26566 CCCGACACCCCGCATGCGCAACAAAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26625  
Db 25645 GAGGGCGCGCTCTCTCGCGCGCGCTCGACGCGCTCGACGCTGCTGCTGCTGCTGCTGCTG 25704  
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27094 CGTCTACAGCGCGGCGACGAGCTCTTTCGCCGGAAGCCAAAGCTCCCGGACGCGC----- 27147 Db  
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28182 CACGGCGCTACCCCCCAAGAACGGGACGGCTCGAGGAGAACGTCGCCCCAGGAGCAT 28241 QY  
27208 GCTCGCTTCTGTAGACGACCAAGGCAAGGCTTCA----- 27242 Db  
28242 GCCTGACGCGAGCCACACGAGCGGCTGCTGCTTACGCTTGGAGCGGCTGCTCTGCA 28301 QY  
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28002 -----CCAGCGCGCCACGGA 28016 Db  
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Db 28077 GGGCGGCTGTGGCGCGGCTGTGGTAAACACGACGACGACCTGCTCTCAC 28136  
Qy 29322 GGGTGGCGCGGACCGGACCGGAGGTGGCGGAGTGGGGGCGGAGCTGGTGGCT 29381  
Db 28137 CTCGCGCAGGCGGAGCGCTCCGGGTGCTGATGTCTTGGAAAGGAGCTCGAAGCTCT 28196  
Qy 29382 GGGCGGAGCGGTGGAGGTCTGCTCGCTCGGACCGCGCGGACCGGACGAGCTGGCGACT 29441  
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Db 28257 TCTGATAAATTCGAGCGCTCACCGGTGCGCGCTGTGATGCGCGGAGGCTCT 28316  
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Db 28317 GACGCGGATCTGCTCGGCGCATGAGCTCGAGCGGATCGACCGGTCTTGGCGCCCAA 28376  
Qy 29562 GCGGACGCTGCGTCTTCTCGACGAGCTGACGCGCGGCGGAGAGCTGTGGCTTTGCT 29621  
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Qy 29622 CATGTTCTCTCGCGGTGGCGGTGGTGGTGGCGCGGAGGCAACTACGCGCGCG 29681  
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Qy 29682 CAACGCGCTCTGACTTCTTCTGCTCATCGCGCGCGCGGAGGCTCGCGCTCTC 29741  
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Qy 29862 GTTGACGCGCTTGGCGGCGGCGGCGGCTTCTGATGCGGCTCGGCTCGGCTCAC 29921  
Db 28674 CTTCATGCGGCTCTTTCGAAACGAGACGCGCTGTCTCGCGGCTTTCGACTTGA 28733  
Qy 29922 GCGGCTAGCGTCTGTGCGGCTTCCGACCGGCTGCGGCTGCTGCAAGGTCTGCTTCA 29981  
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## RESULT 10

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; Sequence 6, Application US/08457335A  
; Patent No. 5723759

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; TITLE OF INVENTION: Genes for the synthesis of  
; TITLE OF INVENTION: antipathogenic substances  
; NUMBER OF SEQUENCES: 22

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; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
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; FILING DATE: 01-JUN-1995  
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; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/457,205  
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; APPLICATION NUMBER: 08/258,261  
; FILING DATE: 08-Jun-1994  
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; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28958 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-457-335A-6

Query Match 10.2%; Score 3140.6; DB 1; Length 28958;

Best Local Similarity 54.1%; Pred. No. 0;

Matches 8239; Conservative 0; Mismatches 6284; Indels 698; Gaps 63;

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Qy 14932 GAAGAGCTGTTGCGCCCTGGTGGCGACCCATCGCGCGCTGTGTGGGCGCATGCCACTCCC 14991  
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Qy 15232 GTCGCGATGGCTGCTCGGTACCCCGGTGATGACGAGGCTGATGATCTCTGGCAGGTG 15291  
Db 14593 GTGGGATGAGTCCCGCTTCCCGGGCGAGCTGGCGACGCCCGGAGGATCTCTGGAGCTC 14652  
Qy 15292 GTCAAGTGGTGGCCATGACGCGGATTCGCCGAGAACCGTGGGTGGGACCTCGAC 15351



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Db 14713 GCGCT-----CGACGCCCGGTCGCTTCCAGTCCGGAGGGGGCTTC 14757  
Qy 15412 CTTTAGGAGGAGGANAATTGATCCGACTTCTTCGGTATCAGTCCGGTGAAGGACTG 15471  
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Db 16108 GACAAGCGGACGAGCACGCTCTCGGACGAGCGAAG----- 16148  
Qy 16912 GCGGAGAAAGACCGGATTCATCTGCTCCGAGAGGCGACCAACGCCCGGATGCGC 16971  
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Qy	17512	AAAAACCTCCCAACCAAAAAGCGCTTCACACTCCCCCCACACAAACCCGATCTCTCAACCAA	17571
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Qy	17572	CTC-----CACGAGCACCCAAACCTTCACCTACCCACCCACCCACACCCGCCCTC	17622
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Qy	17623	ATCACCGCCAAACACCCACCCGACCAACTCTCACCCCCCACTTACTGGACCCCAACAAGCC	17682
Db	16834	GTCAACGGCACCAAGGCTCGAGCGCTCGAGCTCGACGGCGCTACTGGTATCGAAACCTC	16893
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Db	16894	CGGCAAAACCTCTCTTCTCGAGCGGACCGAGCGCTCTCGACGATGGGATCGCTTC	16953
Qy	17743	TACATCGAATCTCGGACCCGACACACCTTCAC-----CACCTTCACCCACCAACCTCCC	17799
Db	16954	TTCTGTCAGAGTCAGCCCTCATCTCCGTGCTACGCTCGCCCTTCGGAGACCTTCGAGCGC	17013
Qy	17800	AACACCCCCAACCAACCTTCACCTCACCCACCCCAACCAACCCCAAAACCCACCTC	17859
Db	17014	TCACCGCTCGATCCGCTGCTGCTCGGCTCCATTTCGACGGACGAGGCCACCTCCCGGT	17073
Qy	17860	CTCACCAACTCTGCAAAACCAACAACAACCTGGACAACCAACCACTACACCAACCAACAC	17919
Db	17074	CTCCTTGCTCTTTGGGCGAGCTCTATGGCCGGGCTTCACGCGCGAGTGAAGGCGCTTC	17133
Qy	17920	AACCAACCCACACCAACCAACCTTCGACCTCCCACTCCCACTACCTTTCCAAACCAACGAC	17979
Db	17134	TTGCGGCTTCGCTCCCGCAAGGTCCTACTCCCACTACGCTTCGAGCGGAGCGGT	17193
Qy	17980	TACTGGCTCGAAAGCACACAGCGCGGTGCGGATCCGTTTCGGGTTCCGGTTCCGGCGG	18039
Db	17194	TTCTGCTCGACGCGCCCAACGACACCCGAA-----GGGCTGCTCCCGTGG	17244
Qy	18040	GCAGGACTCGCGCGGACGCGAGAGGTGGAGTCCGCTTCGGAGCGCGTGGCCCGC	18099
Db	17245	CCGATCATGGCGGTTTGGCAAGCCATCGAAGCGGGGACCTCGACGCTCAACGCGC	17304
Qy	18100	CAGGACTGGAAGGTGCGGACACGCTGCGGTGCCCTCCCGCGGCTTCGACAG	18159
Db	17305	CAGTCC-----ACGCGGACGCGGACGACGCGCGCGCGCTTCGCGCTG	17349
Qy	18160	GTGTCGCCGCACTCTCGCTGGCACCGCACCAACACGACCAAGCCCGCATCAACACC	18219
Db	17350	CTCTCTCCACCTCTCGAGTTTACACACGAGCCAGAGGACGAGACGCTCGACACC	17409
Qy	18220	TGGAACCTACAGAAACCTTGAAACCTTCACCTCCCAACA-----CCCAACCAACCCAC	18276
Db	17410	TGGCGCTACCGCATCAGTGGAGGCTCTGACCAACCGCGCCACAGCCCGCGACCTCGCC	17469
Qy	18277	CAAACTGGCTCATCGGCATCCCGAAACCCAGACCCACCCCAACATACCAACATC	18336
Db	17470	GGCACTTGGCTCTCTGTCGCTCCGCTCGGCGACGACGCGCTCCCTCGCAACGCTC	17529
Qy	18337	CTACCAACCTCTCACACACACGGCATCACCCCATCCCTCACCTCAACCAACCAACCCAC	18396
Db	17530	ACGATGCGCTTACCCGCGCGCGCGGTGTCTCTCGCGCTTGGCTTGAGCAGGTTTAC	17589
Qy	18397	ACCAACCCCAACACCTTCACACACCCGACAAACAGCCCAAAACCAACCAACCGGACCC	18456
Db	17590	ATAGCGCGCGGCTCTTCACCGAGCACCTTGGCGAGGCTGTTCGAGAGTGC-----CG	17646
Qy	18457	ATACCGGCGTCTCTCCCTCTGCGCTTCGACGAAACACCCCAACCCCAACCAACCCAC	18516
Db	17647	ATTGCGGCGTGTCTCTCTCTCTCGCTTCGCTCGACGAGCGCCCTTCGCGAACATCGCCGC	17706
Qy	18517	ACACCCACGGCACCTCTCTCAACCTTCACCTCACCCCAACCAACCAACCAACCCACCA	18576
Db	17707	CTGCCGCGGGCTTGGCTCTCTCGCTGCGCTCTGTCGAAGCTCTGCGGACTCTCGGCTC	17766
Qy	18577	CCAACCCCTCTCTGGTACGCCACCAACAAAGCCCAACCAACCCCAACCAACCGCCCTC	18636

Db	17767	GAGGCTCCCTTGGGCTCTTACGCGCGCGCGTCTCGATTGGACATCTCGACCCACTC	17826
Qy	18637	ACACACCCACCAAGCCCAACCTTGGGACTTCGCGCGCACACACCTCTCTCGAAACACCCC	18696
Db	17827	GCCCATCCACCCAGGCATGATCTGGGGCTTGGGCGCGGTGCTCGGCTCGAGCACCCC	17886
Qy	18697	ACCCACACGCGCGGAATCATGACCTCTCCCAACACCCCAACCCCAACACCTTCAACAC	18756
Db	17887	GAGCGGTGGGGGGCTCGTGACCTCGGCGAGCGCTCGACGCGAGCGCCGACAGCGCGC	17946
Qy	18757	CTCACCAAAACCTCACCAAACCCACACCAAAACCAAACTTCGCATCGCACACACCGGC	18816
Db	17947	TTGCTCTCCGCGCTCTCCCCAGCGCCACAGCAAGAAGCAAGCTTCGCGCTCGCGCCGCGC	18006
Qy	18817	ACCCACACGCGCGCTCACCCCAACACCTTACCCCAACCAACCAACCAACCAACCCACC	18876
Db	18007	CTCTAGCAGCGCGCTTCGTCGCGCCCGCTCGGGATGCGCTTCGCGCTCGGGCTTC	18066
Qy	18877	ACCCCCACGGAACCACTCATACACGCGGAACCGCGCGCTTCGCAACCAACCTCAC	18936
Db	18067	ATGCCCGAGGACCATCTCATCACCGGTGTACCGCGCATTTGGCGCTCACGTGCTC	18126
Qy	18937	CACCACTTACACACCAACCAACCAACCAACCTCTCTTACACAGCGGAACCGGCCCC	18996
Db	18127	CGATGGCT---CGCTCGAAAAGCGCTGAGCACTCTGCTCTATCAGCCGACGAGGGGCC	18183
Qy	18997	CACACCCCCAGSCACAACTCTACCAACCAACCTTCAACAAAAGGCATCCACTCAAC	19056
Db	18184	CAGCCGAAGGCGCGTGAGCTTCACGCCGAGCTACGCGCCTCGGCGGGGTCACTC	18243
Qy	19057	ATCACCACTTGGACACCAAGCAACCCAGCAACTTCAACAACTCTCAACACCATCCCC	19116
Db	18244	TTGCGCGGTGGATGTGCGCGACAGGAGCGTGTGCGCACGCTTCTCGAGCAGCTGAC	18303
Qy	19117	CCAAACACCCCC---TCACCAACGTATCTACACGCGAGGATCTCTCGACAGCCAC	19173
Db	18304	GCGGAGGGCCACAGGTGAGCGCGGTGTCCACGCGGGCGGCATCGAGCCCAACGCTCG	18363
Qy	19174	CTCACCAACTCACCCCCACCACTCAACACGTCCTCGCGCCAAAGCCACAGCGCC	19233
Db	18364	CTCGCGCACTTCATGAGGATCTGCGCGAGTGTCTCGGCAAGGTACAGGTGCA	18423
Qy	19234	CACCTCTCCAACTCACCAACCAACCCCCCTCAACGCGCTTCGCTCTACTCTCTCC	19293
Db	18424	AGACACTCCAGACCTGTCTGCGCTCTCGACCCCTCGAGCGCTTGTCTCTCTCGTCC	18483
Qy	19294	GCGCGCGCACTTTCGGGCAACCGGCGAAGCCAACTACGCGCGAGCCAAAGCTTACTC	19353
Db	18484	GCGCGGCTGTCTGGGGCGCGGCAACAAGAGCGCTATGCGCTTCGAAACGCTTCTCTC	18543
Qy	19354	GAGCGCTCGCCACACCGCCACACCAACCTCCCGCCACACAGCATCGCTTGGGGC	19413
Db	18544	GATGCTTCGCGGAGCAGCGCGGCGAGCTTGGGCTGACGCGGACATCGTGGCTTGGGGC	18603
Qy	19414	ACCTGGCAAGGAAACGGACTGGCGACTGTGTAAGTTCAGCGAACAATCTCCGCGCGCGGG	19473
Db	18604	GTGTGGGGCGGGCGCATGCTACCGGGCTCTTGGCAGCCCACTAGAGCAAGCGGT	18663
Qy	19474	ATGTTCCGATGCGCGCGAGTTGGGGTCAAGCTGTGTGACGGCGGATCGCGAGGGG	19533
Db	18664	CTGTGCGCATGCGCCCTCTGCTGCGCGTGGCGAGCTCGCGCTGGAGCAACAC	18723
Qy	19534	CGCGCGAGTCTCTGTGCGCCATATCGACTCGAAGAAATTGGGACCGGTTCTCTCCAGC	19593
Db	18724	GAGACACCTTACCGTGCACATCGACTGGGCGCGCTTTCGCGCTTCGTTTTCAGCGCC	18783
Qy	19594	AAGTCGTGCGTCTTGCTCGAG---GACCTTCCCAAGGACAGGAACTGAGGAGCGCGC	19650
Db	18784	GCTCGCTCCGCGCGCTCTCTGCGGATTTGCCCCGAGGCGAGCGCGCTCTCGAAGCCAGC	18843
Qy	19651	AG-----TACCGTTGAGCAGACGAGAGCAAAACCTTCGCGCAACTCTCATGGGTGG	19704

Db 18844 GCCGATGGCTCTCCGAGCAAGACGGGGCCACAGGCTCTCTCGACAAGCTCCGAAACCGC 18903  
Qy 19705 TCACGTTCCGACGAGAAAGAGAGTGTCTAGCCTCGTCCGATCCACTCCCGCGAGTG 19764  
Db 18904 TCGGAGGCGAGAGATCCACTGCTCTCTCGTGGTGGCCACGAGCGGCTCTGTC 18963  
Qy 19765 CTCGGGCGGAGAGATCCGAGGCCATCCCGCCGGTGGCTTTTCAGGGATCTAGGGTTTC 19824  
Db 18964 CTGGGCCATACCGAGCGCTCCAGAGTCCAGCCGCCCAAGGGCTTCATGGACCTCGGCTTC 19023  
Qy 19825 GACTCGCTTGGCGGCTGGAGCTTCGCAACCACTTCGAGCAGACAGACGAGTGGCTTCG 19884  
Db 19024 GATTGCTCATGACCGTGGAGCTTCGTGGCGCTTCGACAGGCGACCGGCATCAAGCTTC 19083  
Qy 19885 CCGAGGACTCTGCTCTTCGATTACCCAGCGCCACCAAGCTCGGCCAAATTTCTGCTCTCC 19944  
Db 19084 CCGGCCACCTCGCTTCGACCATCCCTCTCTCATCGGCTCGGCTCTTCTTGGCGGAC 19143  
Qy 19945 GAGATCGGAGATTTCAGGCCCGACA-----ACTCAACTCCGTTCCG 19986  
Db 19144 TCGCTCGCCACGCGCTCGGCGAGGCTCTCCGTGAGCGGAGCGCGCGCTCCG 19203  
Qy 19987 CGACCCCGGAGAGCTGATGAGCGGATCGGCATCGTGGCATGGCTGTGCTTCC 20046  
Db 19204 GCGCTTCGCTCGGCGAGGACAGGCCCATCGGCATCGTCGGCATGGCTTCGCTTGGCG 19263  
Qy 20047 GCGGAGTGACCTCGCGGAGACACTTCGGGATCTGATCTCTCGAGCAGGACGATC 20106  
Db 19264 GCGGCGATCGGCGATGTGACGCTCTTTGGGAGTTCTCGCCAGGAGCGAGCGCTC 19323  
Qy 20107 GCGGATTCGCCACGAGCGGCTGGGACCTTGGACACGCTCTAGACCCCGACCCGAC 20166  
Db 19324 GAGCCCATTCGCCCATGCC- --GATGGGATGCGGTCGCTCTACGACCCGACCCGAC 19380  
Qy 20167 CACCCCGGACCTGTACTACCCGAAACGCGGATTCCTCTAGACGCGAGGCCACTTCGAC 20226  
Db 19381 GCCAAGGCGAAGAGTACGTCCGGATGCGCGCATGCTCGACAGGTTCGACCTCTTCGAT 19440  
Qy 20227 GCGGAATTCCTCGGATCAGCCCGCGAAGCCTCGGCATCGACCCCGACCAAGACATC 20286  
Db 19441 CTGGCTTTTGGGATCAGCCCTCGGAGGCGAAATCTCGACCCCGACGACGCTG 19500  
Qy 20287 CTCCTCGAAACCGCTTGGGAAACCATCGAACCGCGGATCAACCCCGACACCTTCAC 20346  
Db 19501 CTCCTCGAATCTGCTGGCTGGCTCGAGGACGCGGATCGTCCCTCCACCTCAAG 19560  
Qy 20347 GGCACCCCGAGGATCTTACCGGACCAAGAGACAGGACCAAGCGGACACATCGT 20406  
Db 19561 GATTCTCCACCGGCTCTTCGTGGCATCGGCGCGAGCGAATACGCACTGCGAATC--- 19617  
Qy 20407 CAGGCGCCGAGCGGTACGAGGGATTGCTCTGACCGGGGAGCCACACGATCGCTCC 20466  
Db 19618 ACGAGCTCGAAGAGGTGAAAGGTATGCCCTTCAAGGACACCGCGGGTCTTTGCGGG 19677  
Qy 20467 GCGGAAATCTCTATCATCTCGGTTGGAAGGCGCTGCGGTCACTCGACACAGCGTGT 20526  
Db 19678 GCGGCTTGGCTCTACGCTCGGCTTCAAGGCGCGGCTCTCTCGTTCGACACCGGCTGC 19737  
Qy 20527 TCCTCTCGCTGCTGCTGCTGACCTCGCTCGGCTGCGAGTCCCTCAGGTCGGTGAATGAC 20586  
Db 19738 TCCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 19797  
Qy 20587 ATGGCTTTGGCGGGGCGGCGGCTCATGACACCCCGATCACCTTACCGAATTCGCG 20646  
Db 19798 CTCGCGCTCGCGGGGCTCTCGGTATGGCTTCCCGGGGCTCTTCGTCTCTCTTCC 19857  
Qy 20647 CGCCAAACGCGGACTCGCCCGCGAGCGGCTTGAAGGCGTTCTCGGCGGCGCTGACGCT 20706  
Db 19858 CGCATGCGTCTTTGGCGCGCGATGGCGCTTCCAGACCTTCTCGACCAACCGCGAGCGG 19917  
Qy 20707 ACCGCTGGGTTGAGGTTGGGATGTGTGTTGGAGCGGCTCTTCGACGCGCGCGCG 20766  
Db 19918 TACGGAACGGAAGAGGCGTCTGCTCTTGGCTCTCGAGCGGCTCGGCGACGCGCTCGCC 19977

Qy 20767 AACGCTACCGTGTCTTGGCGGTGGTGGCTGGCTGAGTGGCTGCAACACGAGACGGTTCGAGC 20826  
Db 19978 CGAGGACACCGGCTCTCGCTTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGGTGGCTGG 20037  
Qy 20827 AACGCTTGAACCGGCGGCAAGCGGCGCTTCCAGAGCGGCTTCATCGGCGAGGCTTCGCG 20886  
Db 20038 AGCGGCTACCGGCGGCAAGTGGCACTTCCACCAAGAGGCTTCTCGGCGCGGCTTCAC 20097  
Qy 20887 AACGCGGACCTGACCCCGCGGAGCTGATGCGGTGGAGGCGCCAGGACCGGCAACCT 20946  
Db 20098 GAGGCCATATGCGGCTTGGCGAGCTCGATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTG 20157  
Qy 20947 TTGGCGGACCGGATCGAGGCGGCGGCTCTCTCGGACCTACGAGACGAGACCGTCCCGG 21006  
Db 20158 TTGGGAGACCCATCGAGGTGCAAGCCCTGGCGCGCTTACGCGGATGGCAGACCGCT 20217  
Qy 21007 AACGGGCGTGTGGCTGGCTCGTCAAGTCAAGTGGCTTCCGCGGCGGCGGCGGCGG 21066  
Db 20218 GAAAGCGCTCTCTTCTCGGCGCACTCAAGACCAATTTGGGCACTCTCGAGGCGGCTCC 20277  
Qy 21067 GCGGTGGCGGAGTGAATCAAGATGTGATGGCTTCCGCGGCGGCGGCGGCGGCGG 21126  
Db 20278 GGCCTCGGCGGCTGCGCAAGATCGCTGCTTCCGCGGCGGCGGCGGCGGCGGCGG 20337  
Qy 21127 CTCCACGCGGATGAGCGCTCGCGCATGTGGACTGTGCGGCTGCGGCGGCTGCGTGTG 21186  
Db 20338 CTCCACACGACCGCGGCAATCCCTGATCGATGGATGCGCTGCGCATCGACGCTGTC 20397  
Qy 21187 ACGGAGAGGCTGCTTGGCGCGG---CGGAGAGGCGGCGGCGGCGGCGGCGGCGG 21243  
Db 20398 GATCCACAGGCGGCTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTCC 20457  
Qy 21244 TCATTTCGGGCTCAGCGGACCAACCGCCAGCTATCTCGAAGAGAGCAGCGCGGCGG 21303  
Db 20458 GCCTTCGGACTCTTCGGGACCAACCGCCAGCTTATCTCGAAGAGGCTTCCG- - - - -C 20510  
Qy 21304 GTTTCGGGCGGACCAACCGCGCGGAGGATGCGGTAGTGGCGGAGGAGGCTCTGCGCGG 21363  
Db 20511 GATCCCGAGCGCGGAGCCACCGCGGCGACG- - - - -TCGCGTGCAGCGCTTCCCG 20564  
Qy 21364 AGTCTCGGCTGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 21423  
Db 20565 AGCC-----TGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 20616  
Qy 21424 GCCAGGCGCTGCGACCGGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 21483  
Db 20617 GCGGAGAGGCTTCGCGGACACCTCTCGCCACAGACGACCTCGCTTGGCGGATGTAGCC 20676  
Qy 21484 TACACCTTCGCGGCGGCGGCTGTTTCGACCAACCGCGGCGGCGGCGGCGGCGGCGG 21543  
Db 20677 TACTGCTGCGGCGGCGGCTGCTTTCGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTG 20736  
Qy 21544 GCGGACCTTCTTCGAGAGCTCAGGAGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 21603  
Db 20737 GCGGAGAGGCTCTCTCGCGCTCGATTGCTGCTGCGCGGAGGAGGAGGAGGAGGAGGAG 20796  
Qy 21604 ATCCACAGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 21663  
Db 20797 GTGCTGAAAGCGGAG-----CCACGGCAAGGTGCTGCTTC 20835  
Qy 21664 ATCTGCTCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 21723  
Db 20836 GTCTTCTGCGGAGGCTCGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 20895  
Qy 21724 CCGGCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 21783  
Db 20896 CCGGCTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 20955  
Qy 21784 CCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 21843  
Db 20956 TGCTGCTCGGCTGCT-----CCGCGGCGGAGGAGGCGGCGGCGGCGGCGGCGGCGG 20994

Qy	21844	CTGCTCAGCAGACCCCGTATAGCCCGAGCCGCGCCTCTTCGCGCTTCAGGTGCGCCTCCAC	21903
Db	20995	CCGCTCAGCCGGGTTCGACGTGGTTCGACCGCGCGCTCTTCTCGATGATGTCTCGCT--GG	21051
Qy	21904	CGCTCTCTACCCGAGGGTACCAATACACCCCCCACTACTAGCGCGGACACTCCCTCGCG	21963
Db	21052	GCGGCCCTGTGGCGCTCATTGGCGGTTCGAGCCCGAGCGGGTGTGCGCCATAGCAGGGC	21111
Qy	21964	GAATACACCGCCGCCACCTTCGCGGGCATCCTCACTTCACCGACGCGACCCACCTCATC	22023
Db	21112	GAGTCCGCGGGCGTGTGGCGGGCGCTGTCTCGAGGACGTCGCAAGCTGGTG	21171
Qy	22024	ACCAACGCGCC--ACCTCATGCAAAACAATGCCCGCCCGGACCAATGACACCTCCAC	22080
Db	21172	GCGTCGCGAGCGGTGCGCTCGTGGAGCTCGCGGCGAGGGGCGCATGGCGCGGTGGAG	21231
Qy	22081	ACACCCCAACACATCACCAACCACTTCACGCGCCCAAGAAAAGACTTCGCGCATGCC	22140
Db	21232	CTGCGGAGGCCGAGGTTCGACGCGCGCTCCAGCGTATGGCGATCGGCTCTCCATCGGG	21291
Qy	22141	GCCATAAACACCCCACTCCCTCGTCATCAGGGGCAACCCCAACCGTCCAAACATC	22200
Db	21292	GCGTCAACAGCCCTCGTTTCAAGATCTCGGGAGGCCGCTCGGTTCGCGCGCCTG	21351
Qy	22201	ACCACCTCTGCCAACAAAGGCATCAAAAACAAACCTCCCCCAACACCGCTTC	22260
Db	21352	CTCGCGATCTGGAGTCCGAGGGCGCTTCGCGCTCAAGCTGAGTTAGACTTCGCTCC	21411
Qy	22261	CATCCCCCAACCAACCCCTCTCAACCAACTCCACGAGCACCCAAACCTCACC	22320
Db	21412	CATTCGCGCAGGTTCGAGTCGATTCGCGAGACTCTCGATCTCTGTGTGGTTCGAG	21471
Qy	22321	TACACCCACCCCAACCCCTCATCACGCGCAACCCCAACCGGACCAACTC-----	22374
Db	21472	CGGGCTCGAGGGCGTCCGTTCTACTCAGGTGAGGGCGCGCGATCGACGGAGC	21531
Qy	22375	---CTACCCCCCACTATGGAGCCCAAGCCGCAACACCGTCGACTACGCCACACC	22431
Db	21532	GAGCTCGACCGCGCTACTGTTACCGAACTCCGGCAGCGGTCCGCTTCGACAGCT	21591
Qy	22432	ACCCAAACCTTCACCAACAGCGGCTCACCACTATCGAATCGGACCCGACAAACC	22491
Db	21592	GTGCAAGGCT---CCTTGGCGGAGAACATCGCTTCTTCTGTGGAGTGAAGCCCACT	21648
Qy	22492	CTCACACCTCTACCAACCAACCTCCCAACACCCCAACCAACCTCACCCTCACC	22551
Db	21649	GTGCTGACTTGGCTTGACAGACTCTTGAAAGCTCGGAGGCTCGCGGGCGGTGGTC	21708
Qy	22552	CACCCCAACACACCCCAACCCCTCTCAACACCTCGCCAAACCAACCAACCACC	22611
Db	21709	GGCTCTGTGGAGCGAGGAGGGATCTAGGCGCTTCTCTGTCTCGCTCTCCGAGCTC	21768
Qy	22612	TGGGACCCCAACCACTACCCACACCAACCAACCCCAACCAACCACTTCGAC	22671
Db	21769	TAGCTCAACGGCTTCGCGCTTGATTGGACGAGATCTTCGCCCGCGGGAAGGGGTGG	21828
Qy	22672	CTCCCACTTACCCCTTCACACCAACCACTACTGTGCTCGAACTACCGAGCGCCAAAC	22731
Db	21829	CTGCCCACTTACCCCTTCAGAGCGAGCGCTTCTGTGCTCGAGCTTCACGGCAACCG	21888
Qy	22732	AGCCCGGTCAAGGGGTTCTCGCGCTCGGCTCCAGACACGCGCGAGTCGGAGTCTGG	22791
Db	21889	GCCGGGTCAACCACTTGTCTCGCTCGAGGGC-----GGTTGCGAGGCCATCGAG	21942
Qy	22792	GACGGGTGAACGAGGAGACCTTCAGAGCTTCGCCGAAACCTTCGACATCGACGCTCT	22851
Db	21943	AGCGGGAATATCGACGCGCTCAGCGGCCAGCTCCAGTGGACGGGACGAGCAGCGCGC	22002
Qy	22852	GCTCTGACACGGTGTGCCGCACTCTCGCTTCGACCGGCCACCAACCAACCAAGCC	22911
Db	22003	GCCCTTGCCCTGCTCTCTCCACCTTCGAGCTTTTCGCCACGAGGGGCAAGAGCAGGG	22062
Qy	22912	CGCATCAACCTGGACCTACCAAGGAAACCTGGAAACCCCTCACCCTCCCAACCAACCAC	22971

Db	22063	ACGGT	CGAGCGCTGGCGCTACCGCAT	CACTGGGAAGCTCTGACCA	CCGCCACCA	CGCC	22122
Qy	22972	CAACCCCA	---CCAAACCTGGGTCTATCGGCAT	TCCTCCCGAATA	CCGACACCA	CCACCCCCAC	23028
Db	22123	GCCGACTGGCGGGACCTGGCTCTCTGTC	GTGCGCGGCTCTGGACGACGCGCTC	TCGACGACGCGCTC	TCGACGACGCGCTC	TCGACGACGCGCTC	22182
Qy	23029	ATCACCAACATCTCTACCAACTTCA	CCACCAACGCGATAC	CCCCCAT	CCCCCTCATCTGC	23088	
Db	22183	CCCTCCGCGCTACCGAGCGCT	CGCCGCGCGCGCGGCTCTCGCGCTGCGCGCTG	22242			
Qy	23089	AACGACACCGACACAAACCCCAAC	ATCTCACACACACCTTCCACCA	CCCTCCACCA	CACCCGACAA	23148	
Db	22243	AGCCAGCCCACTGACGCGAGGCTCT	TCGCGCGAGCACCTTGC	CGCAGCGCTTG	-----	22295	
Qy	23149	GCCCAAAACACACACACCGGAC	CCCATACACGCGCTTCTCTCCCTCTCG	CCCTCGCCCTCGACGAA	23208		
Db	22296	-----	CGCGAGACCGGCGCTCGCGCGTCT	CGTCTCTCGCTCTCGCTCTCGACGAA	22347		
Qy	23209	ACACCCACCCCAACACCCCAACAC	CAACACCGGACCTCTCTCAACT	CAACTCA	CCCTCCCTCC	23268	
Db	22348	AGTCCCTCGCGACCA	TGCGCGCTGCGCGGACTCGC	CTTCTCGCTCA	CCCTCGCT	22407	
Qy	23269	CAAAACCCACACCAACCCCAAC	CAACCCCTCTGTGTACGACACCA	CAACACGAC	23328		
Db	22408	CAAGCCCTCGGCGACATCGCTCT	CGACGCGCTTGTGTGCTCTT	CAACCGCGCGCGCTC	22467		
Qy	23329	ACCACCAACCCAAACGACCCCT	CTCACACCCACCCCAAGCCAA	CTGGGACTCGCC	23388		
Db	22468	TCCGT	CGGACATCTCGACCCCATCGCCCAT	TCGACGCGAGTGAT	CACTGGGCGCTGGGC	22527	
Qy	23389	CGCACCACTCTCTGAAACAC	CCCCCAACACCGCGGAAT	CATCGACT	CTCCCAACAC	23448	
Db	22528	CGCGTCTGGCTCGGCTCGAGCA	CCCCCGAGCGCTGGGAGGCT	CGTCTGAC	GTGGCGCAGCG	22587	
Qy	23449	CCACCCCGCACACCTCTCAC	CACTCAACCAAA	CCCTCA	CCCAACCCCA	23508	
Db	22588	ATCGACCGGAGCGCGCTGGCGCG	CTTGTCTCCGCGCTCTCGCCCT	CGCAACGAT	GAGAC	22647	
Qy	23509	CAACTCGCATCGCACACCGCAC	CCCAACACCGCGCTCAC	CCCCCGCTCAC	CCCCCACACCTCAC	23568	
Db	22648	CAGTCTCTCTCGCCCGCGGGT	TTACGCTCGCGCTCGT	CGCGCTCGCTCGGCTCGGC	22707		
Qy	23569	CCCACACCAACCAACCCCAAC	CCCCCAACCGGAA	CCCTCAT	CACCGGCGAAC	23628	
Db	22708	GACGCGCGCGCAGTACTT	CAAGCCCGAGGCA	CCCTCTCAT	CACCGGAGCAC	22767	
Qy	23629	GGCGCCTCGCACCACTCTCA	CCCAACACTCA	CAACCAACCA	CCCAACCA	23688	
Db	22768	GGCGCGCTGGCGCTCAC	GTCTCGCGCATGGCT	---CGTCTGAGAGGGCGAG	CACTCTC	22824	
Qy <sup>1</sup>	23689	CTCTCACGAGCGAACCGGCG	CCCCCACACCCCAACGAC	CAACCTCAC	CACCCCACTC	23748	
Db	22825	GTCTCATAGCGCGAGGGG	CCCAACCGCGGCGCTCGGAGCT	CAACGCGAGCTC	CAACGCGAGCTC	22884	
Qy	23749	CAACAAAAGGATCCACCT	CACCATCACACCTCGAC	ACACGACCA	CCGACCACTC	23808	
Db	22885	ACGGCCTGGGCGGCGTCACTT	TCGCGGTGTGTGTGCGCGA	CAGGAGCGCTGT	22944		
Qy	23809	CAACAACTCTCAACACCAT	TCGCCCAACACCC	---TCACACCGT	CATCCACAC	23865	
Db	22945	GCCACGCTCTCGAGCAGCT	CACGCGCGAAGGT	CGCAGTCCGCGCGT	GTTCACGCG	23004	
Qy	23866	GCAGGCGTCAATCTCTT	CGCCCGGTTCGGAACCGAT	TCCTCTCTTCGTT	23925		
Db	23005	GGCGGATCGGGCGCAC	CTCGCTCGCGCA	CTCTCTCATGGAGCT	CGCGACGTT	23064	
Qy	23926	ACGGCAGCGAAGCAACGGG	CGCGCATTCGTGAT	GAGTCTCTCTCGA	CCATGAAACG	23985	
Db	23065	GTCTCTGCCAAGGTCT	AGCGCAGGGAACCT	CCAGCA	---CCTGCTCGGTCT	CGACCC	23121
Qy	23986	CTTGAAACATTCATCTCTT	CTCTGTCGGCGCGCT	TGGGCGAGCGGGAAT	CACTGATG	24045	

Db 23122 CTCGACGCCCTTCGTCTCTTTTCGTCCATCGCAGGCGTCTGGGGGGCGGCAACAAAGCC 23181  
Qy 24046 GCATATCGCGGCCCAACATACCTTGGACGGGCTCGGACGCGCATCGTCAGACACATGGA 24105  
Db 23182 GGATAGCCGCCGGAACCGCTTCTCGACGCCCTGGCGCACGCGGCGCATCTTGA 23241  
Qy 24106 CTTCCGGGGGCAATCGATCCCTCGGGCCCTTGGGCCGGAAGGCAATGTCGCCCGGTGAT 24165  
Db 23242 CAGCCGGACACGCTCGGTGTGGGGCGGTGGGGCGGCGGTGGTATATTCACGGGG 23301  
Qy 24166 GCGGCTCATGTTACTCTGAAAGCGCGCATCTGCCGATGGAGCCGATGGGCTC 24225  
Db 23302 CCCCTGGACCCAGCTGGAGCAACGTCTGTCTGCCGATGGCCCTTTCGTGGCGGTG 23361  
Qy 24226 GGGGCAATTCATCTGTCGGGGCGCAGCGGCCGAATTCAAACCTGATCATCGCGACATC 24285  
Db 23362 GCGGCGCTCGCAAGCCCTGGAGCACGACGAGA---CACCGTACCGTTCGCCGACATC 23418  
Qy 24286 GACTGGAGCGCTTCGTCCCGGCTTCACCGCTCGAGCCACAGCCCGCTCATCGAGGAC 24345  
Db 23419 GACTGGGCGCGCTTTCGCGCTTCGATCAGCGTCTGCTCGCTCGCGCGCTCTCTGCGGACT 23478  
Qy 24346 ATTCCGGAGTTCCGCAAGCGGCTCAGGAGCTGGAAGCAGCTCGCTCGAGCCAAAGACG 24405  
Db 23479 TGCCGAGAGCGCGCCCTCGAAGACAGAGAAGGCGCGCTCTCTCGAGCACGCGCCGG 23538  
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Db 23539 CCCCCG-----ACCTCTCGACAACTCGGAGCGCTCGGAGAC 23580  
Qy 24466 AAGCAGAACAGGTGTCTCGGCTTGATTCGGAAGGATCTGACACGTTCTCGGCTT 24525  
Db 23581 GAGCAGCTCGCTGTCTCGCGCGCTGTGTGCGACGAGACGCGCCCTCTGCTCGGCCAC 23640  
Qy 24526 CGTAATCCGAAGGCATCAGAGCCAAACGAGCTTCGCGGACTCGGCTTCGACTCGCTG 24585  
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Db 23761 CTGCGCTTCGACCATCTCTCTCATCGCTCGCGCTCTTCATGCGGACTCGCTCGCC 23820  
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Qy 24826 GTACGTTTCGCGAGCACTGTGGGAATGCTCGCTTCGGGTAAAGCAAGCTATCGGCGTC 24885  
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Qy 25126 CCCACCGGAGTCTTCGCGGGAATCAACGCTCAAGACCACGCGCGCATATCCGCAAAAGC 25185  
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Db 25060 GATACCCGAGGCGCTTGGCGCGCGCACGAAGATGGCAGTTCGCGCGCGCGCATCTCC 25119  
Qy 26026 TCATTTCGGCGTTCAGCGGACCAAGCCCGCATCATCTCTCGAAGAGCAACCACTCCCCAG 26085  
Db 25120 GCCTTCGATTTCTCGGCGACCAAGCCCACTCATCTCTCGAAGAGCTTCCCGCGCGCTG 25179  
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Db 25231 TGGCGCGTCTCTGTCGCGGAGGACGAGGCGCGCGCTCCGCGCGCGCGAAGCGGCTC 25290





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Db 27501 CATGCGCGCGAGCGGTGCGCTCTCGGACAGAGGTCTCGACCTCGGGACGAGGTGCC 27560  
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Qy 28722 TTCCCGGAAGCCCCCGGGAGCGGACCGAGGCTCGAGGCGCGCGCGAGCTGCT 28781  
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Qy 29202 GCGAGGCTGCTTCTTTCGCGGCGGAACGCTGCTGATCACCGCGGAAACCGGTGCT 29261  
Db 28017 CACAGGCTCCCGCGAGGCTCGAGGACCGCTCTCATCAGGAGGACCGCGCAGCT 28076  
Qy 29262 GGGCGGCTGCTGCGCGCGGCTGCTGAGAGGCGACGCGCTGCGGATCTGTTGCTGCG 29321  
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Qy 29322 GGGTGGCGCGGACCGGAGCGCGAGGTGCGCGGAGTTGCGGGGAGCTCGGTGGGT 29381  
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Qy 29382 CGCGCGGACGAGGTGCTGCTGCTGCGACGCGCGGACCGGCGAGCTGCGCGACCT 29441  
Db 28197 GGGGGCTTCCGTCACTCGCGCGGTGCGAGCTGCGGCGGATCCAGGACCT 28256  
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Db 28257 TCTGGATAACATTCGAGGCTCAACCGGTGCGCGCGCTGCTGCTGCTGCGCGCGGCTCT 28316

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Qy 29622 CATGTTCTCTCGCGGTGCTGCGGTGCTGCGCGGAGGCAACTAGCGCGCGC 29681  
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Qy 29682 CAACCGCTCTCTGCTTCTTCTGCTGCTGCGCGCGCGCGAGGCTGCGCGCGCTCT 29741  
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Qy 29862 GTTCGACGCGCTTGGCGGACGCGGCGGCTTCTGATGCGCGCTCGGCTCGACTCAC 29921  
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Qy 29922 GCGCGTACGCTGCTGCTGCGCGCTGCGCACCGGCTGCGCGCTGCTGCAAGGCTCTGCTCA 29981  
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## RESULT 11

US-08-729-214-6  
; Sequence 6, Application US/08729214  
; Patent No. 5817502  
; GENERAL INFORMATION:  
; APPLICANT: Ligon, James M.  
; APPLICANT: Hill, Dwight Steven  
; APPLICANT: Ryals, John Andrew  
; APPLICANT: Hammer, Phillip E.  
; APPLICANT: van Pee, Karl-Heinz  
; APPLICANT: Kirner, Sabine  
; TITLE OF INVENTION: Genes for the synthesis of  
; antipathogenic substances  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ciba-Geigy Corporation  
; STREET: 520 White Plains Road  
; CITY: Tarrytown  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/729,214  
; FILING DATE: TBA  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP5  
; TELECOMMUNICATION INFORMATION:





18997 CACACCCACGCAACACCTCACACCCAACTCCAAACAAAGGATCCACCTCACC 19056  
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19057 ATCCACCTCGGACACCAACAGCAACCCAGCAACCACTCCCAACACCACTCCC 19116  
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20038 AGCGCATCACCGCGCGCAATGCGACCTCCACCAAGAGTCTCTCGCGCGCGCTTCCAC 20097  
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21127 CTCCACGCGGATGAGCGCTGCGCGCATGTGAGTGTGCTCGGCGGCGGCGGCGGCGG 21186



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Qy	21187	ACGGAGACGGTCCCTTGGCCCGG---CGGGAGGGGCGCGCGGGGACGAGTGTC	21243	22261	CACCTCCCCACACCAACCCCATCTCAACCAACTCCACACGACCAACCAACCCCTCACC	22320
Db	20398	GATGCCACGAGGGGTGGCGCGCCACGAAGATGCGAGTCCCGCGCGCGCGGCTCTCC	20457	21412	CACCTCCGCGAGGTGAGTCTGATTCGCGACGAGTCTCTCGATCTCTCTGTCTGTGGTTCGAG	21471
Qy	21244	TGATTCGGCGTCAGCGGCAACCAACGCCACAGTATCTTCGAAGAAGCACCCCGCAGAC	21303	22321	TACCAACCAACCCCAACCCCTCATCACCGCCCAACACCCCAACCCCAACCAATC-----	22374
Db	20458	GCCTTCGGAATCTCGCGCAACCAACGCCACAGTATCTTCGAAGAGGCTCCCG-----C	20510	21472	CGCGCTCGACGGCGGTCCCGTCTTACTCCACGGTGAGCGCGCGCGATCGACGGGAGC	21531
Qy	21304	GTTCGGGGGACCAACCCCGCAGAGGATGCGGTAGTGGCGAGGAGGCTCTGCGCGC	21363	22375	---CTCACCCCGCACTACTGACCCCAACAGCGCGCAACACGTCGACTACGCGACACAC	22431
Db	20511	GATCGCGAGGCGGACCCACCGCGCACAGC-----TCGGCTCGACGCGCTTCCCGC	20564	21532	GAGCTCGACGCGCGCTACTGTGTACCGGAACCTCGCGGACCGCGTCTGCGACGCT	21591
Qy	21364	AGTCTCTGGGTGTGGCCGTGGGTGTGGCCAGTCCAGCGCGCCCTGCGCGCCAG	21423	22432	ACCAAAACCTCCACCAACACGCGTCAACCTACATCGAACTCGGACCCGACAAACAC	22491
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Qy	21424	GCCAGGCGCTGACGCCCACTCAACCAACCAACCGCGCTCGACCTCGCGACGTGGA	21483	22492	CTCACACCTCACCCACCAACCTCCCAACACCCCAACACCAACCTCACCTCACC	22551
Db	20617	GCCAGAGGCTCCGCGACCACTCTCGCGCCACGACGACCTCGCTGSCCGATGTAGC	20676	21649	GTGCTGACCTTGGCTTTCACGAGCTCTCGAAGCGTCGGAGCGCTCGCGCGGTGCTC	21708
Qy	21484	TACACCTCGCCACGCGCGCGCGTGTTCGACCAACCGCGCCACACCTCATCGCGCGGAC	21543	22552	CACCCCAACACACCCCAACCCCTCTCTACCAACCTTCGCAAAACCAACCAACAC	22611
Db	20677	TACTCGCTCGCCACCAACCGCGCTTACTTTCGAGCACCGTSCCGCTCTCTGTGTCCACGAC	20736	21709	GGCTCTCTGTGGAGCGACGAAGGGATCTACGGCGCTTCTCTGTCTCTCGAGCTC	21768
Qy	21544	CGCGACACCTCTCTGCAAGCACTCCAGGCACTCGCGCAGGCGAACCACCCCGCGCTC	21603	22612	TGGCACCCCAACCACTACACCCACCAACCAACCAACCAACCAACCAACCAACCTCGAC	22671
Db	20737	CGCGAAGACTCTCTCGCGCTCGATTCTGCTCGCCAGGAGCGCGCGCCCGAGCACC	20796	21769	TAGTCAAGCGCTTGGCGCTGATTTGGAGAGATCTCTGCCCCCGGGAAGGGGTGCGG	21828
Qy	21604	ATCCACAGCAGCGCCCGCAGCGGACCGGACCGGGAGCGCGAGGAAGACCGCATTC	21663	22672	CTCCCCACCTACCCCTTCCAAACCAACCACTACTGGCTCGAACTACCCAGCGGCCCAAC	22731
Db	20797	GTGCTCGAAGCGGAG-----CCACGGCAAGGTCTCTTC	20835	21829	CTGCCCCACTACCTTCCAGCGGAGCGCTTCTGGCTCGAGCGCTCCACGCGACCCGCC	21888
Qy	21664	ATCTGCTCGGACAGGGACCAACCGCCCGGATGGCCCAAGGCTCTACCAACCCAC	21723	22732	AGCCCGGTAAAGGGGTTCGCGCGTTCGGCTCGAGTCCAGACACCGCGAGTCGAGTCTGG	22791
Db	20836	GTCTTCTCGGCAAGGCTCGAGTGGGAAGGATGGCCCTCTCCCTGCTCGATACCTCG	20895	21889	GCCGCGTCAACCACTTGTCTCGCTCGAGGGG-----GGTTCTGCGAGCCATCGAG	21942
Qy	21724	CCGCTCTTCGCGCGCGCACTCAACGACATCTCACCCACTCGACCCCGCCACCTCGACCC	21783	22792	GACGCGTGAACGAGGAGCTCCAGAGCTCGCCGAAACCTCGACATCGAGCGCTCT	22851
Db	20896	CGGCTCTTCGGGCAAGCTCGAAGGTGCGAGCGCGCGCTCGCGCCCAAGTGGACTGG	20955	21943	AGCGGAATATCGACGCGCTCAGCGCGCAGCTCCACGTGGAGCGGCGAGCGCGCGCC	22002
Qy	21784	CCCTCTCTCCCTCTCTCAACCAAAACGACAAACGACGACGACGAGGACGCGCGCGCA	21843	22852	GCTCTGGAACGCGTGGTGGCGGCTCTTCGCCCTGGCAACCGCCCAACCAACGACCAAGCC	22911
Db	20956	TGCTGCTCGCGTGT-----CCGCGGAGGAGGCGCGCGC	20994	22003	GCCTTGCCTGCTCTTCCCACTTCGCGAGCTTTCGCGAGCGGCGGCAAGAGCAGGCG	22062
Qy	21844	CTGCTCCAGCAGACCCGTAACCGCAGCGCGCTCTTTCGCTTCAGAGTTCGCTTCAC	21903	22912	CGATCAACACTCTGACCTACAGGAAACCTTGGAACCCCTCACCTCCCCCAACACCCAC	22971
Db	20995	CCGCTCGACCGGTCGACGTGGTCCAGCCCGCGCTTTCTCGATGATGCTCTCGCT---G	21051	22063	ACGCTCGACGCGCTGGCGCTACCGCATCACGTGGAAGCTCTGACGACCGCGCACCGCC	22122
Qy	21904	CGCTCTCTCACCGAGGCTACACATCACCCCGCACTACTACGCGGACACTCCCTCGGC	21963	22972	CAACCCCA---CCAAACCTGCTCATCGCATCCCGGAAACCCAGACCCACCCCGCCAC	23028
Db	21052	GCGCGCTGTGGGCTTCATGGGCTGAGCCCGAGCGCGGTGTGGCCATAGCGAGGCG	21111	22123	GCGAGCTTGGCGGCACTTGGCTCTGTGTGCGCGCGCTCTTGGAGCGAGCGCGCTC	22182
Qy	21964	GAAATCACCGCGCCACCTCGCGGCTATCTCACCTCACCGAGCGCACCAACCTCATC	22023	23029	ATCACCAACTCTTCAACCACTCCACCAACCAACCGGCTACCGCCATCCCTCTCACTGTC	23088
Db	21112	GAGATCGCGCGCTGTGTGGGGGCGCTGTCTGCTCGAGGACGCTGCGCAAGTGTGTG	21171	22183	CCCTCGCGCTCACGAGGCGCTCGCGCGCGCGCGCGCGCTCTCGCGTGGCGCTG	22242
Qy	22024	ACCAAGCGGCG---ACCTCATGCAACCATGCCCCCGCGCACCATGACCAACCTTCAC	22080	23089	AACACACCAACCAACCCCAACCTTCACCAACCTTCACCAACCTTCACCAACCCGACAA	23148
Db	21172	GCGTTCGCGAGCGTGTGCTGTGAGTCTCGCGGCGAGGGGCGCATGCGCGCGTGGAG	21231	22243	AGCAGGCGCACCTTGAGCCGCGAGGCTCTCGCCGAGCACTCTGCGCGAGGCTTG-----	22295
Qy	22081	ACCACCCACACATACCAACCACTCACCGCCCGCAAGAACGACTCGCCATCGCC	22140	23149	GCCCAAAACCAACCAACCGGACCCCATCACCGGCTGTCTCTCTCTCGCCCTCGAGAA	23208
Db	21232	CTGCGGAGGCGAGGTGCAACGCGCTTCAGCGCTATGGCGATCGGCTCTTCATCGG	21291	22296	-----CGCGGAGACCGCGCGCTCGCGCGCTGTCTCGCTCTCTCGCCCTCGAGAA	22347
Qy	22141	GCCATCAACACCCCACTCTCTGCTATCAGCGGACCGCCCAACCGTTCACACATC	22200	23209	ACACCCACCCCAACCCCAACCAACCAACCGGACCTCTCTCAACCTCACCTCTCCCC	23268
Db	21292	GCGATCAACAGCCCTCTGTTACAGACGATCTCCGCGGAGCCCTCTGCGCTCGCGCCCTG	21351	22348	AGTCCCTCGCGGACCATCGCGCTGCGCGGAGCTCGCTCTCTCGCTCACCTCTGTC	22407
Qy	22201	ACCACCTCTGCAACACAGGCAATCAAAACCAAAACCTTCCCAACCAACCGCTTC	22260	23269	CAAAACCAACCAACCCCAACCCCAACCCCTCTCTGTTAGCGCAACCAACCGCCAC	23328
				22408	CAAGCCCTCGCGACATCGCCCTCGAGCGGCTTGTGGCTTTCACCCGCGGCGCGCTC	22467



24580 TACGACGCGGAGAGGGCTCGTCTGCTTGGCCCTCGAGCGGATCGGCGACGCCCTCGCC 24639 Db  
25546 AACGCTCACCCTGCTCCTCGCGCTGGTGGCAGTGGCTCAACACGACGGTGGAGC 25605 Qy  
24640 CGGAGACACCGGCTCCTGCTCGTCCGCGGCAACCGCATCAACACGACGGCGCTCG 24699 Db  
25606 AACGCTCTGACCGCGCCCAACCGGCGCTCCAGCAGCGGTGTCATCCGTGAGCGCCCTGGCC 25665 Qy  
24700 AGCGGTATCACCGCCCAACCGCACCTCCAGCAGAGAGGTCTCTCGGGCGCGCTCCAC 24759 Db  
25666 AATCGGAGACTGACCCCGCGCATGTGACGAGTGGAGGGCCAAGGCAACCGGACCACT 25725 Qy  
24760 GACGCCCGCATCACCGCGCGCATGTCGACGTCGTGAGTGGCATGGCAACCGCACCTCG 24819 Db  
25726 CTGGGGACCGATGAGGCCCGAGCACTCTGGCGCGCTACGGACAAACCGCCCGCCAC 25785 Qy  
24820 CTGGGAGACCCCATCGAGGTGCAAGCTTGGCGCGCTACGCGAGCGGACAGCCGCT 24879 Db  
25786 CACCGCCCTTGTGGCTGGGATCCCTCAAAATCGGAGCGGCAACGACAGCGCCCGCG 25845 Qy  
24880 GAAGAGCTCTCTTCTCGGCGGCTCAAGACCAACATCGGCATCTCGAGGCGCGCTCC 24939 Db  
25846 GCGTGGCGGAGTCAATCAAGATGTGATGCGCTTGGCAACGCGGTGTGCAACAGACC 25905 Qy  
24940 GCGCTCGCGGGCGTGGCAAGATGTCGCTCCGCTCCGCAACGACGCGCTGCGCCCGCACC 24999 Db  
25906 CTCACGTTGAGACGCCACCGCCAGTGGTGGTCCAGGCGGAGTACAACTCTCTG 25965 Qy  
25000 CTCACGCGACCCACGCAATCCCTCATCGAGTGGAGGCGCTCGCCATGACGTCGT 25059 Db  
25966 ACACAAACCGGTGCTGCGCGCGCCGACCGCGCGCGGCGGCAACGACGCGCGGTGCA 26025 Qy  
25060 GATACCCCGAGGCTTGGCGCGCGCACGAGATGAGAGTCCCGCGCGCGCGGATCTCC 25119 Db  
26026 TCATTTGGCGTCAAGCGGCAACCGCCACATCATCTCGAAGAGCAACCACTCCCGAG 26085 Qy  
25120 GCTTTGGATTCGCGGCAACCAACCGCCACGTCATCTCGAAGAGGCTCCCGCGCGCTG 25179 Db  
26086 GACAGGATACCGACGACGACCGCTGCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 26145 Qy  
25180 CGCGCGAGCGCGCACCTCAAGCGCGGCTCGCAAGCGC-----TCCCGCGCG 25230 Db  
26146 CTTCCGCTGCGGTGCGCGAGGCTGAGGCGGCTGCGGGCGGCGAGGCGGCGGCGGTTG 26205 Qy  
25231 TGGCCCGTCTCTGTCGCGCAGGAGGCGCGGCTCGCGCGCGCGGCGGAGCGGCTC 25290 Db  
26206 GCGCAGTACGTGGCAGCGCGCGGACATGTCACTGCGGACATTTGGTGGGCTTGCGCC 26265 Qy  
25291 CGCGACCACTCTGTCGCGCACGACGACCTCACCTCGCGGATGTGGCTATTCTGCTGGCC 25350 Db  
26266 CGCGCGCGGCGTACTGGAACACCGCGCGTCTATCTGGCGCGGACCGCGAGGAATG 26325 Qy  
25351 ACCACCGCGCGCACTTGAGACACCGCGCGCTCTCTGTAAGCCCAACACGCGACGAGTCT 25410 Db  
26326 GCGCAGGCACTGACAGCGCTGCGAGCGCGGAAACCCCAACATACACACAGGCGCAC 26385 Qy  
25411 CTCTCGCGCTCGACTGCTGCGCCAGGACAGCGCGCGC-----GAGCAGCGTCTC 25464 Db  
26386 ACCCGGGCGGTGACCGCGCGGCTGCTTTCTGTTTCCCGGACAGGCGCGCGAGTGG 26445 Qy  
25465 GGACGAGCGGAAGCCACGGAAGCTGCTTTCTGTTTCTGTTGCGGAGGCTCGCAGTGG 25524 Db  
26446 GCGCGGATGGGCTGACCTGCTACCTCTCACTGCTTCCGCGGTTGCGGCAACATCGACGA 26505 Qy  
25525 GAAGGATGGGCTCTCTGCTGCTGACTCTCGCGCGCTTCTCGCGCTCAGTCTGAAGCA 25584 Db  
26506 TCGGAGAAAGCCCTCACCGCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26565 Qy  
25585 TCGGAGCGCGCTGCTCTCACGTCGAGTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 26644 Db  
26566 CCGCAGCAACCGCGATGGCAACAGCGGAGCGGTGCGCGCGCTGCTTTCAGCATCATG 26625 Qy

25645 GAGGCGCGCCCTCTCTCGACCGGCTCGAGCTGTACAGCCCGCGCTCTTTTGGCGTCAATG 25704 Db  
26626 GTCTCCCTCGCGCGCTGTGGCGCTCTAGCGCATCGAACCCGACGCGGTCTCTCGGCCAC 26685 Qy  
25705 GTCTCCCTGGCGCGCTCTGGCGCTCGCTCGGCGTAGAGCCCGCGCGCTCTCTCGGCCAC 25764 Db  
26686 TCCAGGAGAGAAATCGCGCGCCACATATGCGCGCGACTCAGCCTGTAAAGACGCGCC 26745 Qy  
25765 AGTCAGGCGGAGATCGCGCGCTTGTGTGACGCGCTCTCTCTCTCGAGGACGCGGCC 25824 Db  
26746 AAAACCGTTGACCTGCGCAGCGCGCACTGGCGCGCTGACGAGCGCGGGCGCCATGGCC 26805 Qy  
25825 CGCATCGCGCGCTGCGCAGCAAAAGCGCTCACCGCTGCGCGCAACGCGGGCCATGGCC 25884 Db  
26806 TCAGTGGCGCTGCGCGCGCGAGCTGAGCAGCTCATTTCCGAAACGCTGGGAGGAGGCGAG 26865 Qy  
25885 GCGTGTAGCTTGGCGCTCGAAGCTCCAGACCTTACCT---CGTCTCTTGGGCGACAGG 25941 Db  
26866 TTGTGGTGGCAGCCCTCAACGCGCCCACTTCCACCACTGCTTCCGCGCAACCAAGGCG 26925 Qy  
25942 CTCTCCATCGCGCGCTCAACAGCCCGGCGCTCGTGTCTCGCGAGCGCGCGCC 26001 Db  
26926 GTGATGAGGTGCTGGCGCACTGACGACACCGCGCTACGCGGCAACGATCCCGCTC 26985 Qy  
26002 ATCAGCGGCTGATCGACTCGCTCACCGCAGCGAGGTCTTTCGCGCAAAAGTCCGCTC 26061 Db  
26986 GACTAGCGCTCCCACTGCGCGCGCTCCAAACCGCTTCCAGCAGCACTCTTCCGACCTGCTG 27045 Qy  
26062 GACTAGCGCTCCCACTGCGCGCGCTCCAAACCGCTTCCAGCAGCACTCTTCCGACCTGCTG 27121 Db  
27046 GGAGACATCAACCGCGCGCTCCACCGCTGCTTCTTCCACCGTGGAGGCACTGG 27105 Qy  
26122 GCCAATCGCTCTCGGAGCTGAGTCTCTTATTTGACCGTCAACCGGACCAAG 26181 Db  
27106 CTGAGACCAACACCTTGGAGCGCGCTATCTGATGACGCAACCTTCCAGCGCGCTCGC 27155 Qy  
26182 CTCAGCGCTCGAGCTCGACGCGCGTACTGATGATGAAACCTTCCGCAACCGTCTG 26241 Db  
27166 TTCAGCAGCGCATTCAGACCTTACGACGCGGACGCGCGCTTCTTCCGAAATCAGC 27225 Qy  
26242 TTCTGAGCGGACGAGCGGCTCTCTGACGATGGGCTATCTTCTTCTGAGGTGAGC 26301 Db  
27226 CCCACACCACTCTGCTCCCGCATCGAAGACCAACCGAAGACCAACCGAAGATC 27285 Qy  
26302 CCCATCCGCTGCTACGCTCGCTCGCGAGCTTGGAGGCTACCGCTCGATCC 26361 Db  
27286 ACCGAGCGGAGCGCTCGCGCGGAGCAACGACACCACTTCTTCTTCTTCTTCTTCTG 27345 Qy  
26362 GTGCTGCTGCTTCTTCTGAGCGGACCACTTCCGCGCGCTGCTTCTTCTTCTTCTG 26421 Db  
27346 GCCACACCAACACCGCGCATCGGACACCCACCTGCGCAGCAGCTTACACCCAA 27405 Qy  
26422 GCGAGCTCTTACCGAGGCTCG-----CGCTGAGTGGAAAC 26460 Db  
27406 ACCACACCAACCAACCGCGCATCGCTGAGCTGCGCGCTTCCAGCTTCCAGAC 27465 Qy  
26461 GCTTCTTGGCGCTTGGCTCCCGCAAGGTCTCTTCCCGCTTCCAGCTTCCAGAC 26520 Db  
27466 CAGCACTACTGCTTCAACCAACCAACCAACAA---CAACCGACCTTCCAGCAGCGGCTC 27522 Qy  
26521 GAGCGCTTCTGCTGAGCGCTTCCAGCGGCGGCTGCGCGCTGCGCGCTGCGCGGCTG 26580 Db  
27523 ACCCCACCAACCAACCGCTTCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGG 27582 Qy  
26581 ACCTCGCGGACCAACCGCTGCTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCTT 26640 Db  
27583 CTACTCAACCGCGCTTCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTT 27642 Qy  
26641 GTCTTTCAGAGCGGCTTCTTCTTCCAGCGGCTTCCAGCGGCTTCCAGCGGCTTCTTCT 26700 Db  
27643 GGCATGCTCTTCTGCGGCGGCTTCTTCCAGCTTCTTCCAGCGGCTTCCAGCGGCTTCTT 27702 Qy  
26701 GGCATACCTTCTTCTGCGGCGGCTTCTTCCAGCTTCTTCCAGCGGCTTCTTCCAGCTTCT 26760 Db

Qy	27703	GTGACTGCCCCCTCGGGTGGAGAACTGACCCCTGACGACACCGTTGGTGTGATTCGCCGACACC	27762
Db	26761	GTGGGCTTGACACCGTGAAGACGTACGCTCGACCCGCCCTCGCTCTCCCATCGACG	26820
Qy	27763	GAGACGTGAGTTGAGAGTTCACCGTTTCGGGAGCCGATGAGAGTGGCCATCGCGCCCTC	27822
Db	26821	GGCCCGTCTCTCTCCAGATCTCCGTTCGGGCCGCGGACGCTGTGACGAAAGGGCGCTC	26880
Qy	27823	GCATCCACTCGTACTCCGACACCGCTGCTCGCGGACCGGGAGTGGACCCGCTACGCC	27882
Db	26881	TCGGTTCA---TAGCCGGCGACGACGCGCTTCAGATGCGCCCTGGATCTGCCACGCC	26937
Qy	27883	ACGGCCCTCTCTACACACCGCGGACACCGGATCACCGTCCGACACGACACGAGCGCG	27942
Db	26938	AGCGCTCTCTCGGCAAGCTAGCCCGTCCATTGGCTTCGATGCTC-----	26984
Qy	27943	TGCTTCGGGGAGCTGGCCCCCGCCGGCGGACGCCATCGAACTGGGGCGAGCTCTAC	28002
Db	26985	-----CGCGATGGCCCCCTCGGGCGCCACCCAGGTGGACACCCAAAGGTTTCTAC	27036
Qy	28003	GGTGTATGGCGGGACTCGGCATCGCTACGGGCGGCTCTTCAGAGGGCTGC-ACGC	28061
Db	27037	GCAGCCCTCGAGAG---CGCTGGGCTTGTATTGGCCCCGAGTTTCAGGGGCTTCGCCCGC	27093
Qy	28062	CGCTGAGGTTTCGGCGACGATGCTTCGGCGGAGTGGCTTCGCGGGAAGAGGCTCTGCG	28121
Db	27094	CGTCTAAGCGGGCGACGAGCTCTTCGCGGAAGCCAGCTCCCGGACGCCG------	27147
Qy	28122	CGATGCTCCGGCGGGGCTTTCGGTGTTCACCGGCGCTTCTCGACGGGCGCTCGACGC	28181
Db	27148	CGAAGGAGCGCGCTCGTTTTCGCTTCACCGCGGCTCTCGACAGCGGCTTCGAGGC	27207
Qy	28182	CAGGGCTCACCCCCAGAAAGGGAGCGCTCGACGGAGAACTGTCGCCAGGAGCAT	28241
Db	27208	GCTCGCTTTGTAGACGACGAGCAAGGCCCTTCA-----	27242
Qy	28242	GCCTGACCGGCGACCCACAGGCGGACCTGCGGTTTCAGCTGAGGGGGTGTCTTCTGCA	28301
Db	27243	-----GGATGCCCTTCTCTGGAGCGGAGTATCGCTGCG	27276
Qy	28302	CACGGGGGAGTTTCGGTGTTCGGGTACGCGTGTTCGCGAGTTCGCGAGCACGGTAATGC	28361
Db	27277	CTC---CGGTGGAGCCACCACTTCGCGGTGCGGTTTCCACCGTCTGAGGGGAAATCCTC	27334
Qy	28362	CGTGGCCCTCACCGCGGCCACGAGGACGCTCGGCGGTTGGTACGATCGAGTTCGCTCGC	28421
Db	27335	GGCTCGCTCTCTTCGCCGACGCGAGGCGAACCCATCGCTTCGGTGAAGCGCTCGC	27394
Qy	28422	GCTCGCGCCGTTTCCACCGAGGAGTTCGCGCGGCGCGGATCGTACGCCCGGACGCA	28481
Db	27395	CATGGCGCGGCTTCGCGCGAGCAGTCTCCGACAGCCG-----GAGCGTCCCACTCGA	27449
Qy	28482	GTGCTCTTCGACTGAGTTCGGTTTCGGTACGATGCGCGCAACCGCCCTTCGCCAC	28541
Db	27450	TGCGCTCTTCGCGATCGACTGAGCGAGCTGCAAAAGCCCCACC-----TCACCGCC	27500
Qy	28542	CGCGACCGGCTTCGGGGTTCATCGCGCGGGGCTTCCCACTGCCCGGCTGACGGA	28601
Db	27501	CATCGCCCCGAGGGTGGCTCTCTCGGCAAGAGTCTGACCTCGGACACAGGGTGGC	27560
Qy	28602	GCACGACGATGACCGCGTATGACGAGCGCGGACCTGCTTCTGGCTCTGAGCCGCGG	28661
Db	27561	TCTCGACCGC-----TATACCGACCTTGTGCTCTACGAGCGGCTCGACACGAGG	27611
Qy	28662	TGCTCGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	28721
Db	27612	CGCTTCGCTTCCAAAGCCTCGTCTATCGCCCTTTCATCGCTCTGCCCCGAA-----	27660
Qy	28722	TTCCGCGAAGCCCCCGGGAGCGCGGACCGAGGCTTCGAGGCCCGCGCGGACGTGCT	28781
Db	27661	-----	27660





Qy	16012	GC	GGTCAATCAGGACGGTTCGAGCAACGGGCTGACGGGCCCAACGGGCGCGTCCAGGAG	16071
Db	15352	GC	CGTCAACACGAGACGGCGGAGCCAAAGCGCTCACCGCGCCCAATGGCCCTGC	15411
Qy	16072	CGT	GTCTANTCCGCTTGGCCTTGGCCAAACGGCGAACCTGACCCCGCCGACGTTCGATCGGTG	16131
Db	15412	CG	GTTCATTCGGCAAGCGCTTCGACACGCGCGGCTCACTTC	15471
Qy	16132	GAG	CCACGGCACCCGACCACTTTGGCGACCCGATCGAGGCCACGAGCCCTCTCGCC	16191
Db	15472	GAG	GTCAACGGCAACCACTTCGAGACCCCATCGAGGCAACGAGCGTTTTC	15531
Qy	16192	AC	TACGACAGCACCGCCCGGCAACGAAACCGCTGTGGCTGGGCTCGATGAA	16251
Db	15532	AC	TATGGAGGCCCATTTCCAAAGACAGACCCCTCTGGCTTGAAGCGCTCAAGTCCAAC	15591
Qy	16252	AT	CGGCCACGCGAGGCTGCGCAGGTGTGGCGGGGTTCATCAAGATGGTATGGCGCTG	16311
Db	15592	CT	GGGACATCTCAGCGCGCGCGCGCTCGCGGATCATCAAGATGTGCTCGCGTTG	15651
Qy	16312	CG	GAATGGTCTGTGCGCGGGAAGTTTCATGTGGATGAGCCGTGCGCGCATGTGAC	16371
Db	15652	CAG	CAAGTCTTTGCCAAGACCTTCATGCCAGATCCCTTCCCGCCACATCGACTGG	15711
Qy	16372	TC	CGGGGGCGGTGACGTGTGACGAGAGACGGTGCCCTGCGCCCGGGGAGGGCGG	16431
Db	15712	TT	CTCAGGATCGTAAAGCTCTCTGAACGAGAGCGCGTGGCTGACGACAGCAG	15768
Qy	16432	CT	CGCGGGGACGAGGTGTCATCGTTGCGGCTCAGCGGCACCAACGCCACGTATCCTC	16491
Db	15768	CT	CGCGCGCGCGGTGTTCTCTGTTGCGGCTTCGCGCACCAACGCGCATGTATCTC	15828
Qy	16492	GA	AGAAAGCACCCGCCACAAACATCCGTCGAGACACACCCCGCGACGCGCCCGGAGAA	16551
Db	15828	GA	AGGCTCCCGCGCCA-----	15847
Qy	16552	GC	AGCGCGACGATGTTTCGGGGGAAGCGCGCGGACGACGCGGTACCGCGGGAA	16611
Db	15848	----	CGCGGGCGAGTCAGGCGCTTTCACAGCGCTGATCGACGCGCTCCCGCGCGGTG	15902
Qy	16612	GC	GACTGGTCTGCTGCGCGCAGTCCAGGGGTGCGCGTGGCTGTGCGCCAAAGTCG	16671
Db	15903	GC	CGTCTGTC-----TGTCGCGCAGGAGC	15927
Qy	16672	CAG	CGGCGCTGCGCGCCAGGCGCCTGACGCGCCACTCACGACCAACCCCGGC	16731
Db	15928	GAG	CGCGCTGCGCGCCAGGCTCAAGGCTCGCGACACCTGCTCGCCCAAGCGAC	15987
Qy	16732	CT	GACCTGCGCGACGTTCGGGTACCTTCGCGCACGCGCGCGCGGTTCGACACCGC	16791
Db	15988	CT	CACTCGCGCATGTGGCTATTTCGCTGGCCACCAACCGCGCGCCACTTCGAGCACGC	16047
Qy	16792	GC	CACTCATCGCGCGACCGCGACACTTCCTGCAAGCACTCCAGCACTCGCCGCA	16851
Db	16048	GC	CGCTCTGCTAGCCACGACCGCGACGAGTCTCTCTCGCGCTCGACTGCTGCGCCAG	16107
Qy	16852	GG	CAACCCCAACCCCGCGTTCATCCACAGCAGCGGCCACGAGCGGGAACCGGGAG	16911
Db	16108	GA	AGCCCGCACCGGACACGCTCTCGACGAGCGGAAG-----	16148
Qy	16912	GC	CGAGGAAGACCGCATTCCTGCTCGGACAGGGCAACCAAGCGCCCGGATGCCC	16971
Db	16149	--	CGAGGCAAGTGTCTTCCTTCCTTCGCGAAGGCTCGCATGTGGGAAGGATGCCC	16206
Qy	16972	CAG	GGCTCTTACACACCAACCCCGCTTCCTGCGCGCGCACTCAACGACATCTGACCCAC	17031
Db	16207	CT	CTCTCTGCTGACTCTCTCGCCCGCTTCGCGCACACAGCTCGAAGCATCGAGCGCGG	16266
Qy	17032	CT	GACCCCACTCGACCAACCCCTCTCTCTCGCCCTCTCAACCGAGACCCCAACCCAG	17091
Db	16267	CT	CGTCTCACTGAGGTGAGCGCTGCTCGCGCTCTGCGCGGGAACGAGGGCGCCCC	16326

Qy	17092	GACCA	CACACCTT	CGAAG	AGCGGCGCACTGCTTCAGCAGACCCCGTACGCCAGGCC	17151
Db	16327	TCCTC	CGACGGGT	CACGCTGTG-----CAGCCGCGCCTCTTT	16365	
Qy	17152	GCCTCTT	CGCCTT	CCAGTCCGCTCCACCGCCTCTCACCGCTCTCACGAGGCTACCATCACC	17211	
Db	16366	GCGGT	CATGGTCTCCCTGCGCGCCTCTGCGGCTCGCTCGGCGT	CGA-----G	16413	
Qy	17212	CCCACT	ACTAGCGCGGACATCCCTCGCGGAAATACCGCGGCCACCTCGCGGGCATC	17271		
Db	16414	CCGCG	CGCGT	CGTCCGCCACAGCGAGATAGCGCGCCTTCTGTCGAGGCGCT	16473	
Qy	17272	CTCAC	CTC	ACGACCGCACTATACCCAAAGCGGCACCTCATGCAAAACATG	17331	
Db	16474	CTCTC	CT	CGAGACGCGCGCGCATCGCGCCTGCGCAGCAAAAGCGTCAACACGCTCG	16533	
Qy	17332	CCCCCGG	CACCATGACACCTTCACACCA	CCCCCGCACCATCACCCACCTCACC	17391	
Db	16534	CGGCAAC	CGGGCATGCGCGCGT	CGAGTCTGCGGCTCCGACCTCCAGCATCCTCGCT	16593	
Qy	17392	GCCAC	CGAAAGCA	CGCTCGCCATCGCGGCATCAACACCCACCTCCCTCGT	17451	
Db	16594	CCCTG	GGGCGCAGGCTCTCATCGCGCGCTCAACAGCCCCCAGGGCCACGCTCGTATCC	16653		
Qy	17452	GGCAC	CCCCC	CCACACGATCAACACCCCTCTGCCAACAAAGGATCAAAACC	17511	
Db	16654	GGCGAG	CCCGCGCGTGCAGCGCTGATCGACTCGCTCACGCGAGCGAGTCTTCGCC	16713		
Qy	17512	AAAACT	CTCCACCAAAAGCGCTTCCATCTCCCGCAGACCAACCCCATCTCTCAACCAA	17571		
Db	16714	CGAAG	AGTCCGCGT	CGACTACGCTCCCATCAGCCCCAGATGGAGCGCGTCCAAAGACGAG	16773	
Qy	17572	CTC-----	CACGAGC	ACACCAACCCCTCTACTACCCACCCACCCACACCCCCCTC	17622	
Db	16774	CTCGC	CGAGGTCTAGC	CAACATCGCTCTCGAGCTGGAGTCCCTCTTTATTCGACC	16833	
Qy	17623	ATCAC	CGCCAAAC	CCCCACCCCGACCAACTCTCTACCCCCCCTACTTGGACCCCAACAGCC	17682	
Db	16834	GTCA	CCGGAC	CACAGGCTCGACGGCTCGAGCTCGACGGCGGTACTGGTATCGAAACCTC	16893	
Qy	17683	CGCAA	CCGCTGCACTACGCGACGACACCCGAAACCTTCACCAACAGGCGTCAACACC	17742		
Db	16894	CGCAAA	ACCGTCTGTCTCGAGCGCAGCCGAGCGGCTCTCGACGATGGGATCGCTTC	16953		
Qy	17743	TGAT	CGAACTGGACCCGCACAACACCCCTCAC--	CACCTCACCCACCAACCTCCCC	17799	
Db	16954	TTCGT	CGAGT	CAGCCCTCATCCCGTGTCTACGCTGCGCTTCGCGGAGACTGGAGCGC	17013	
Qy	17800	AACAC	CCCCACCA	CCCTCACTCCACCCACCCACCCACCCCAACCCCACTC	17859	
Db	17014	TCAC	CGCTCGATCCCGTCTGCTCGCTCATTTCGACGCGACGAAGGCCACTCCCGGT	17073		
Qy	17860	CTAC	CAACCTCGCCAAACACACACACCTGGACCCCGCACCACTACCCGACCA	17919		
Db	17074	CTCTT	GTCTCTTGGCGCGAGCTATATGGCGCGGCTCA	CGCCGAGTGGAAAGGCTTC	17133	
Qy	17920	AACCA	CCCCAC	CACACCCACTCGACTCTCCCACTCCCACTCCCTTCCACACCCAGCAC	17979	
Db	17134	TTCG	CGCCTT	CGCTCCCGCAAGTCTCACTCCCACTCAGCTTTCAGCGGAGGCT	17193	
Qy	17980	TACT	GTGCTCGAAAGCACAGCGCGGTGCGGATCCGGTTC	CGGGTTCGGGTTCGGGGCGG	18039	
Db	17194	TTCT	GGCTCGACGCCCCCAACGCACACCCGAA-----	GGGCTCGCTCCCGCTCG	17244	
Qy	18040	GCAG	GACTGCGGGCGGACGGGAGAGGTGGAGT	CGCGTTCGGGAGCGGTGGCCCCGC	18099	
Db	17245	CCGAT	CGATGGGCGGTTTTTGGCAAGCCATCGAAACGCGGGGACCTCGACGCGCTCAGCGGC	17304		
Qy	18100	CAGGA	CTGGAAACGTCGCGACACGCTCGCGTGC	CGTCCCCCTCGCGCGGCTTGACACG	18159	
Db	17305	CAGCT	CC-----	ACGGGACGGCGACGACGAGCGCGCCCTCGCCCTG	17349	
Qy	18160	GTGGT	CGCGCACTCTTCGCTTGGCACCGCCACCAACACGACCAAGCCGATCAACACC	18219		

Db 7737 GCGAGCTGGGGCTACCGCATGCTG- GAAGGGCTCCGGCGCGAGGGGTCCGAG 7795  
Qy 4348 GACTGGAAACGCTGGCGACACTTCGCGCTGCCCCCTCCGGCGCTGGACACGCTG 4407  
Db 7796 GCGACCGGCTGTCCGGCGCGCTGGCTCCGCTCAAGCGGAGAACATCCCGCGAGGCG 7855  
Qy 4408 GGGCCCGGACTTCGCGCTGGACCGCGCAACAAGACGAGCCGCGATCAACACTGG 4467  
Db 7856 GCGCGCTGTCTACCGCGCTGTCAAGCGCGGGGAGAGGTGAGGTGTGACGGCGGG 7915  
Qy 4468 ACCTACGAGAAACCTGGAAACCTCTCAACCTCCCAACCAACCAACCAACCAAC 4527  
Db 7916 GCGAGACGAGACCGTAGAGGCTCCGGCGCGCGCTCAAGCACTGACG----- 7963  
Qy 4528 TGGCTCATGGCATCCCGAAACCAAGACCAACCCCATCATCAACCAATCTCTAC 4587  
Db 7964 ----- 7963  
Qy 4588 AACCTCAACACAGGAGATCAACCCCATCCCTCAACCTCAACCAACCAACCAAC 4647  
Db 7964 ----- 7963  
Qy 4648 CCCCAACACTTCACACACACCTCTCAACACCGACCAACCAAGCCCAACCAACCAAC 4707  
Db 7964 ----- 7963  
Qy 7964 ----- 7963  
Qy 4708 GAGCCATCATCGCGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4767  
Db 7970 GACGGCTTCAACCGCGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8000  
Qy 4768 CCCCAACACCAACCGGACCGCTCTCAACCTCAACCTCAACCAACCAACCAACCAAC 4827  
Db 8001 ----- 8000  
Qy 4828 CACCCACCAACCGGCTCTGTGATAGCGCAACCAACGCGCAACCAACCAACCAACGAC 4887  
Db 8048 GGAATCAAGGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8107  
Qy 4888 CCCCTCAACACCGCAACCGCAACCGCAACCGCAACCGCAACCGCAACCGCAACCGCA 4947  
Db 8108 ACCCGCGCGACCGGACCGGACGATGTCTGTGGGCTGTGGCGGTGTGTGTGTGTGT 8167  
Qy 4948 CACCCACCAACCGGCTGTGATAGCGCAACCGCAACCGGCAACCGGCAACCGGCAAC 5007  
Db 8168 CACCCGAAACGCTGGGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8227  
Qy 5008 CAGCACTTCAACCAACCGCTCAACCGCAACCGCAACCGCAACCGCAACCGCAACCG 5067  
Db 8228 GCGCACTGTGTACCGCACTCTCCGGCGCAACCGGAGGAGACGATGCGCATTCGCAAC 8287  
Qy 5068 ACCCGCAACCAACCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5127  
Db 8288 ACCCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8347  
Qy 5128 ACCCGCAACCGGCAACCGCTCATCAACCGGAGGAGGAGGCGGCGCTGTGTGTGTGT 5187  
Db 8348 GACTGGCAACCGCAACCGCTCATCAACCGGAGGAGGAGGCGGCGCTGTGTGTGTGT 8406  
Qy 5188 CTACCAACCAACCGCTCAACCGCAACCGCAACCGCAACCGCTGTGTGTGTGTGTGT 5247  
Db 8407 -CGCGGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8464  
Qy 5248 GGGCGGCAACCGGCAACCGCAACCGCTCAACCGCAACCGCTGTGTGTGTGTGTGTGT 5307  
Db 8465 GGGGAAAGCGCGCGGAGCAACCACTCAACCGGCAACCGCTGTGTGTGTGTGTGTGT 8524  
Qy 5308 CTACCACTCAACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5367  
Db 8525 GTACACATGTGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8584  
Qy 5368 ATCCCGCAACCAACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5427  
Db 8585 ATCCCGCGGAGACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8644

Qy 5428 ACCCTCAACCAACCTCAACCGGCAACCGCTCAACCAACCGCTGTGTGTGTGTGTGTGT 5487  
Db 8645 ATCTGGAGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8704  
Qy 5488 GCGCACTCTCTCAACCAACTTCAACCAACCGGCTGTGTGTGTGTGTGTGTGTGTGTGT 5547  
Db 8705 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8764  
Qy 5548 TCCCGCGCGCAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5607  
Db 8765 TCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8824  
Qy 5608 CTGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5667  
Db 8825 CTGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8884  
Qy 5668 GCGACCTGGCAAGGAAACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5727  
Db 8885 GAGCGGTGGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8944  
Qy 5728 GCGGCGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5788  
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Qy 5769 ----- 5768  
Qy 9005 CCGGAGACGACCGGATACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9064  
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Qy 9065 TCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9124  
Qy 5875 GCGCGGAAAGGAGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5925  
Db 9125 GCACGGGACACGCGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9184  
Qy 5926 CACAAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5985  
Db 9185 GCGGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9244  
Qy 5986 CGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6045  
Db 9245 GCGGCGGAGCGCGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9304  
Qy 6046 TCGTTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6105  
Db 9305 GCTTCAAGGACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9364  
Qy 6106 AAGGCAAGGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6165  
Db 9365 CGGAGGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9424  
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Db 9425 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9484  
Qy 6216 ----- 6215  
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Qy 6250 GTACCGAGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6309  
Db 9545 GACGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9604  
Qy 6310 GCGGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6369  
Db 9605 CCGGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9664  
Qy 6370 GACCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 6429  
Db 9665 GACCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9724

QY 2134 TGGCTGACGGCGACCGGCTGGGGCGAGGGCGCTGGAGTCTGTGTGAGCGG 2193  
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 Db 5807 CTGTGGAGACCGCGCGCGACGAGACCACTGGCTCGGCTGGCTGGCGGAGCGCTTG 5866  
 QY 2254 AACCAAGACGCTGCTCGAATGAGGCTGACCGCGCGGACGATCGGCTCGAGAGCGGCTG 2313  
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 Db 5927 ATCCGCGCGCTGCTGGCGAGCGCGGCTGAGACCTCGAGTGTGAGTGTGAGTGTGAG 5986  
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 QY 2434 GGGCAG---CGGGCGGTCGACAGCGCGCTGTGGCTGTCTGAACTCAACATCGG 2490  
 Db 6047 GGGCAGGCGCGTGAAGAGAGAGACGCTGGCGCTGGCTGTGAGTGTGAGTGTGAGTGTGAG 6106  
 QY 2491 CACACATAGCTGCGCGGCTGTGGGATGATCGAATGAGTGTGAGTGTGAGTGTGAGTGTGAG 2550  
 Db 6107 CACACATAGCTGCGCGGCTGTGGGATGATCGAATGAGTGTGAGTGTGAGTGTGAGTGTGAG 6166  
 QY 2551 GGGGCTTGGCGGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2610  
 Db 6167 GAGCTGTGCTGAGAGACGCTGAGACGCTGAGACGCTGAGACGCTGAGACGCTGAGACGCTGAG 6226  
 QY 2611 GGGGCGGTCGCGCTGTCGACGAGGCGGTCGCTGAGGCGGAGAGCGGCGAGGCGGCTG 2670  
 Db 6227 GGGGCGGTCGCGCTGTCGACGAGGCGGTCGCTGAGGCGGAGAGCGGCGAGGCGGCTG 6286  
 QY 2671 CGGCGGCGGAGATGCTGCTGTCGAGATCGGCGGACGAGATGCGATGATGATGATGATGATGAT 2730  
 Db 6287 CGGCGGCGGCGCTGCTGCTGTCGAGATCGGCGGACGAGATGCGATGATGATGATGATGATGAT 6346  
 QY 2731 GAGGCGGCGGCGGCGGCGGCTGCTGCTGCGGCGGAGGCTGTCGAGGCTGTCGAGGCTGTCGAG 2790  
 Db 6347 GAGGCGGCGGCGGCGGCGGCTGCTGCTGCGGCGGAGGCTGTCGAGGCTGTCGAGGCTGTCGAG 6406  
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 QY 2971 TCGCTTGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3030  
 Db 6538 ---GGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6592  
 QY 3031 GTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3090  
 Db 6593 GTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6649  
 QY 3091 GAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3150  
 Db 6650 ---CTGATGAGCGGAGCGGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6688  
 QY 3151 TTGCTGCTTCCCGAGCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3210  
 Db 6689 TTGCTGCTTCCCGAGCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6748  
 QY 3211 TCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3270

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 QY 3331 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3390  
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 Db 6929 GGTATCGAACCCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6988  
 QY 3451 TGTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3510  
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 QY 3511 GCGCG---TGTGCGGCGCGGCGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3567  
 Db 7049 GCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 7108  
 QY 3568 GAGCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3627  
 Db 7109 CTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7162  
 QY 3628 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3687  
 Db 7163 ACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7222  
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 Db 7223 GCGGAGCGGATTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7282  
 QY 3748 CAGCCCTGCGGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3807  
 Db 7283 GAGATCATGAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7342  
 QY 3808 GTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3867  
 Db 7343 GTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7402  
 QY 3868 TACTGTACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3927  
 Db 7403 TACTGTACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7461  
 QY 3928 GATGAGGAGCAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3987  
 Db 7462 ---GCTGAGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7504  
 QY 3988 GAGAGCACCGAGAGCAGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4047  
 Db 7505 CCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7564  
 QY 4048 GACAGAGCAGCGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4107  
 Db 7565 CAGGAGGCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7624  
 QY 4108 ACACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4167  
 Db 7625 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7685  
 QY 4168 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4227  
 Db 7686 ---GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7720  
 QY 4228 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4287  
 Db 7721 GCGCG---CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7736  
 QY 4288 GGCAGCTGCGGCGGAGCGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4347



Db	14909	CACGGACGGGACGGGCGGTGACGGGCAACAGCCGCTGCGCTGGGGTCGTTGAAGTCCAA	14966
Oy	13113	CATGGGGCACTCCATGGCCCTGTGGGGGTGTGGGCGGGGTATCAAGTGTGATGGCGCT	131727
Db	14969	CATGGGACACACCAGGCGCGCGCGGGGTGTCTCCGGGTGATCAAGATGTGTCCAGGCGCAT	150287
Oy	13173	GGGGAATGATGTGTGTCGCGCGGGAAGTTGCAATGTGAATGAAGACCGTCCGATATGTGAACAT	132232
Db	15029	GGCGCAAGGCGTCTTGCCGGAAGAGCTTCAAGTGGAGAACCCCAAGCAAGGTGAACATG	150887
Oy	13233	GTCGCGGGGTGCGGTGACGTTGCTGACGAGAGACGATGCTCTGGCCCGCGC---GGAGAGG	132887
Db	15089	GTCCGCGGGCGCGGTTCAGGCTGCTCAACGAGGCGATGATGATGGCCCGAACAGGGCGACGG	151487
Oy	13280	GGCGCTACGCGGGGCGAGAGTGTATATTGCGGTGACGCGGCAACAGCCCAAGTCAAT	133497
Db	15149	CGGACTGCGGAGGGCGCGGCTCTCTCTTCCTTCGCGGTGACGCGGAGCAAGCGCGCACTCGT	152087
Oy	13350	CCTGAGGGAAGCAACCGGCCCAACAATCCGCTGAGACACACCGCGCGACGACGTCCCGGG	134097
Db	15209	GCTGGAAGGCGCCCGG-----CGGCCGAAG	152347
Oy	13410	AGAAATCAGCCGCGACAGAGATGCGCGGTAGTGGCGATGAGAGCTGTGCGGCAAGTCCAG	134697
Db	15235	AGACCCCTGCGCTCCGAGAGCGACCCCGGCGGTCAAGCGT-----CGGTGGCGCGCG	152867
Oy	13470	GGTGTGCGCGGTGCTGTGTGTGGGCAAGTGTGCAAGCGGCGCGCTTGCGCGCCAGCGCCAGCG	135297
Db	15287	CCTGTGCTCCGTGTGTGTGTGTGGGGAAGACTCCGGCGCGCTGGAAGCCCAAGTGGAGCG	153467
Oy	13530	CCTGACAGGCCCACTTCAACCAACAC---CGGCGTGTGACTGTGGCGGAGCTGGGGTA	135837
Db	15347	CCTGCGCGCGTTCGCTGTGCAAGGAGCGCTGACGAGCGCGCGAATCCGAGCGCGGTGCTGCG	154067
Oy	13584	CACCTTGCACCAAGCGCGCGCGCGGTTCGACCAACGCGGCCCACTCATGCGCGCGCACCG	136437
Db	15407	CGTACTGGCGCGCGCGCGCGCGCGCGGATTTGAGACACCGGCGCGTGTGTCTGGCACCGGACA	154667
Oy	13644	CGACACCTTCTCTGCAAGCACTTCAAGGCACTGCGCGGAGGGAACCCACCCGCGGTCAAT	137037
Db	15467	GGAAGATTTGCGCGAGCGGCTGACCGGCTCGGAAAGACTGATATCGGGGACGCGCTTC---	155237
Oy	13704	CCACAGACAGGCGCCCAAGCGGGAACCGGGAGAGCGCGAGAAACCGCATTCAT	137637
Db	15524	-----GGAAGTGGGCGGGATGGCGTTGCT	155477
Oy	13764	CTGTCTCGGACAGGGGACCCCAAGCGCCCGGATGAGCCACAGGCGTTCACACACCAACCC	138237
Db	15548	GTTCGCCGGGTTCAGGAGCGACGAGTGGGCGGGATGGGCGCGGAATCTTGTGAAGTGTGCA	156077
Oy	13824	CGTCTTGGCGCGCGCACTTCAAGCAATGTGACACCACTTGACCCCACTTGAACCAACCC	138837
Db	15608	GGAAGTTGCGGCGCGCCATGAGCCGAGTGTGAGAGACGGGCGTCTCCCGCTAATGTGAATGTGCT	156677
Oy	13884	CTTCTTCCCCCTCTCAACCAAGAACCCCAACCCAGACCAACCAACCTTGAAAGAAC	139437
Db	15668	GCTGGAAGGCGGTGTCTCGGAGGCGGC-----GGG	156977
Oy	13944	GGCGGCACTGTCTCAGAGACCGGCTAAGCGCCAGCGCGCGCTTGCGCTTCAAGTGTGC	140037
Db	15698	CGCGCCACGCTGGAGGGGTTCACGTCGTTCAGCGCCGTGATCTTGTGCTGATAGGATTTTC	157577
Oy	14004	CTTCCACCGGCTCTCTCAACGAGGATTCACATCAACCCCACTAATACGCGGACACTTC	140637
Db	15758	GCT---GGGAAAGTCTGGAGAGACCAACAGCGCGTGTGAGCGCGGCTGTGGGCACTTC	158147
Oy	14064	CTTGGGGAATCAACGCGCGGCCCACTTGGCGGACATCTTACCTTCAACGAGCGCACAC	141237
Db	15815	GCAAGGAGATTCGCGCGCGCGTACGATGTCGCGGCTTCAACCTTGAAGACGCGCGCGG	158747
Oy	14124	CTTCATGACCAACGCGGCCCACTCATGCAAAACATATGCCCCCGGAC---CATGACAC	141807
Db	15875	CGTGTACCTTGGAGCAAGTTCATATGCGCGCCCACTTGGCGGGAAGGCGGAGTAT	159347

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OY      14181  CCTCCACACCAACCCCCACCAACATATACCCACACACCTACCGCCACGAAACGACCTCGC 14244
Db      15935  CTCCCTGCCTTCAGCAGGAAAGCACCCCGACGCGCATGAGAACTCCACGGAATTGC 15999
OY      14241  CATCGCGGCATCAACACCCCACTTCCTGTCATCAGCGACCCCCACACGCTCCA 14300
Db      15995  GATCGCGCGGTCAACAGGCCCCACCGGCACCGTGTTTGGGGGACCCCAACGATCCA 1605
OY      14301  ACAATATCAACACCTCTGCCAACAAGGCAATCAAAACCTTCCCAACCA 14366
Db      16055  AGACCTGCTCAGGCGGTGTAGAGGCGCGGAGTCCGCGACGGAATATCCCGTGACTA 16111
OY      14361  CGCCTTCACACTCCCCACACCAACCCCATCTCAACCAACTGCACAGACACCCAAAC 14420
Db      16115  GCGCTCCCAAGCGCCCACTGCAAGCATCAGAGCGAACTGGCGAGGTCTCTCCCGG 16177
OY      14421  CTTCACTTACCAACCAACCCCAACCCCTCATCAGCGCAACCCCAACCCCACT 14486
Db      16175  GCTCAGCCCGGAGACCTGAGGTCCGTTCTTCGACACTGAAGCGCTGATCAC 16233
OY      14481  CCTACCCCCCACTACTGAGACCAAGCGCCCAACCCCTGATGATGACCAACAC 14544
Db      16235  CGACCCGAGTCTCAGCGGACCTAATGTATCGCAACCTTCGCGACCGGTCCGCTTCCG 16299
OY      14541  CCAAAACCTTCACCAACAGCGGCTCAACCACTCATGGAATCGAGCCGACCAACCT 14600
Db      16295  CCCCAGCTGTGAGACCTCGCACCAAGCAAGGCTTACCACTTATGAGGTCAAGCC 16355
OY      14601  CACCAACCTTACCAACGAGCAACCTTCCCAACACCCCAACCAACCTCAACCTCA 14666
Db      16355  CCAACCCGCTCTCAACATGACCTTCCCGAGACCTCACCGGCTCGGACCTT---CCG 16411
OY      14661  CCCCCACCAACACCCCAACCAACCTCTCAACCAACCTCGCAAAACCAACCAACCT 14722
Db      16412  CCGGAAACAAGGAGCGAGAGCTGTGTCACTTCACTCGCGAAGCTGAGCAACG 16477
OY      14721  GCAACCCCAACACTACACCCACCAACCAACCAACCCCAACCCCAACCAACCTCGACCT 14780
Db      16472  CTTCACTATGACTGAGCTGGGCGCCGCTTC---TCCCAACGAGCAACCGGCAACCAACCGAGCT 16522
OY      14781  CCCCACCTACCCCTTCCACACCACTACTGTGCTCA 14819
Db      16529  CCCCACCTACGCTTCCAGCGCGGTCACTACTGCTCCA 16567

RESULT 14
US-09-105-537-5
/ Sequence 5, Application US/09105537A
/ Patent No. 6265202
/ GENERAL INFORMATION:
/ APPLICANT: Sherman, D.H.
/ APPLICANT: Liu, H.
/ APPLICANT: Xue, Y.
/ APPLICANT: Zhao, L.
/ TITLE OF INVENTION: DNA encoding methymycin and pikromycin
/ FILE REFERENCE: 600.438US1
/ CURRENT APPLICATION NUMBER: US/09/105,537A
/ CURRENT FILING DATE: 1998-06-26
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 5
/ LENGTH: 36778
/ TYPE: DNA
/ ORGANISM: Streptomyces venezuelae
US-09-105-537-5

Query Match      9.6%; Score 2951.8; DB 4; Length 36778;
Best Local Similarity 54.4%; Pred. No. 0;
Matches 8436; Conservative 0; Mismatches 5722; Indels 1361; Gaps 69;

OY      8  GGATGACGCGGGGAAAGAACCCCGCTTCGCGCAGGGAGGTCTCGAGTGGCCGACG 67

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11174 CGGACCGGACCGGCGCATCATCCGTTCCGCTCTGCAATCCATGTCGACCCCGGACG 11233  
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11234 CACTGCGCTCTTTCGATGCGGCGCTTGCTGCTGGAACCGCGCGGCTCTGCTGCGCGGAC 11293  
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11294 TCGCTCGCGCGCGCGCGCGG----- 11316  
12872 GCGCTGACCGCGCGCGCGCGGACGCGCGCGGACGACCGCGCGGATCCGCGCGC 12931  
11317 -----CCGCTGCTGAGGACCTCTGCGCGCGCGCACCGCGCGCGGACCGCG 11363  
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11395 --GCCGACGCTGACCGCGCGCGCTGCGCGGACGACGACGACGACGACGACGACGACG 11452  
13052 CGGTCACGCTCGCGCGACCGGCGCGGACGCTGGAACGCGCGCGCGCGCTGCTG 13111  
11453 TCGCGCTGCTCGCGCTCGACATCGGACGCGCTCTGCGGACGACGCGCGCGGACGACG 11512  
13112 TCGAGTTCGCTCGTCCGCGGAGCTGCGGACGACGCTGCGGACGCGCGCGGCTGCG 13171  
11513 CCGCGCGCGCGCTCTGCGGACGCTGCGCTTCTGCTCTGACCGCGCGCTGGAATGCG 11572  
13172 AGCGCGGACGCGGCTCTCTGACGCTGCGCTTCTGACGCTCTGACGCGCGCGCTGCG 13231  
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13292 GCGCGCGGACGCTGCGCTCTGACGCTGCGGACGCGGCTCTGCGGACGCGGCTCTG 13351  
11672 -----AGCGACGACGCGGACGCGGCTCTGCGGACGCGGCTCTGCGGACGCGG 11696  
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11697 -----CCCGCTGCTGCGGACGCTGACGAACTCGAACTCGCGCTCTGCGGCTG 11749  
13412 AGCGACGCGGCTGCTGCGGACGAACTGACCGCGCTGGAAGCGCGCTTGTGCTGACG 13471  
11750 AACCGACGCGGCT--AGCGAAAGTCACTCTGCGGCTGAACTGCTCATGTTGAG- 11805  
13472 TCTCGGACGCGCGCGGAGCGGAACTCTGGAAGCACTGCGGCTCTGCGCTGATG 13531  
11806 -----TGGAACGACCGCGGACGCTGCGGCTGAACTGCTCATGTTGAG- 11845  
13532 TCAAGGCGGACGCGGACGCGGACGCGGCTCTGCGGACGCGGCTCTGCGGCTG 13591  
11846 AGGACG----- 11852  
13592 CGGACGCGGCTCTGCGGCGCGCGGACGCGGACGCGGCGGAGTGAAGACGCGCGG 13651  
11853 -----GAAGTTCACATCGGACGAAAGAGGCTGAGATTTTCAATTCATTTGACGAGC 11905  
13652 GAGTCCGCGGCTTCAAGACGCTCTGCGGAGGAACTTTTGGCGCTCTGACGAGAGC 13711  
11906 TCGGCTGCTGACGCGGACGCTGCACTCTGCGCGCTGATTCG----- 11949  
13712 CGAGGACGAGCTGATCTCTGCGGACGCTGCGCTCTGCGCGCGGACCGCGTCCGCGG 13771  
11950 -----CTGCGCGCTCTGAGAGCTGAGT 11972  
13772 CTGAGCTGAGATCACTTCACTGCGGCTCTGCGGCTCTGCGGACGAGCTG 13831  
11973 GCAATTGCGGATGAGGAGGCTCTGAGATCTCAAGCGGCTGACCTGCGGACCTG 12032

13832 GTCCAGGTGAACGAGGAGATCTCTGACTACTCTGCTGCTGACGCGGACGCTCA 13891  
12033 CCGGACTGCGCGCTGCTGATCGAGTGTGTGACGCTGAGCAGGACGCTGCGGATTTGT 12092  
13892 CGAGGCGCGCTGCGGCTCTGCGGAGCTGAGGCGGACGCGGCGGAGCTGCGGATCTGT 13951  
12093 GGGGATGCGCTGCTGATCCGAGGCGGCGGACGCTGACCGGCGGACGCTGCGGATCTGT 12152  
13952 CGGATGCGCTGCGGCTCTGCGGCGGCGGCTGCGCTCTGCGGAGACTGTGCGGCTGT 14011  
12153 CAAGTCCGACGCGGACGCTATCGGAGGCTTCCGACGCGGCTGGAATGGAACCTGAGAC 12212  
14012 GCGCGGCGGAGGACGCGGACGCTGCGGAGTTCGCGGAGACGCGGCGGCTGAGAGG 14071  
12213 GCTTCAAGACCGGACCGGACCGGCTGAGGACGCTGACGCGGCGGACGCGGAGGCTTCT 12272  
14072 CCGTCAAGACCGGACCGGAGGCGGACGCGGAGGCTTACCGCGGAGGCGGAGTTCCT 14131  
12273 CTATGACGCGGCGGCTTCAAGCGCGGCTTCTGAGTGTGACGCGGCTGAGAGGCTGCG 12332  
14132 GTACGAGGCGGCGGAGTTCGAGCGGCTTCTTGGGATCTGCGCGGCGGAGGCTTCTG 14191  
12333 AATGACCGGCGGACGCGCTGCTGCTGGAACGACTTGGGAACTTTCGAAACGAGCGG 12392  
14192 CATGACCGGCGGACGCGCTCTCTGAGGCGCTCTGAGAGGCTTTCGAGACGCGG 14251  
12393 AATGACCGGAGCTCACTGCGGAGGCGGACGCGGCTTCTGAGGAGTCAATCCGGA 12452  
14252 GATCCGCGGCGGACGCGGCGGCGGACCTCGGTGCGGCTCTTCAACCGGCGGAGATGAC 14311  
12453 GGACTACGACGCGGAGTACACATCAAGCGGCTCAAGCGGCTGAGGCTGACTGCTGAC 12512  
14312 GACTACCGGACGCGCTCTGACGAGT--GTCCGAGGAGCTGAGGCTTACTGAGGAC 14368  
12513 TGGACGCGGACGATTCGCTGAGGCGGCTGATCTCTTCAACCTTGGGCTTCAAGGCG 12572  
14369 CGGACGCTCGGAGTGTGCGCTGCGGCGGCGGCTGAGACGCTTGGCTGAGAGGCG 14428  
12573 TGGCATCACTTCAACGCGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12632  
14429 GCGCTGCTGAGGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14488  
12633 AGCGCTCGGCTCGGATGATGACGATGCGGCTGCGGCGGCGGCTGCTGATGAGGCG 12692  
14489 GCGCTGCGGACGCGGAGTGTGACATGCGCTGCGGCGGCGGCTGAGCGCTGATGAG 14548  
12693 TCCCTTCTGCTTCAACGAGTCTCTGCGGACGCGGCGGCTGCGGCGGCTGCA 12752  
14549 GCGGACGACTTCTGCTGAGTTCAGCGCTGAGCGGCGGCTGCGGCGGCTGCA 14608  
12753 GCGCTTCTGCGGCGGCGGAGCGGACGCGGCTGCTGCGGAGGCTGAGGAGTCTGCTG 12812  
14609 GTCTTCTCTGCTGAGGCGGAGCGGACGCGGCTGCTGCGGAGGCTGCGGCTCTGCT 14668  
12813 GAGGCGGCTCTGCGGCGGCGGCGGACGCGGCTGCTGCGGCTGCTGCTGCTGCTG 12872  
14669 CGAGCGCTCTGCGGCGGCGGCTGCGGAGGCGGCTGCTGCGGCTGCTGCTGCTG 14728  
12873 CCGCTTCAACGAGGCGGCGGACGCGGCTGAGCGGCTGAGCGGCTGCTGCTGCAAGT 12932  
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12933 CAAGTCACTGCGGCGGCTTGGCGGACGACGCTCTGCTGCGGCTGCTGCTGCTG 12992  
14789 GCGCTGCTGCTGCGGCTTGGCGGAGCGGCTGCGGCTGCTGCGGCTGCTGCTGCT 14848  
12993 GAGGCGGACGCGGAGGACGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGCTGCTG 13052  
14849 CGAGGCGGACGCGGAGGACGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGCTGCTG 14908  
13053 AGCTTACGCTGAGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13112



Dh 10591 GCCGCGCTGCTGCGGACCCGCGACACCCGCTGCTGCGCGCGCTGCTGACCTTCG 10650  
Qy 9046 ACTGACGATGAGCGCTTCTTTCAGAGGCGCTTGTCTTTAGAGTGCATCCGTGCTGCT 9105  
Db 10651 GACCGGAGACGGGCTGCTGCTCAACGGCGCGCTCTCCCTGCGACACCCCGTGGCTCGG 10710  
Qy 9106 GACCATGCTGCTGCGGCGACGCTGCTGCTGCTGCGGCGCACTTCTCTGAACTCGCCCT 9165  
Db 10711 GACCAACGCTGCTGCGGAGCGCTGCTGCTGCGGCGCGCATGAGTCACTCGCGCGG 10770  
Qy 9166 CATGCGGCGCATATAGTGGGCTGCGACCGAGTGAATGACCTGATGCTGATGCTGCG 9225  
Db 10771 CACGCTGCGAGACTCGGCGGCTTGTGCTGATGATGCGGAGCTGACCTCTTGAACCTG 10830  
Qy 9226 GTGATTCCTGATGATGAGTGGTGTGATGATGATGATGATGATGATGATGATGATG 9281  
Db 10831 GTACTGCGCGACAGTGGGCGCTGACGCTGCGCGTGAACGTTGCGGCGCGCGCGAGAG 10890  
Qy 9282 ---GAGGGGCGCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 9336  
Db 10891 CCGGATGCGAGTCCGCGCGGAGCGCGACCGCGCTGCTCCCTGCACTCGCGGCTCGCC 10950  
Qy 9337 GATGATGCGGAGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9396  
Db 10951 GACGCGCGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 11010  
Qy 9397 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9456  
Db 11011 CCGGAGCTTCCCGTGGCGCGCGACCGTGGCGCATGTTGGCGCGCGCGCGCGCGAGAG 11070  
Qy 9457 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9516  
Db 11071 GTGCGCTGACGCTCTTACAGAGCGCTGACAGGAGAGAGAGAGAGAGAGAGAGAG 11130  
Qy 9517 TTTTGGGAGCTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9576  
Db 11131 TTTCAGGGGCTGAAACGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 11190  
Qy 9577 CC-----GAGAGAGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATG 9624  
Db 11191 CCGCGCACAGAAATGCGACCGCGCGCGCGCGAGACCGCGCGGAGAGAGAGAGAGAGAG 11250  
Qy 9625 TTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9684  
Db 11251 GCCCTTACGCGATCACAACCGCGCGCTGCTGACAGCTTGTGACAGCGATGCGGTCG 11310  
Qy 9685 GAGGGGCGGAGTTCCGAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 9744  
Db 11311 GGTCTCTGACAGAGCCGAGAGCTGTCGCGCTCCCTTCACTGAGAGGATGACCGTG 11370  
Qy 9745 CACCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9804  
Db 11371 CACCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 11418  
Qy 9805 CTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9864  
Db 11419 ACGGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11478  
Qy 9865 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9924  
Db 11479 CCGCTTACAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11525  
Qy 9925 CCGCGGAGTTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9984  
Db 11526 GATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 11585  
Qy 9985 CAGCGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10044  
Db 11586 ACAAGACCGGACCGCACTTGTGATGATGATGATGATGATGATGATGATGATGATG 11634  
Qy 10045 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10104  
Db 11635 -----GACGAGCTGAAAGTGTGCGCGCGCGCTGAGATGCGCGGAGCGTGTGAGAT 11681

Qy 10105 GGTGAGGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10164  
Db 11682 -----CGGCTTACACCCGACCTGCGCGCGCGCTGTCCAGAGATGATGATGATGATG 11733  
Qy 10165 CGGTTGCGGATTCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 10224  
Db 11734 CCGGCGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 11793  
Qy 10225 GACGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10284  
Db 11794 GGTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 11853  
Qy 10285 GAGCATCCGAGACCGGATTCCTCTGACCTGACACCGACACCGGACCGACCTGAC 10344  
Db 11854 CACCTGCGGAGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 11913  
Qy 10345 ACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10399  
Db 11914 TCCGCGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 11973  
Qy 10400 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10459  
Db 11974 ACCGCGGAGACCGAGAACCGCGCGCTTGTGATGATGATGATGATGATGATGATGAT 12033  
Qy 10460 GACTTGAATCATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10519  
Db 12034 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 12093  
Qy 10520 CCGAGTGCCTGCGCGAGCGCTGCGGATGATGATGATGATGATGATGATGATGATGATG 10579  
Db 12094 GCCCTGACAGACCGGACCATGAGCTGAGCGCTGCGCTGCGCTGCGCTGCGCTGCG 12151  
Qy 10580 GTGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10639  
Db 12152 GACCGCGGACCGGAGCTGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 12211  
Qy 10640 TGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10699  
Db 12212 GCTGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 12271  
Qy 10700 TGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10759  
Db 12272 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 12331  
Qy 10760 GCTTGGGAGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10819  
Db 12332 CCGTGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 12391  
Qy 10820 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 10879  
Db 12392 CCGTATCTGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 12451  
Qy 10880 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10939  
Db 12452 TCTCTCTGAGGAGACCTGCGCGCGGATGATGATGATGATGATGATGATGATGATGAT 12511  
Qy 10940 CCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 10993  
Db 12512 CCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 12571  
Qy 10994 CCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 11053  
Db 12572 CAGGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 12631  
Qy 11054 ACGCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 11113  
Db 12632 ACGCGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 12691  
Qy 11114 CCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 11173  
Db 12692 CCGCGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 12751



Db 6250 ACCCCGCGGACCGGACCGGACCTGCTCTGAGGCGCTCGCCGCTCTGAG 6309  
 Qy 4948 CACCCACCCACGCGCGGAAATCATGACTCTCCCAACCCCAACCCCAACCTCTC 5007  
 Db 6310 CACCCGAAACGCTGGGCGCGCTCGTCACTCCCGCCAGCCGATCCCGCCCTC 6369  
 Qy 5008 CAGGACTTCAACCAACCTCTCAACCCCAACCAACCAACCTCTGCTTCCGAC 5067  
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 Qy 5068 ACCGACCCCAACCGCGCGCTCTCAACCCCAACCTCTGACCCCAACCAACCAACCC 5127  
 Db 6430 ACCGACTTCAAGCCCGCGCTCTCGCGGACCTCTCAAGGAGCTGCGCCACCGC 6489  
 Qy 5128 ACCCCACCCCGGAAACCACTCTCATCCGCGGAAACCGCGCCCTCGCAACCCAC 5187  
 Db 6490 GACTGGACAGCCCAAGGACCGTCTCATACCGGCGGACCGGAGCCCTGGGACCA- 6548  
 Qy 5188 CTCAACCCACCTTCAACCAACCAACCAACCTCTCTCTCAACCGGAAAC 5247  
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 Db 6607 GCGGAAACGCGCGCGGAGCCACCACTCAACCGCGGAACTCAACCGCATCGCGCGC 6666  
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 Qy 5368 ATCCCGCCCAACACCCCTCTCAACCTGATCAACCGGAGGATCTCTGACGACG 5427  
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 Qy 5428 ACCCTCAACCACTCAACCCCGCAACCAACCAACCAACCTCTCGCGCAACCCCAAC 5487  
 Db 6787 ATCTGAGACAGCTTACCGCGGAGAGTTCGCGCGGCTCACCTGAGGAGCGCTCGC 6846  
 Qy 5488 GCGCACTCTCTCAACCACTCAACCAACCAACCCCTCTCAACCGCTCTCTCTACTC 5547  
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 Qy 5548 TCCCGCGCGCACTTGGGCGCACCGCGCAACCAACCAACCTGACCGGACCGCTTAC 5607  
 Db 6907 TCCGCTGAGGACTCTGCGGCTATCCCGGTGAGGCACTAGCGCCGACCAACCGCTAC 6966  
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 Db 6967 CTGACGCGCTTGGCGCTTGGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTG 7026  
 Qy 5668 GCGACCTGCAAGAAACGACTCGTATTCGCAAGGCGCGGCACTTCTGACCGC 5727  
 Db 7027 GGAAGCTGGAGAGTGGGCGATGCGCGCTGACGCGCTGAGCGCGAGCGCTGCGCAC 7086  
 Qy 5728 GCGGCTTTCGACCTTCAACCGGAGTTCGCGCGAGC----- 5768  
 Db 7087 CAGGCGCTGCGCGGATGAGCCCGGAACTCGCGCTGCGCGCACTGAGTTCGCGCTCGC 7146  
 Qy 5769 -----GTTCAGCGAGCGGATTCGCGGACCAACCGCGCTATGCTCATTCGCGAC 5820  
 Db 7147 CGGAGCGAGCGCGGATACCGTTCGCGGACATTCGAGACCGCTTCTACTTCGCGTAC 7206  
 Qy 5821 ATCGACTGAGACGATGAGACACACTCTGAGACGAGGAGCTG-----GTGAGCGG 5874  
 Db 7207 TCTTCGCGTCCGCGGAGCGCTCTGTCAGAGAGCTGCGCGAGTTCGCGCGATCATTCAC 7266  
 Qy 5875 GCGCGGAAAGGAGCGAGCTTCGAGCGCGCGCGCGCGCGCG-----AGTTG 5925  
 Db 7267 GCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7326  
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 Db 7327 GCGGAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7386

Qy 5986 CGAGACATGTGGCGGAGTGTCTCGGACCGGAGCCGAAAGCCATCGCGCGCGACG 6045  
 Db 7387 CGGCGGACGCGCGCGCGCTGCTCGGATGCGCTTCGCGGAGAGTTCGCGCGCGCG 7446  
 Qy 6046 TGTTCGCTGACTGGCTTGCATTCTACGCGCGCTGAGTTCGAAACCTGCTGATC 6105  
 Db 7447 GCTTTCAGGAGATGCGCTTGCATCGCTCGCGGTGTCGAGCTTCGCAACAGGCTGAC 7506  
 Qy 6106 AAGGACAGGAGCTCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6165  
 Db 7507 CGGCGGACCGGCTTCACTGCTGCGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7566  
 Qy 6166 CTGCGCGTACACTGCGAGAACCACTGCGGCGCAACGAGCGAGTTCGCG----- 6215  
 Db 7567 CTGCTGCTGCTGCTGCGAGGAGTCTCGGTCGAGGAGAGCGCGCGCGCGCGCGCG 7626  
 Qy 6216 -----TCTTCAGCGGAGCGCTTACCGCGCGGCTTCT 6249  
 Db 7627 TCCGCGCGCTGCGCGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7686  
 Qy 6250 GTCAACGAGCGGATGCGCATGCTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6309  
 Db 7687 GACGAGATCCGATGCGATGCTGCGATGAGCTGCGCTACCCGCGTGAATCCGCGAC 7746  
 Qy 6310 GCGGACGACTTCTGAGATCTGATCTCTCCGAGGAGCGGATGCGCGGATTCGCCAC 6369  
 Db 7747 CCGAGGACCTGTGCGGATGCTGCTCGAGGCGCGGAGGAGATACCGCGCTTCCCGAC 7806  
 Qy 6370 GACCGCGCTGGACCTGGAACAGCTTACGACCCCGGACCCCGGACCTCGCGACCTG 6429  
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 Qy 6670 ACCGATGCTTTCGACCTGAGCGGAGCGCGCGGAGCTATCTCGGCTGATCTCGTAC 6729  
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 Db 8227 GCGCTGACCTGCGGCTGCGGCTGCTGCGGAGCGGAGTTCGAGTTCGCGGCTGCGG 8286  
 Qy 6850 GGTGACGCGGATGCTGCTCGCGGCTGCTGCTGAGGTTTTCGCGGACCGGAGTTCG 6909  
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 Db 8347 GCGCGGAGCGGCGGACGAGGCTTTCGCGGAGCGGAGCGGAGCGGAGCGGCGGAG 8406  
 Qy 6970 GGTGAGGAGTTCGCTGCTGAGCGGCTTTCGAGCGGCTTTCGAGCGGAGCGGAGCGG 7029  
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Dp	2288	AGATGGAAGAGGTTGCTCGGGGCGTGTGAAGCCGATGGGGTCCGTGCGGGGTCAATTCCC	2347
Oy	665	TGAGCGTTCCCGCCCACTCCCTTGATGTAGCCCATCGAAGAAAGGGTGTCAAGCGGC	724
Dp	2348	TGACCTACCGCGTCCCAAGCCGGCAGGTGTGAGATCATCGAAGCGAGCTCGCCGAGGTCC	2407
Oy	725	TGCTGCGCATCAACCCACAGCCCTTCCGCATTCCTTTCATCTCTCGGTGACCGCGGCC	784
Dp	2408	TGCGGGGCTCAGCCCGCAGAGGTCTCGCGCGGTGCGCTTCTTCTGCACTCTGAAAGCGCTT	2467
Oy	785	GCTTCGACACCCGCGAGCTAGACGCGGGTACTGTGTACCGCAAACTGTGTGACAGCGGTCC	844
Dp	2468	GGATCAACGAGGCCCTGTCTCGACGGCGGGCTACTGTATACCGCAACTCTGGCCATGTGTGG	2527
Oy	845	GGTTCGAGCCCGCGCGCCGG---CTGCTTTGTGACAGAGGGGCCCAAGAAGTTGTGTGAGA	901
Dp	2528	GCTTTCGCCCCCGCGCTGTGAGACCTGTGGCCACGAGAGGGCTTTCACCTTCGTGTGAG	2587
Oy	902	TGAGCCCGCACCCCGGTGTGTGACCATGTGGCTTTCAGAGAC-----	939
Dp	2588	TCAGGCGCCACCCCGTCTTCAACCATAGGCGCTTCCCGGAGACGTATCACCGGTGTGAGACC	2647
Oy	940	-----CTGCGCCCGGACCTGTGGCGAGACCAACCGGCA	970
Dp	2648	TGCGTTCGAGCAACAGCGCGGTCAAGACCGCGCTGTGTGCTCTCTTCGCGGACATGTGGCA	2707
Oy	971	CCGCGGACACCGGTGATCATGTGGCACTGTGCGCGCGCGCCAGAGGACCTCTGAGCACTTCC	1030
Dp	2708	ACGGACTGCGGGTGCATGTAGAGCCGCTCTCCCTTCGCGACCGGCCACACATCTCGACC	2767
Oy	1031	TGACGTCTCTGCG-----CCACTACGCGGGCATGTGTAGACGTTCGGGCA	1075
Dp	2768	TCCCCACTTAAGCGCTTTCAGACCGAGCGCCACTGGCTGGCGAATGTGAGCGCTCGGCC	2827
Oy	1076	CCACCGGTCTCTTCGCGCACGCTGACCGCGCGTGTCCGCCACGACAG-----	1119
Dp	2828	CGCGGGGCGAGCCCGCGGTGACGCCCGCTTCTTCGCGAGAGCGCGCGCGCGCGG	2887
Oy	1120	-----CAGCAGTTCGTCTCTCTGTGACCTGTGTGCGCGGCCACACATGTGCTGTGAAG	1174
Dp	2888	AGCTTCGACCGGGACGAGCAGCGTGGCGGTGATCTGTGAACAAGTCCGGCGCGACAGGCC	2947
Oy	1175	ACGACGGAAGAGAGCGCACCGCGTGTGATGTCGGGCCATCGGCGAGATTTCGCCCACTCG	1234
Dp	2948	AGGTGCTGGGGTACGCGACAGCGCGGCGAGATGAGGTTCGACCGGACCTTCGTGAGGCG	3007
Oy	1235	GCTTCGACTTCGCTCATGTGGTGTGACATGTGCGCAACCGCTCAGGAAGGCCACCGGCGCTGC	1294
Dp	3008	GTTTCGACTCTCTTGAACCGCGGTGACCTGTGCGCAACCGGATTAAGCGCGCTTGGGCTTAC	3067
Oy	1295	GATTGCCGTGACGCTCATCTTTCGACCAACACAGCGCGGCGCGCGGTGCGCGCGGCTTTC	1354
Dp	3068	GGATGTGGCGCGTTCATGATCTTTCGACTTCCCAACCCCGAGGCTCTGCGGAGAGACTTC	3127
Oy	1355	GGAACGCGCGCGCTGTGGCCACTTCGACGAGGACACCGCGCGCTTACCGGACTTCACTCAGCG	1414
Dp	3128	TCTCTGTGTGACAGG-----GAGGCGCGCGCGCAACCGCGCGGTGCGGAGCGGCT	3180
Oy	1415	GCGACGGAAGC-AGGCGAGCGCGCGGACGACCCGATTCGATCATCTGGCATATGAGTATGCGCT	1473
Dp	3181	CGGTTGGGGGCGCGCGGTGCTGTGACCGAGCCGGTGTGGATGTGTGGCATGTGGCTTGGCGC	3240
Oy	1474	TTCCCGGCGGAGTTCGGGTCCCGAAGGACTGTGTGGAGCTGTGCGCGCTCGGGCGAGAC	1533
Dp	3241	CTGCTCGGTGGGGTGTGCTGTGCGCGGAGGACTGTGTGGCGGCTGTGTGGCGCGCGGGGAC	3300
Oy	1534	GCCATCGGGCGGTTTCCCAACGACCGACCGCGGATGCGCCAGGAACGCGTCAACGCCAGAC	1593
Dp	3301	GCGATCTTCGAGGTTTCCGCGAGGACCGCGCGCTGGGACGTGGAGGGGCTGTACACCCGAT	3360
Oy	1594	CCGACGCAACCCCGGCACTTTATTCGCGAGGAGGGCGGTTCTTTCACGACCGCGGCAC	1653
Dp	3361	CCGAGGACCCCGGCACTGTGTATGTCCCGCAGGCGCGGTTTCATGTGAACGTTCGCGGCG	3420

[illegible]

29082 GCTTCCGCGCCGCGCGGAGGCTGTCAAGCAGCGCTGTGGCGGCGCAGTGTGSC 29141  
27951 GATCGCCCTCCGCAACGCGAAACCCCTCTTCCAGAGCTCTACGCTGCC----- 28001  
29142 CCACGCCGTACCCGCGTACCCGCGCGTACCGCTACGCGGCTACGACCGCTACC 29201  
28002 -----CCAGGCCCGCAGCA 28016  
29202 GGCAGCGGCTCCCTTCTTCCGCGCGAAAGGTCTGATCAGCGCGGAGACCGGTCTT 29251  
28017 CACAGGCTCCCGCGAGCGCTCGAGAGCAGCTCTCATCAGCGGAGGACCGGACGCT 28076  
29262 GGGCGCGCTCTGTGGCGCGCGCATGTGTGAGGCGCAGCGCGGTACGCGCATCTGTGCGC 29321  
28077 CCGCGCTCTGTGGCGCGCGCTCTGTAAACAGCAGCGCGCAGACCTCTCTCTCAC 28136  
29322 GGGTCCGCGCGAGCAGCGCGAGGCTCGCGAGATTGCGGCGCGAGCTCGTGCGCT 29381  
28137 CTTCGCGCGAGGCGCGAGGCTCTCGGCTCTGATGTCTTGAGAGGAGCTGAAAGCTT 28136  
29382 CCGCGCGAGCGTGTGAGGTCTGTGCGCTGCGACCGCGCGGACCGGACAGCTGACCGACT 29441  
28197 GGGGCGCTCGGTACCCCTCGCGCGCTGCGAGCTGTGCGAGTCCAGCTTAAAGGACT 28256  
29442 GCTGACAGCGGATCCCGCAGATCGCGCGCGTGAACCGGTGTGTGAGCAGTGGCGGATCT 29501  
28257 TCTGATTAACATTCCTCAGAGCTTACCCGAGTCCGCGCGCTGTGAGTCCGCGCAGCTCT 28316  
29502 GGCAGCAGCGGTGATCAGTCTGTGCGCGAGCGGCTCGGCGCGCTCTCGGCGCA 29561  
28317 CAGCGCGCATCTGTCTGGCGCGCATGAGCTTCAAGCGGATGAGACCGGTCTTGCGCCCA 28376  
29562 GGGGAGCGTGTGCGCTCTTCTGACAGCTGACGCGCGGCGGACAGCTGTGCGCTTCT 29621  
28377 GATGAGCGCGCTGTGCGCTGATGAGCTACCCAGATTAAGCCCTTGTGCGCTTCTCAT 28436  
29622 CATGTTCTCTCGCGCTCGCGCGTGTGCGCTGCGCGCGCGGAGCACTAGCGCGCGC 29681  
28437 CCTTCTCTGTGCGCGCGCGCTCTCGCGAGCTAGGCTACTCACTAGCGCGCTGCG 28496  
29682 CAACGCGCTCTGAGCTTCTGTGCTGATGCGCGCGCGCGAGGCGCTCGCGCTCTCT 29741  
28497 GAGCGCTTCTCTGATGCGCTGTGCGCACACCGCGCGCGGAGGCGCTCGCTGCTCATC 28556  
29742 TCTGCGCTGTGCGCTGTGAGAGGAGGAGCAGAGGATGAGGAGGCTGAGCTGAGCA 29801  
28557 GCTCGGTGTGAGGAGCAGTGTGCGCGCGAGCGAGCAGATGAGCAGTCAAGCGCGCG 28616  
29802 CATGCGCGGATGAGCGCGCGCGGAAATGCGCGCGCGCTGCGGAGCTGTGCGCT 29861  
28617 CGCGCTCTGTGAGGAGCGCGCGG---CCTTCTCTGAGCTGTGAGGAGGAGTGTGCGCT 28673  
29862 GTTCAGCGCGGCTGTGAGCGAGCGGAGCGGCTCTGATGCGCGCTGTGAGCTGAC 29921  
28674 CTTCAGTGTGCGCGCTCTTCTGAGCAGAGCAGCGCGCTGTGCTCGCGCTGTGAG 28733  
29922 GGCCTGAGCGTGTGTGTGCGCGCTGCGACCGGCTGTGCGCGCTGTGAGAGTGTGCTTCA 29981  
28734 CGCGCTGAGGAGGAGCGCGCGGAGC-----GTCCCGCTGTGTCAAGTGTGCTGCG 28787  
29982 GCTGCTGTGCTGTGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 30022  
28788 CGCTGCGAGCGTGTGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 28828

## RESULT 13

US-09-320-878-19  
Sequence 19, Application US/09320878A  
Patent No. 6117659  
GENERAL INFORMATION:  
APPLICANT: ASHLEY, Gary  
APPLICANT: BETLACH, Melanie C.

APPLICANT: BETLACH, Mary C.  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
FILE REFERENCE: 30062202120  
CURRENT APPLICATION NUMBER: US/09/320, 878A  
EARLIER FILING DATE: 1999-05-27  
EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
EARLIER FILING DATE: 1998-08-28  
EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
EARLIER FILING DATE: 1998-05-06  
EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
EARLIER FILING DATE: 1997-04-30  
EARLIER APPLICATION NUMBER: 60/119,139  
EARLIER FILING DATE: 1999-02-08  
EARLIER APPLICATION NUMBER: 60/100,880  
EARLIER FILING DATE: 1998-09-22  
EARLIER APPLICATION NUMBER: 60/087,080  
EARLIER FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 19  
LENGTH: 38506  
TYPE: DNA  
ORGANISM: Streptomyces venezuelae  
US-09-320-878-19

Query Match 9.6%; Score 2956.6; DB 3; Length 38506;

Best Local Similarity 54.4%; Pred. No. 0;  
Matches 8439; Conservative 0; Mismatches 5719; Indels 1361; Gaps 69;

8 GGAATGAGCGGCGGAGAAACCCGCGCTGTGCGCGAGGAGTCTCGAGTGGCGGAGC 67  
Db 1703 GGCAGAGATCTGCGGAGCGCTGTGCGCGCGCTGTGAGGCTGTGCGGCGGCTT 1762  
Qy 68 AGCGGAGCGGCGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 127  
Db 1763 CCGGTGTGCGGAGTGTGCGGCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1822  
Qy 128 GAGGAGAACTTCTGACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 187  
Db 1823 GTGCGGAATGTGTGACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1882  
Qy 188 CGTTCGCGCGCTTCTGACCTGTGCTGTGAGCAGAGTGTGAGGAGTGTGAGGAGTGTG 247  
Db 1883 CACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1942  
Qy 248 CCGGCTGTGAGCGGCTGTGAGCTGTGCTGAGCGGAGCTTGTGCGCTGTGCTGTGCTG 307  
Db 1943 CAGCGTGTGAGGAGTGTGAGTGTGAGGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 2002  
Qy 308 CGCGCTTGTGCGCTGTGCGAGGAGTGTGAGCGCTGTGCGGAGTGTGAGCAGCTGTGAG 367  
Db 2003 CTTCGGTGTGAGGAGCAGCAGCGGAGTGTGAGCGCGCGGCTGTGCGGAGTGTGAG 2062  
Qy 368 AGATGCGGCGAGCAGCGCTGTGAGGAGTGTGCGGAGCGGAGCGGAGCGGAGTGTGAG 427  
Db 2063 AGATGCGGCGCGCTGTGAGCTGTGCGGAGTGTGAGCTGTGAGCAGCGCGCTGTGAG 2122  
Qy 428 CGCTTGTGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 484  
Db 2123 CCTGTGAGGAGAGTGTGAGTGTGCGGAGCAGCTGTGCGGAGGAGGAGGAGTGTGCTG 2182  
Qy 485 CCGCGAGCGGAGTGTGAGCTGTGCGGAGTGTGAGCTGTGAGCAGGAGCAGCAGCGGCG 544  
Db 2183 CGCTGAGCAGGAGCAGCGCTGTGAGGAGCAGCTGTGCGGAGTGTGAGCAGCAGCGGCG 2227  
Qy 545 GCGTGTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 604  
Db 2228 GCGTGTGCGGCGCGCTGTGAGGAGGAGCAGCGGAGCAGCGGAGCAGCGGAGCAGCGG 2287  
Qy 605 CCGTGTGAGCAGCTGTGAGCGGAGCAGCGGCGGAGGAGTGTGAGCAGCGGAGTGTGCGG 664



Db	25942	CTCTCCATCGCCGCGCTCAACAGCCCCAGGGCCACGCTCGTGTCCGGACGAGCCCGCCGCG	26001
OY	26926	GTGATGAGGTGCTGGCGCATGCAACGACACCGGCGCTACGGGCGCAACGATCCCCGTC	26985
Db	26002	ATCGACGGCGGTGATCGACTCGCTCACGCGACGCGAGGCTCTTCGCGCGAAGGTCGCGCTC	26061
OY	26986	GACTACGCTCCCACTGCGCCCAATGAGAGCGCGCTCCAAAGCAAGCTCGCCGAGGCTCA	26121
Db	26062	GACTACGCTCCCACTGCGCCCAATGAGAGCGCGCTCCAAAGCAAGCTCGCCGAGGCTCA	26121
OY	27046	GAGACATCAACCCCCAGCGGTTCACCGGTGCGGTTCTTCTCAACCGGTGAAGGCACTGAG	27105
Db	26122	GCCAAATCGCTCCTCGGAGGTGGAGACTCCCTTTATTGACCGTCAACGCGACACAG	26181
OY	27106	CTGGAACACAAACCTTGAGAGCGCGCTTATGTATCCGCAACCTTCACAGCCCGTCCCG	27165
Db	26182	CTGACGCGCTCCGAGCTCGAGGCGGCGTATCGAGTATGAAGCTCCGGGAAACCGTCTG	26241
OY	27166	TTTCAGCCACCGCATTCAGACCTTCAGACGAGACGAGACCGCGCTTATTCGAATCAGC	27225
Db	26242	TTCTCGACCGGACCGAGCGGCTTCCTGAGAGTGGCATGCTTCTTGTCTGAGGTCAAG	26301
OY	27226	CCCCACCCCACTCGTCCCGCGGATCGAAGACCAACCGAAGAACCAACCGAAGAACATC	27285
Db	26302	CCCCATCCCGTCTCAAGCTCGGCTCCCGGAGACCTGGAGCGCTCACCGCTCGATCCC	26361
OY	27286	ACCGCGACCGGACGCTTCGCGCGCGGAGCAAGACACCCACCGCTTCTCAACGCGCTTC	27345
Db	26362	GTGTCGTGCGCTCAATTTCAGCGGAGAGAAAGGCACTCGCGCGCTGCTCTCTCTGG	26421
OY	27346	GCCCAACACCAACACACCGGAGATGGAGACACCAACCTGGACCAACATACCCAA	27405
Db	26422	GCGAGCTCTCTACCCGAGGCTCG-----CGCTCGACTGGAGAC	26460
OY	27406	ACCCACCCCAACCCCAACCCCAACCCCAACCCCAACCTGACCTGGACCTAACCCCTTCAACAC	27465
Db	26461	GCTTCTTTCGGGCTTCGCTTCCTCCGCAAGTCTCCCTCCCACTAACCCCTTCAACAGC	26520
OY	27466	CAGACTACTGGCTCCAAACACCAACCAACAA-----CAACGACCTTCACCAACCGGCTTC	27522
Db	26521	GAGGCTTTCGGCTCGAAGCTCCACAGGCGCAGCTGGCGAGCGTCCGCTCCGAGGCTCG	26580
OY	27523	ACCCCAACCAACACCCCTCTCTACCGGCAACATCAACCTCTGGCGAACAACACAA	27582
Db	26581	ACCTTCGCGCAACACCGCTGTCTGGGCGCGCGCTGCTCGCGCAACCGCATGAGCTTT	26640
OY	27583	CTACTCAACGCGCGCTCTCCCTACAGCAACCAACCCCTGGCTACCGACCAACGCTCGC	27642
Db	26641	GTTTCAACAGAGCGGCTCTCTCTCGACAGACACCGGTGCTGMAAACAACGTCCTTC	26700
OY	27643	GGCATGTCTCTCTGCGCGGCAACCGCGCTCTCGAATCGGCTTCMAACCGGCGAAGCG	27702
Db	26701	GGCATTACCTGCTCGTGGCAAGCGCGCTCTCTGAGCTGGCTCTGATGTGCGCATCTC	26760
OY	27703	GTGACCTGCCCTCGGAGTGAAGAACTGACCCTTGACAGCAACGTTGTGTATCCCGACACC	27762
Db	26761	GTGCGCTTCGACACCGTGAAGAGTCAAGCTGACCCCGCTGCTCTCCATCGAG	26820
OY	27763	GAGACCTGACGTTTGACGGTTCACCGTTTCGGGACGCGATGAGAGTGGCATTTGCGGCTTC	27822
Db	26821	GGCGCGTCTCTCTCCAGATCTCCGTGCGGCGCGGAGCGTGTGAGAGAGGCGGCTTC	26880
OY	27823	GCGATCACTCTGTAACCTGGGCAACGCGGTGTCGCGGAGACCGGAGTGAACCCGTACGCG	27882
Db	26881	TTCGTTTCA---TAGCGGCGGCGACGAGCGGCTTCAGAGTAGGCCCTTGAAGCTGCGACGCG	26937
OY	27883	ACGGGCTCTCTCAACAACACGCGGCAACCGATCAACCTGTGCGGACACGCAACGAGACGCG	27942
Db	26938	AGGCGCTCTCTCGGCGAAGTACCGGCTCCATTTGCTTGATGTCT-----	26984
OY	27943	TGCGTTGGCGGAGCTGAGCCCGCGCGCGCGGCGGCGACCCATGAACTGAGCGACGTTAC	28002

Db	26985	-----CGGAATGAGCCCCCTCGGGGGCCACCCAGGTGACACCCAAAGTTTCTAC	27036
OY	28003	GATCGTATGCGCGGCACTGGAACATGACTACGGGCGGCTCTTCCAGGGCGCTGC-ACGC	28061
Db	27037	GCAGCCCTCGAGAG---CGCTGGGCTTGTTATGACCCCGAGTTCCAGGAGGCTCCGGCCGC	27093
OY	28062	CGCCTGAGAGTTTGGGCGACGATGTCTGCGCCGAGGTGCGTCTGCCGGAAGAAGCTTGGC	28121
Db	27094	CGTCTACAAAGGCGCGGCACAGAGCTTTCGCGAAGCMAAGCTCCCGAGCGCGC-----	27147
OY	28122	CGATGCTCCGGCGGCGGCTTCGAGTGTTCACCCGGGCTTGCTCGAGCGGACCTTGACGC	28181
Db	27148	CGAAGAGAGCGCCGCTGTTTGCTCCCTCCACCCCGCCTGCTGACAGCGCCTTGTGACGC	27207
OY	28182	CACGCGCTCACCCCGAGAACGAGGAGCGAGCTGACGAGAAAGTCGCCAGAGAGCAT	28241
Db	27208	GCTGCGCTTTGTAGACGACAGGGAAGGCTTCA-----	27242
OY	28242	GCTTGACGCGGACGCCACCAAGGCGGACTGCCGTTCACTGAGAGCGGCTGTCCCTGCA	28301
Db	27243	-----GGAATGCCCTTCTGTGGAGGAGTAGTATCCTGGC	27276
OY	28302	CACGCGGCGGAGTTCCGATGTTGCGGCTGAGGCGCTGTGCGGACGCGACAGTAAATGC	28361
Db	27277	CTC---CGATGGAAGCCACACCTTCGGCGCTTTCCTTCACCGTCTGAGAGGGAATCTTC	27334
OY	28362	CGTGGCCCTACCGCGGCGGACGAGAGAGCGTGGCGCGGTGTGACGATCGATCGCTGC	28421
Db	27335	GGCGTCGCTCCTCGTCGCGAGCCGAGAGGCGAACCATCGCTGGGTGACMAAGCCTGCG	27394
OY	28422	GCTGCGGCGGCTGTTCACCGAGAGCTGGCGCGGCGCGGATCTGAAGCCGAGACGA	28481
Db	27395	CATCGCGCGCGCGTCCGCGCAGAGGCTCCGACAGCCCGG---GAGCGTCCCACTCGA	27449
OY	28482	GTCGCTCTTCGACGTGACGTGGGTTTTCCGATCCAGTGGCCCGGCAAGGCCCTTCCGCCAC	28541
Db	27450	TGCCCCCTTCGCAATGACTGGAGCGAGCTGCAAAAGCCCAAC-----TACCGCGC	27500
OY	28542	CGCGGACCGGCGCTGTGGCGGTGATCGAGCGCGGCGCTTCCCAACTGCCGCGCTACAGGA	28601
Db	27501	CATGCGCCCGAGGGGTGCCCTCTCCGCGACAGAAAGTCTCGACTTCGGGACCAAGGATGC	27560
OY	28602	GCAAGAGACGTGACCGCGTATGACGAGCGCGGCGACCTGTTCGGCTCTGAGACCGCGG	28661
Db	27561	TCTGGAACGC-----TATACGACCTTGCTGTACGACAGCGCCTCGACCAAGG	27611
OY	28662	TGCTCCGCGCGCGCGGTGTGCTGATGTGTCTGATGTGTGTGCGCCACACAGAAAGCCGGAATG	28721
Db	27612	CGCTTTCGCTCAAGCTGTCATGCTGCCCTTCCTTCATCGTCTGTGCCGA-----	27660
OY	28722	TTCCGCGAAGCCCGGAGGAGCGGAGACGAGGCTTGCAGAGCCCGGCGGACGTGCT	28781
Db	27661	-----	27660
OY	28782	GCAAGTGGGCGTGTGCAACGAGCTGCCTGTCGAGCGAGCTGCGCGAGATGTTGGCCAG	28841
Db	27661	-----GGGACCTCATGCGAGCGCGCGGACGACACCGGCAAGCGCTGACCT	27710
OY	28842	GCTCCAGGCTTGCTGGGTGGGAGCGAGGCGCTCCGACAGCAAGCCGGGCTGTCTGTACGTTG	28901
Db	27711	CTTGCAAGCTTGAGCTGCGGACGAGGCGCTCCCTCTTCGCGCTTCGCGCTGTGTACCG	27770
OY	28902	CGGCGGAGTGGCGCGGCGCTCCGAGGACGATGCGAGCTGAGCCCGGAGGCGCGGCTGTG	28961
Db	27771	ACGCGCGGCTGCCACCCAGGCTGAGAGAGAGCTCAAGGAGCTTCGCTCACGAGCCTCTTG	27830
OY	28962	GAGGCTGGTGCCTTCCGCGGAGTCCGAGACCCGAGACCGCATCAGCTGTGACTTGTGA	29021
Db	27831	GGGTCCTGCTCGCTCCGCGAGAGGAGGACCCAGAGGCGCCCTTCGTCCTGTGACT	27890
OY	29022	GCGGAGGACAGAGGCGGAGCCGCTGACGTGGCGACGCGGCTGAACTCGCGGAGCGGCA	29081
Db	27891	CGACGACAGGAGGCTCCGACAGCGCCCTGTCTCGCGCGGCTCGACGCGMAAGAGCCGA	27950

24706 GACCTAGACGAGAGAGACGCGGCACTGTGAAATGCTCTCCCGCAATGGCCCATCGG 24765  
23821 CAGGCCCTTGCGACGAGGCTCTCCGCCGAGGCGA-----CGCCCGCGGCTCCGC 23871  
24766 CGTACCGTGAAGAGCAGAACCGATCGGCATCATCGATATGCAATGTCCTTCCCGCGCGC 24825  
23872 CGCGCTCGAGGAGAGAGCCCATTCGCTGTCGGCATGGCCCTGCGCTGCGCGGCGCGC 23921  
24826 GTAACGTTCTGCGGAGCACTGTGGGAATTGCTGCTTCCGGTAAAGACGCTTATCGCGTTC 24885  
23932 GTCCGGAGATGTGACGCGCTTTTGGGAGTTCTTCACCAAGGCGCGCACCGGCTCGAGCCC 23991  
24886 TTCGCCGACGAGCGCGGCTGGGACCTGAGCAGCGCTTACAGCCCGGACCCGACCACCCC 24945  
23992 ATTCCAC--AGAGCGGCTGGAGAGCGCGGTGCGCTTACAGACCCGACCCGACGCGCAC 24048  
24946 GGCACCTGTACAGCCCGAAGACGCGGATTCCTTACGCGCGCAGGCGCACTTTCAGCGCGAA 25005  
24049 GCGAAGAGCTACGTCCGGCATGCGCGATGCTCGACCATATGACCTTTCGACCCCTGCGC 24108  
25006 TTCTTCTGGGATACGCCCCCGGAGCGCTTCCGATGAGACCCCGAGACGATCTCTCTTC 25065  
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25126 CCCACCGAGTCTTTCGCGCGGAATCAACGCTCAAGACACGCGCGCATATTCGCGCAAGC 25185  
24229 CTCACGGGAGTCTTTCGCGCATCTGCGCGGGAATACGCGATG-----CAGAG 24279  
25186 CGTGAATGAGAACCATTCAGAGGCTTACGCGCTGACCGGAGATTCGCGGAATGTGCGCTC 25245  
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25246 GGCAGGAGGCTTACACGCTCGGAGCTCGAAGGCGCGGCTGCGGTGATACGCGGT 25305  
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25306 TCGTGTGCTGTGTGCGCTTTCATTTGGGCGCGCAGCGCTTCGTCGCGGTGATGTTTCG 25365  
24400 TCTCTCGCTGCTGCTCTCTCCACCTCGCTGCGCAAGCCCTCGACAGGCGGAGTGCAC 24459  
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24460 CTCGCGCTTGGCGGAGTGTGCTCATGATCTCCCGACAGACCTTCGTCATCTTTTC 24519  
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24520 CATTGCGGCGCTTGGCGCGGAGCGGCGCTTCAGACCTTCTCGAGCAACGCGAGCGC 24579  
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25546 AACGCTACCGGTCTCTGGCGGAGTGTGAGTGTGAGAGCGGCTTCGACGCGCGTTCG 25605  
24640 CGAGAGACCGGCTCTGCTCTCTGTCGCGGAGCAGCGCATCAACACAGCGCGGCTGCG 24699  
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24700 AACGCTACCGGCGCGGCGCGGCGCTTCGAGAGCGGCTTCGAGGCGCGCTGCGCGC 24759  
25666 AATGCGGAGCTACCGCGCGGCGGAGTGTGAGAGTGTGAGAGCGGCGCGGCGGAGCT 25725  
24760 GACGCGCGGAGTACCGCGCGGCGGAGTGTGAGAGTGTGAGAGCGGCGCGGCGGAGCT 24819  
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24820 CTGGGAGAGCGGATCGAGGCGGAGGCGGCGGCGGCTTACGAGCGAGCGGAGCGGCT 24879

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24880 GAAAGGCTCTCTTCTGGGCGGCTCAAGACCAACATCGGAGCATCTGAGAGCGGCTTC 24939  
25846 GCGGTGGCGGAGTATCAAGATGTGTGAGCGCTTCGCGCAACGCGCTGCTCCACAGACC 25905  
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25906 CTTCACGTGAGACGAGCCACCCCGGAGTGCATGTGTTCACAGGCGGAGTCACTCTCG 25965  
25000 CTCACGCGGAGCCACGAGAAATCCCTCATGAGTGGAGGCGCTGCGCATGACGCTGCTC 25059  
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26146 CTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 26205  
25221 TGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 25290  
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25321 ACCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 25410  
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26386 ACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26445  
25465 GAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 25524  
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26686 TCCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 26745  
25785 AGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 25824  
26746 AAAACGTTGAGCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 26805  
25825 GCGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 25884  
26806 TCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 26865  
25885 GCGGCTGAGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 25941  
26866 TTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 26925

Db	21649	GTGCTGACCTTGGGCTTGACGAGCTCTCGAAGCGTCCGAGGGCTCGGCGGGTGTCT	21708
OY	22552	CACCCCAACCAACCCCCAAACCCACTCTCTCAACCACTGCGCAAAACCAACACACC	22611
Db	21709	GGCCTCTGTGGAGCGAGAGGGAGACTACGAGCGCTCTCTCGCTCTCCGACTC	21768
OY	22612	TGGCAGCCCCACGACTACACCCACACACACACACCCACACCCACACCCACTCGAC	22671
Db	21769	TACGTCACAGGCTTGGCTCGGATTTGGACGACGATCTGCGCCCCGGAGAGCGGGTCCG	21828
OY	22672	CTCCCACTTACCCCTTTCACACCAACCACTACTGAGCTCGACATACCCAGCGCCAAAC	22731
Db	21829	CTGGCCACTTACCCCTTTCAGCGGAGCGGCTTGTGGTTCGACCGCTTCAGCGGACCCGC	21888
OY	22732	AGCCCCGCTCAAGGCGTTCTCGCGCTCGGCTTCGACACCGCCGAGTCCGAGTTCTGG	22791
Db	21889	GCCGCGCTCAACCACTTGGCTCGCTCGAGGGGC-----GGTTTGGCAGGGCCATCGAG	21942
OY	22792	GAGCGGCTGACGAGGAGAAAGCTTCAGAGCTCGCCGAAACCTTCGACATCCAGCGCTT	22851
Db	21943	AGCGGAAATTCGACGCGCTTCAGGAGCACTCCAGTTGACGCGACAGCAGCGCGCC	22002
OY	22852	GCTCTGACACAGGTGTGTCGCACTCTCGGCTTGGCACCGGCAACCAACGACCAAGCC	22911
Db	22003	GCCCTTGCCTGCTCTTCCACCTTCGCAAGCTTTCGACGAGCGGCAAGGAGAGGAGC	22062
OY	22912	CGCATCAACCTTGACCTTACAGGAAACTTGAAACCCCTCACCTTCCCAACCAACCAC	22971
Db	22063	ACGGTCACGCGTGGCGCTACCGCATCAGTTGAAAGCTTCGACACCGCCACACAGGCC	22122
OY	22972	CAACCCCA---CGAAACTGTGCTATATGGCCATCCCGGAAACCGACCAACCAACCCAC	23028
Db	22123	GCCGACCTGGCGCGACCTTGGCTCTCTGTGTGTCGCGCGCTCTTGACACACACGCGCTC	22182
OY	23029	ATCAACCAACATCTCTCAACCACTTCACACACAGGAGATACCCCACTCCCGTCACCTGTC	23088
Db	22183	CGCTTCGCGCTACACGAGGGCGCTTCGCCGAGCGGCGCGGCGCTTCGCCGCTGGCCTTG	22242
OY	23089	AACCAACCAACCAACCAACCCCAACCTTCACACACACCTTCACACACACCCGACAAACA	23148
Db	22243	AGCAGGCGCAACCTTGACCGCGAGGCTTCGCCGACGACTGCGCCAGGCTTG-----	22295
OY	23149	GCCCCAAACCAACCAACCGGACCCCATATCAGGCTGTCTCTCTCTCGCTTCGACGAA	23208
Db	22296	-----CGCCGAGACCGGCGCGCTTCGGGCGGTCTCTCGCTCTCTCGCTTCGACGAA	22347
OY	23209	ACAACCCCAACCCCAACCCCAACCAACCAACCGGAGACCTCTCAACCTTCAACCTTCCC	23268
Db	22348	AGTCCCTTCGCGACACATGCGCGCGCTTCGCGGAGACTGACTTTCGCTCACCTTCGTC	22407
OY	23269	CAAAACCAACCAACCAACCCCAACCAACCCCTCTGTGATGCGCAACCAACCAACGCTCAC	23328
Db	22408	CAAGCCCTTCGGGACATTCGCGCTTCGACGCGCTTGTGGCTCTTACACCGCGGAGCGCTC	22467
OY	23329	ACCAACCAACCCCAACGAGCCCTTCACACACCTTCACCAACCCCAACCTTGGAGACTCGC	23388
Db	22468	TCCGTCGACATTCGCGACCCCATATGCCATCCGACGACGAGCGATGACTGGGAGCTTGGGC	22527
OY	23389	CGACACCACTCTCTCGAAGACCCCAACCCCAACCGCGGAAATATGACTTCCCCACAC	23448
Db	22528	CGGTCTGTGGCTTCGACACCCCGAGCGCTGGGAGGAGCTGTGACCTTCGCGCCACAG	22587
OY	23449	CCCAACCCCAACCCCTTCACCACTTCACCAACCCCTTACCCCAACCCCAACCAAC	23508
Db	22588	ATGAGCGCGAGCGCGCTGGGCGCTTGTCTTCGCGTCTTCGCTTCGACATGATGAGAC	22647
OY	23509	CAACTGCGCATTCGACACACCGGACACCAACCGCGCGCTTCAACCCCAACCAACCTTCAAC	23568
Db	22648	CAGCTCGCTCTCGCGCGCGGAGTTCTAGCTTCGCGCGCTTCGTCGCGGCTTCGCTGGGC	22707
OY	23569	CCCAACCAACCAACCAACCCCAACCCCAACCGAACCAACCTTATATCAGCGGAGAAC	23628

[illegible]

OY	20347	GGCAACCCCAACGGAGCTTACCCGGACCAAGACACAGACACAGCGGACACATCCGT	20406
Db	19561	GATTCTCCCAACGGCGCTTCTGTGGGATGGCGGACGACCAATATCCACTGGAAAC---	19617
OY	20407	CAGGCCCCAGACGGGTATCCAGAGGATTTGTCCTTACCGGGGACGACACAGATCCGCTTC	20466
Db	19618	ACGAGCTCCGAGAGGCTGAGAAAGGTATAGCCCTCGAAGGACCGCGGGGTCTTTGGCCGG	19677
OY	20467	GGCGGAATCTCTCATCTCTCGGGTTGGAAGGCGCTGCGGTACCTTCGACACAGGTGT	20526
Db	19678	GGGGGCTTGGGCTTACAGCTCTGCGCTGCAAGGGGCGCGGCTCTCGGTTCACACCGGCTGC	19737
OY	20527	TGCTCTCGCTCGAGCGGCGCTGCACTGCGCTGCGACGATGCGCCCTTAGAGTCCGGATGATGACCC	20586
Db	19738	TCTCTCTCGCTCTGCTGCGCTTCACCTGCTTCGCAAGCCCTCCGACAGGGCGAGTGCAC	19797
OY	20587	ATGGACCTTTGGCGGGGCGGACCGCTCATGACCAACCCCGATCACCTTTCACCAATTCGCG	20646
Db	19798	CTCGCCCTCGCGCGGGCGGCTCTCGGTATGGCCTCCCGGAGCTTTCGTCTGCTTC	19857
OY	20647	CGCCACGCGGACCTCGGCGCCCGACGGGCGTTTGGAGGCGTTTCGGGCGGGCGGTAGCGGT	20706
Db	19858	CGCATCGGTGTTTGGGCGGCGCCGAGTGGCGCTCCAGACCTTCTTGACCAACGCGACGGCG	19917
OY	20707	ACCGGCTGGGATGAGGATGTGGGATCTGTGATGAGCGGCTTCCGACGCGCGCGCG	20766
Db	19918	TACGGAAGCGGAGAGGGCGTGTGTCTTGGCCCTGAGGCGGCTGGGCGACGCGCTCGCG	19977
OY	20767	AACGGTACCGGTCTCTGCGCGGTGTGCGTGGACATGATCGGTCACACAGACGGTGTGAC	20826
Db	19978	CGAGGACACCGCGCTCTGCGCTCTGTCGCGGCGACCGCCATGAAACATACCGCGGCTGTG	20037
OY	20827	AACGGTCTGACCGGCGCCCAACGGGCGCTCCGAGAGGCGTCAATCCGCGACGGCGCTCGCG	20886
Db	20038	AGCGGCATCACCGGCGCCCAATGACACTTCCACCAAGAAAGTCTTCGCGCGCGGCTTCAC	20097
OY	20887	AACGCGGACCTGACCCCCCGCGACGTCGATGCGGTGAGGCGCAACGGACACCGACACT	20946
Db	20098	GACGCCCCATATCGGCGCTCGCGACGTCGAGTGTGTAATGCATGGCACCGGACCTTC	20157
OY	20947	TTGGGCGGACCGGATCGAGGCGCCAGGCGCATCTCGGACACTACGAGAGAGACCGTCCCGCG	21006
Db	20158	TTGGGAGACCCCATATGAGGTGCAAGCCCTGACGCGCGCTTACGCCGATGTGCMAACCCGCT	20217
OY	21007	AACGGGCGGTGTGGGTGGGCTCGGTCAATTCACCGTCGAGACACACAGGCGCGGCGG	21066
Db	20218	GAAAAAGCTCTCTCTTCTGGGCACTCAGAACCAATTTGGCATCTCGAGGCGGCTTC	20277
OY	21067	GGCGTGGCGGAGTGAATCAGATGTGATGGCCCTTCGCGCACCGGACACTCCACCGACT	21126
Db	20278	GGCGTGGGCGGCGTGGCCAGATGTGCGCTCTCCCTCGCANTAGCGCCCTGCCCCACAC	20337
OY	21127	CTCCACGCGGATGAGCGCGGTGCGCATGTGGACTGTGCGCGGAGTGCAGGCTGCTG	21186
Db	20338	CTCCACACGACCCCGCGCAATCCCTGATGTGAGTGGGATGCGTCCGATCGACGTCTGC	20397
OY	21187	ACGAGACGATGCTTCGTGCGCGG---CGGGAGGGGCGGCGCGCGCGGACGAGTGTCA	21243
Db	20398	GATGCAAGAGGGGCTGGGCGCGGCAAGAAATGGCAGTCCCGCGCGCGCGCGGCTTC	20457
OY	21244	TCAATTCGGCGCTCAAGCGGACCAAGGCCACGTCACTCTCGAAGAAACACCGCGGACGAC	21303
Db	20458	GCTTCGGAGCTCTCCGGACCAACGAGCCACGTTATCTCGAAGAGGCTCCG-----C	20510
OY	21304	GTTCCGGGAGGACACACCGCGGACGAGAGATGCGGATGTGATGACAGAGAGGCTGTGCGCG	21363
Db	20511	GATCCCGAGGCGGAGCCACCGGCGGACAGC-----TGGGTGCGAGCGGCTTCCGCG	20564
OY	21364	AGTCTCGGAGGTGTGGCGCTGTGCTGTGTGCGGCAATGCGACGCGGCGCTTCGCGCGCAG	21423
Db	20565	AGCC-----TGGCGGTGTCTCTGTGCGGCGAGGACGAGCGGCGCGGTGCGCGCCAG	20616

QY	21424	GGCCAGGCGCCGTGACGCGCCACCTTCACGACACACCCGGGCTGACCTCGCGACGCTCGGA	21483
Db	20617	GGCCAGAGGCTCCGGACCACTCTCTGGCCACGACGACCTGCGCTTGGCGATGAGC	20676
QY	21484	TACACCTTCGCGCACGCGCCGCGGCTTTCGACACACGCGCCACCTCATTCGCGCGAC	21543
Db	20677	TACTCGCTCGCAACACCGGGGCTACTTCGACACCGATGAGCAGCTGCGGCTTCGTGGTCCAGAC	20736
QY	21544	CGGACACCTTCTCTGCAAGCATCTCAGGCACTTGGCGGAGGMAACCCACCCCGCGTC	21603
Db	20737	CGCAGAGCTCTCTTCGCGGCTCGATTGGCTCGCCAGAGGAGGCGCCCGCCGAGCAC	20786
QY	21604	ATTCACGACGCGCGCGGAGCGGGACCGGGAGGCGCGAGAAAGACCGCATTC	21653
Db	20797	GTCCTCGAAGAGGCGGAG-----CCACGGCAAGGTGTCTTC	20835
QY	21664	ATCTGCTCGGACAGGCGACCCACGCGCGGATGGCCACGCGCTTACACACCCAC	21723
Db	20836	GTCCTTTCCTGGGACAGGCTTCGCGAGGAGATGGATCCCTCTCCTCTGCTCATACCTCG	20895
QY	21724	CCGCTTTCGCGCGGACATTCACGACATTCGACACCATCGACCCCGACCTCGACAC	21783
Db	20896	CCGATCTTTCGGGACAGCTTCGAGGCTGAGCGCGCCCTGCGCCACGTTGACTGG	20955
QY	21784	CCCTCTCTCCCTCTTCACCCAAAAGACMAAGACMACAGACGAGGACGCGGCGCA	21843
Db	20956	TGCGTGTGCGGGTGT-----CCGCGGAGGAGGAGGCGGCGCC	20994
QY	21844	CTGCTTCAGACGACCCCGTATGCGCCAGCCCGCTCTTGGCTTCCAGTGGCGCTTCAC	21903
Db	20995	CCGCTTCAGCGGGTTCGAGTGTTCAGCCCGCGCTTTCATGATGATGTCTCGCT--GG	21051
QY	21904	CGCTCTCTCACCGGCGCTACACATCACCCCGCATTAAGCGCGGACATCCCTCGG	21963
Db	21052	GGCGCCCTGTGGCGCTCCATGGGCGTTCGAGCCGACGCGGTGGTGGCCATGACAGGCG	21111
QY	21964	GAATTCACCGCGCGCCACTGCGCGGCACTTCACCTTACCGACGCGACACACCTCATC	22023
Db	21112	GAGATCGCGCGGCTGTGTGGCGGGCGCGCTTCCTCGAGAGCCCTCCAGAGCTGGTGG	21171
QY	22024	ACCCAGGCGCG---ACCCTATGCAAAACATGCGCCCGGACCAATGACACACCCCTCCAC	22080
Db	21172	GGCGTGGGACCGGTGCGCTCTGTGAGCTTCGCGGCGAGGGGCAATGGCGCGGTGGAG	21231
QY	22081	ACGACCCGACACCATCACCCACACCTGACCGCCACGAAACGACCTTGGCATGGC	22140
Db	21232	CTGCGGAGGCGGAGTTCGACCGCGGCTTCAGCGGATATGAGCATGGGCTTCTCAATCGGG	21291
QY	22141	GGCATCAACACCCCACTCCCTGTGTATATAGGGGACCCCGCCACACCGTCCACACATC	22200
Db	21292	GGATTCACAGCCCTCGTTTCACGACATTCGAGGAGCCCTCGCGTGTGCGCGCCGTG	21351
QY	22201	ACGACCTCTGCGCAACAGGACATCAAAACCAAAACCTCCCGCCACCAACGCGCTTC	22268
Db	21352	CTCGCGATCTGGAGTTCGAGGGGCGTTCGGCCCTCAAGTGAATGACATTTGCGCTCC	21411
QY	22261	CAGTCCCCCAGACCAACCCCATCTCTCAACCACTCCACAGCACACCAACCTTGACC	22320
Db	21412	CAGTCCGCGCGAGTTCGATTCGATTCGAGACCTCTCGATCTCTGTGTGAGCTCGAG	21471
QY	22321	TACACCCGACCCGACACCCCGCTCATACCGGACACCGCCACCCGACCACTC-----	22374
Db	21472	CCGGGCTTCGAGGGGCTCCGTTCTACTCCACGATGAGGGCGCGCGATCGACGGGAGC	21531
QY	22375	---CTCACCCCGCATCTAGGACCCCAAGCCCGCAACCGTGCATTACGCGCACAC	22431
Db	21532	GAGCTCGACGCGGCTCTACTGTACCGGAACTTCGCGACGCGGATCGCTTCGACAGCGCT	21591
QY	22432	ACCCAAACCTTCACCAACAGCGCTCACCACTTACATGAACTGGAGCCGACCAACAC	22491
Db	21592	GTCGAGGCGCT---CTTTCGAGGAAATCGCTTCTTGTGGAGGTGAGCCCCGATCTCT	21648
QY	22492	CTACACACCTTCACCCACCAACCTTCGCCAACCCCGACACACCTTCACCTCAC	22551

Db 17350 CTCTTCCCAACCTCTGAGCTTCAACACAGGCGCCAGAGACGAGCTGACACC 17409  
OY 18220 TGGACCTACGAGGAAACCTGAAAACCCCTGACCCCTCCCAACA---CCACCAACCCCAAC 18276  
Db 17410 TGGCGTACCGGATCACTGTAAGAGCTTCAACACGCGCGACGCCCTGCGACTTGCC 17469  
OY 18277 CAACCTGCTCATTCGCACTCCCGAAACCCAGAACCCCAACCCCAATCAACCAACATC 18336  
Db 17470 GGCACCTGCTCTCTCGTCTGCGCGCTCGCGGAGACGCGGCTCCCTGCAAGCTC 17529  
OY 18337 CTACCAACTCTCAACCAACGCGGATCAACCCCATCCCTTCACTTCAACCAACCCAC 18396  
Db 17530 ACCGATGCGCTTACCGCGCGCGCGCGCTGCTCGCGCTGCGCTGAGCCAGCTTCA 17589  
OY 18397 ACCAAGCCCAACACCTCCCAACAACCCCAACAACCCCAACCAACCAACCCCAACCC 18456  
Db 17590 ATTAGCGCGCGCGCTCTCAACGAGACCTGCGGAGGCTGTTCCGAGACTGCC---CCG 17646  
OY 18457 ATCAGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18516  
Db 17647 ATTGCGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 17706  
OY 18517 ACACCCACCGGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18576  
Db 17707 CTGCGCGCGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 17766  
OY 18577 CCAACCCCGCTCTGTAAGCGACCAACCAACCAACCAACCAACCAACCAACCAACCC 18636  
Db 17767 GAGGCTCTCTTGTGCTCTTCAACGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCT 17826  
OY 18637 ACACACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCC 18696  
Db 17827 GCGCATCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCC 17886  
OY 18697 ACCCAACCGCGGAAATCATGAGCTTCCCAACAACCCCAACCCCAACCCCAACCCCA 18756  
Db 17887 GAGCGTGGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 17946  
OY 18757 CTCACCCAAACCTCTCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCC 18816  
Db 17947 TTGCTCTCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18006  
OY 18817 ACCCAACCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18876  
Db 18007 CTCTAGCAAGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18066  
OY 18877 ACCCCCAACCGGAAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18936  
Db 18067 ATGCCCCGAGGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18126  
OY 18937 CACCACTCTCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCC 18996  
Db 18127 CGATGCT---GCTGAAAAGGCGCTGAGCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 18183  
OY 18997 CACACCCCAACCGGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19056  
Db 18184 CAGGCGGAAAGGCGCGCTGAGCTCTCAACGCGGAGCTACCGCGCTCGCGCGCGCTCAAC 18243  
OY 19057 ATTCACCACTGCGGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 19116  
Db 18244 TTGCGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18303  
OY 19117 CCACAAACACCC---TCAACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19173  
Db 18304 GCGGAGGCGGCAACGATGAGCGCGCTGTTCAACGCGCGCGCACTGAGCCCAACGCTTCCG 18363  
OY 19174 CTACCAACCTCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCC 19233  
Db 18364 CTGCGCGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18423  
OY 19234 CACCTCTCTCAACCACTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 19293

Db 18424 AGACACTCTCAACGACTGCTCGCTCTCTCAACCCCTCTCAACCCCTTGTCTCTCTCTCT 18483  
OY 19294 GCGCGCGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19353  
Db 18484 GCGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18543  
OY 19354 GAGCGCTGCGCAACCAACCGGCAACCAACCAACCTCTCTCTCTCTCTCTCTCTCTCT 19413  
Db 18544 GATGCGCTGCGGAGCAGCGCGGCTTGTGGGCTTGAACCGGCAACATCGTGGCTTGGG 18603  
OY 19414 ACTGCGAAGGAAACGATGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19473  
Db 18604 GTTGGGAGGCGCGGCGGCAATGCTCTACCGGCTCTCTCTCTCTCTCTCTCTCTCT 18663  
OY 19474 ATGTTGCGATGCGCGCGGCGGATGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19533  
Db 18664 CTGTGCGGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18723  
OY 19534 CGCGCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19593  
Db 18724 GAGACCAACCTCAACGCTGCGGCACTGAGCGCGCGCTTGTGCGCTTCTCTCTCTCT 18783  
OY 19594 AAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19650  
Db 18784 GCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18843  
OY 19651 AG-----TACGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19704  
Db 18844 GCGGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 18903  
OY 19705 TCAGCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19764  
Db 18904 TCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 18963  
OY 19765 CTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19824  
Db 18964 CTGCGGCAATACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19023  
OY 19825 GACTGCTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19884  
Db 19024 GATTGCTCATACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19083  
OY 19885 CCGAGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19944  
Db 19084 CCGGCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19143  
OY 19945 GAGATCGGAGAGTCTCAACCGGCA-----ACTCAATCTCTCTCTCTCTCTCTCT 19986  
Db 19144 TCGCTCGGCGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19203  
OY 19987 CGACCCCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 20046  
Db 19204 GCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19263  
OY 20047 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 20106  
Db 19264 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19323  
OY 20107 GCGGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 20166  
Db 19324 GAGCCCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19380  
OY 20167 CAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 20226  
Db 19381 GCGAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 19440  
OY 20227 GCGGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 20286  
Db 19441 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19500  
OY 20287 CTCTCTGAAACCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 20346  
Db 19501 CTCTCTGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 19560



[illegible][illegible]





D	16170	CGACTACGCCACCCGCTCAACCAT---GTCCGAGAGGGCATGAGAGGCTACTCTGGGAC	16228
O	12513	TGGAGCGCGGCAAGATTGCGTAGGGCGGTATCTCTACAACTTCGGGCTCGAAGGCC	12572
D	16227	CGGCAACTCCGGCAGTGTGCGCTCGGGCCGCGTCCGATACACGCTTGAGCTGGAGGGCC	16286
O	12513	TGCGATCATATTGACACCCGGTGTCTCTCTGCTGTGTGGCCCTGACATCTGGCTGGCA	12632
D	16287	GGCGGTCACGGTGCACACCCGCTGTGCTCTGCTGTGTGCTTACACTCGCCCTGTGA	16346
O	12633	AGCGCTCGGTCGGGTGATATGACCATATGAGGCTCGAGGAGGGGCGCTCCGTATGGACAC	12692
D	16347	GGCTCTGGCGAAGGCGAAGTGCATAGAGGCTCTCGCGAGGGGTACAGGTATGTGCAC	16406
O	12693	TCCCTTCGTCCTTCAACCGAGTCTCTCGCAGCGGGGCTTGGCGGACAGCGCGGTGCAA	12752
D	16407	GCCCAAGACCTTTCGTGAGTTCAACCGGTCAAGCGGGGCTTGGCCCGGAGCGGCGGTGCAA	16466
O	12753	GGCGTTTTCGGCGGCGCGGACCGGACCGGCTGTCCGAGGGTGTGGGATGTCTGTGT	12812
D	16467	GTCTTCCTCGTCAGCGGCGGACCGGACCACTGTGTCGAGGGGCTGCGGCTCTCTCTGT	16526
O	12813	GGAGGGGCTCCGACGCGCGCGGACACGGTCAACCGGTCTTGGCGGTGTCCGGGGGACG	12872
D	16527	CGAGGGCTGTTCACCGCGGCTCCCAAGAGGCAATGGATCTTGGCGGTGTCCGGGGCAC	16586
O	12873	CGCGGTCAACGAGACCGGCGGACGACCGGCTTGACCGCACCCAGCGTTCGTTCAAGT	12932
D	16587	CGCGGTCAACGAGACCGGCGGACGACCGGCTTCAGCGCTCCGAAAGGGCGGTCCGACGA	16646
O	12933	CAAGTCAATCCGCGAGGCTTTGGCCAAACGACACTTCCCTTGGCGGATGTGATCGGT	12992
D	16647	GCGGCTCATCCGAGGTGCGCGGAGCGCGCGGCTTCACACCTCCGAGGTGACCTGTGT	16706
O	12993	GGAGGGCCCAAGGACCGGGACCAACCTTAGGGGACCGGATGAGAGTCAAGCCCTGTGGA	13052
D	16707	CGAGGCCCAAGGACCGGTATGCGACTCTGGGAGCCGATGAGGCGGAGGCGTCAATCCG	16766
O	13053	AGCCTACGGTACAGACCGCCCCAAGCGGCGCGCCCTCTGTGCTCGAACCTCTCAAGTCCA	13112
D	16767	CACGTACCGGAGAGGGCCGTACCGGCGAACAAGCCGCTGCGCTCGGTGCTTGAAGTCCA	16826
O	13113	CATCGGCACTCCATGCGCGCTGCGGGTGTGGCGGGGTCTAAGAATGTGATGGCGCT	13172
D	16827	CATCGGACACACCAAGGCGCGCGCGGCTGTCTCGGCGTATCAAGATGGTCCAGGCGAT	16886
O	13173	GCGGAATGTCTGCTGCGCGGACGTTGATGTGATGAGACCGTCCGCGATGTGACTG	13232
D	16887	GCGCCACCGGCTCTCGCGAAGAGCTTCACGTGGAACACCGACCGACCAAGGTGGAATG	16946
O	13233	GTCCGCGGGTACGGGACGCTGATGAGGAGACGGTTCCTGTGCGCGGCG---GGGAGGG	13289
D	16947	GTCCGCGGGCGGTCAGCTGTCTTCAACGAGGCCATGAACTGGCCGGAACAGGGCGACGG	17006
O	13290	GCGGCTACGGCGGACAGGATGTATATTTGCGGCTAGCGGACCAACGCGCCACTGAT	13349
D	17007	CGGACTGGGAGGGGCGGCGGTCTCTCTTCCTTGGGCTCAGCGGAGCGAACGCGACTGT	17066
O	13350	CCTGAGGAGACACCGGCGCCCAACATCCGTACAGACACCGGCGAGCGACTCCGGG	13409
D	17067	GCTCGAAGAGGCGCCCG-----CGGCGGAGG	17092
O	13410	AGAAATCAGCGCGCGAGAGATGCGGAGTGGCGATGAGAGGCTGTGCGCGGAGTCCAGG	13466
D	17093	AGACCCCTGCTTCGAGGCGACCCCGGCGGTGAGCGGT-----CGGTGGGCGCCGG	17144
O	13470	GGTGTGCGCGTGTGCTGTGCGGCAAGTGCACGCGGCGCTTGGCGGCCCGAGGCGAGCG	13529
D	17145	CCTGTGCGCGTGTGCTGTGCGGAAAGACTCGGCGCGGCTGGAGCGCCAGATTCGAGCG	17204
O	13530	CCTGACGCGCCACTCCACCAACAC---CGGCGTGAAGCTGGCGGAGCTGGGAT	13583
D	17205	CCTGCGCGCTTCCGCTGCAAGGGCGGATCGAGACGCGCGGATCCGGGCGCGGTGCTCG	17264

OY	13884	CACCTTGGCCCAAGCCCCGCGCGGTGTTTGACAACCACCGCGCACCTTCATGCGCGGCAGC	13613
Db	17265	CGTACTGGCCGGGGGGGGCGGCCGAAGTTTGAAGACACCGGGCGGTGTGTGTGGACCGGACA	17324
OY	13644	CGACACTTTCCTGAAGAACAATTCCAGGACACTCGCGCGGAGGAGAAACCCACCGCGCAT	13703
Db	17325	GGAAGATTTTGGCGCAGCGGTGACCGCTCCGAAAGGACTGTATACCGGACCGCCCTC---	17381
OY	13704	CCACGACGCGCCCAGGCGGGACCGGAGCCGGGAGGCGCGAAGAAAGACCGCATTCAT	13763
Db	17382	-----GGACGTGTGGCGGGTGGCTTCGT	17405
OY	13764	CTGCTCCGGACAGGGGACCCCAAGCCCCGGGCAATGGCGCCAGCGCTTCACACCAACC	13823
Db	17406	GTTCCCGGTCAGGGACGCAATGGGGCGGAATGGCGCAAATCTTGAAGTTCGAA	17465
OY	13824	CGTCTTGGCGCGGCACTCAACGACACTTGCACCCACTTGCAGCCCCCACTTGCACACCC	13883
Db	17466	GGAATTCGCGGCGGCCCATGACGGAATGCGAGCGCGCTTCGCCGTATGTGACTGTGC	17523
OY	13884	CTCTCTCCCTCTCTCAACCCAGAACCCCAACACCAAGACACCAACCTTGAAAGAGC	13943
Db	17526	GCTGAGAGCGGTGTGTCGGAGCGGC-----GGG	17555
OY	13944	GGCGGCATCTCTCAGAGACCCGCGTAGCGGCCGCGCCCTTTGGCTTCCAGGTGCG	14003
Db	17556	CGGCCCAACGCTGAGAGGGGTCAAGTGTGTCAAGCCCGGTGACCTTGTGTATGGTTTC	17615
OY	14004	CTTCCACCGGCTCTCTCAACGAGCTTACCATCACCCCCACTACTACGGCGAACCTC	14063
Db	17616	GCT---GGCGAAGGTCTGGGACGACCAACGCGCTGTAGCGCGCGCGTGTGTGGCCATTC	17672
OY	14064	CGTGGGGAATGACCGCGCGCCACCGTGGCGGCAATCTCACCGCTTACCGAGCCACAC	14123
Db	17673	GCAGGGGAGATGCGCGCGCGGTACGTGCGCGGTGCTTCACTTGAAGACGCGCGCG	17722
OY	14124	CCTGATCACCCMAAGCGCCACCCCTCATGCAACCATGCCCGCGAC---CATGACAC	14180
Db	17733	CGTGTCACTCGTGGGACGAAGTCAATCGCGCCCACTTCGCGCGCAAGGCGGATGAT	17792
OY	14181	CCTTCAACCAACCCCCCAACAATAACCAACCACTCACCGGCCAAGAAAAGACTCGC	14240
Db	17793	CTCCCTCGCCCTCAAGCAGGAAGAACCAACCGCGACGCGCATCTGAGAACTTCCAGGAAATGTC	17852
OY	14241	CATGCGCGCATCAACCCCAACCTCCCTGTATCAGCGGCAACCCCAACCGTCA	14300
Db	17853	GATGCGCGCGGTCAACCGGCCCAACCGCACCGGTGTTTGGGGGAAACCAACCAAGTCA	17912
OY	14301	ACACATCAACAACCTTGTGCCAACAAGGATCAAAACCAAAACCTTCCCAACAACA	14366
Db	17913	AGACCTGCTTAGCGGTGTAGGCGCAACGGGGTCCCGCAACGATCATCCCGTGCATTA	17972
OY	14361	GGCCTTCACTCCCCCCCCACAACAACCGCAATCTCAACAACCTTCAACAGACACCAAC	14420
Db	17973	CGCCTTCCACAGCGCCACGTCATGACATCAGAGCAATCTGCGAGGTCTGTGCGG	18032
OY	14421	CCTCACTCAACAACCCCAACCCCGCTCATCACCGCAACCCCAACCCGACCACT	14480
Db	18033	GCTAGCGCGGGACACTTAGGTGCGTTCTTCSACACTTGAAGGCGCTGATCAC	18092
OY	14481	CCTCAACCCCACTACTGGAACCAACAAGCCCGCAACACTGTGATTAAGCCACCAAC	14540
Db	18093	CGAGCGGTGTGCAGCGGCACTTCTGTGTACCGCAACTTCGCGCAACGCGGTGCGCTTCCG	18152
OY	14541	CCAACCCCTCACCAACCGGCTCAACAATTATCATGTGAATTGGAACCCGAAACAACCT	14600
Db	18153	CCCGCGGTGAGAACCTTGGCAACGACGAAGGCTTCAACCACTTATGAGAGTACGGC	18212
OY	14601	CACCACTCTCAACCAAGCAACTTCTCCCAACACCCCAACCAACCTTACCTTACCCA	14666
Db	18213	CGACCCGCTCTCAACCAATGACCTTCCCGAGACCGTACACCGGCTTGGACCT---CG	18269



Db 11849 CCGCGCTGCGGGGTAGCCACCGCTTTCACCTCCGCGACATGAGCGGACGTCTGACGGG 11908  
 Qy 8539 CTCGACGAGCACCACCAACCTTCACTACACCAACCCACACCCCTTCACTACCGCC 8598  
 Db 11909 TTCCGGGCGCTGAGAGCGGTGAGTTCGGGCGCCCTCTCTGACCGTGTCTCGAAC 11968  
 Qy 8539 AACA-----CCCCCCCCCAACTCTTCAACCCCACTACTAGAACCAACA 8646  
 Db 11969 GTACCCGCGCTGCGCGCCCGCCCGACGACCTGTGAGACCCGAGTACTGGGCTCGGAC 12028  
 Qy 8647 GCCCGACACCGTGTGACTACGACCAACCCCAACCTTCCACCAACGCGCTCAC 8706  
 Db 12029 GTCCGCGGACCGCTTCTCTCGACGCGGTCCGCTGTGCGGACCTCGCGCGG 12088  
 Qy 8707 ACCTACATGAACTGGAGCCGACCAACACCTTACACACCTTACACCAACCTTCCG 8766  
 Db 12089 ACCTGCTGAGAGTGGGCCCCACGCGGTCTTACCGGCACTGACGCGCGGCTCTCGG 12148  
 Qy 8767 AACCCCCCAGCACAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT 8799  
 Db 12149 GACACCCCGCGGATTTCCGCTGCGCGCTTCCGCTGCGCTTCCGCGCGCTTCCGCG 12208  
 Qy 8800 -----CCCCACACACACCCCAACCCCAACCTTCTTCAACCAAC 8835  
 Db 12209 GACTCGCGCGCGCGCGCTCGCGCCCGCGCGCTGTGTGCGGCTGTGCGCGGACG 12268  
 Qy 8836 CTCGCAAAACACACCACTGTGACCCCGCAACCTACCA-----CGACGACCAACA 8892  
 Db 12269 CGGTGGAAGACGAGACGATCGGAGCGCTTGGGAGGAGGACGACCGACGACGAG 12328  
 Qy 8893 CCCCACACCCACAC-----CCACTGTGACCTTCCCACTTAC 8928  
 Db 12329 CCGGACTGCGGACCGCTTCCGCGCGCTCGCGCGGACCGCTGTGACCTGTGACGATAC 12388  
 Qy 8929 CCGCTTCAACACCACTACTGTGTGAAAGACACACCGCGGTGCGGACCGTGTG 8988  
 Db 12389 TCCCTTCCGCGGACCGCTACTGTGTGAGCGCGCGCGCGGACCGCGGTGTGACAC 12448  
 Qy 8989 GGAG-----CGGACTGACCCCAACCGGACCGGCTTGTGCGGCGGACATTTGAACTGGG 9045  
 Db 12449 GCGGCGCTGCTGTGCGGACCGCGGACCGGCTGTGCGGCGGCTGTGACGCTTCCG 12508  
 Qy 9046 ACTGACGTGAGAGCGCTTGTGAGAGCGGCTTGTGAGGATCGACCTGTGCTGCT 9105  
 Db 12509 GACCGGGAAGCGCTGTGTGACCGGCGCGCTTCCCTGCGACCAACCGTGTGCTCGG 12568  
 Qy 9106 GACCATGCGGTGTGCGGACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9165  
 Db 12569 GACCAACCGGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12628  
 Qy 9166 CATGCGGAGCACTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9225  
 Db 12629 CACGCTGCGAGTCCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12688  
 Qy 9226 GTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9281  
 Db 12689 GTACTGCGGAGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12748  
 Qy 9282 ---GAGGAGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9336  
 Db 12749 CCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12808  
 Qy 9337 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9396  
 Db 12809 GACGCGCGCGCGGTACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12868  
 Qy 9397 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9456  
 Db 12869 CCGGACCTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12928  
 Qy 9457 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9516  
 Db 12929 GTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 12988

Qy 9517 TTTTGGGGCTGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9576  
 Db 12989 TTCCAGGGGCTGAAACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13048  
 Qy 9577 CC-----GAGGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9624  
 Db 13049 CCGCGCACGAAATGTGACCGCGCGCGGACCGCGAAGCGCGGAGGTGTGTGTGTGTGT 13108  
 Qy 9625 TTGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9684  
 Db 13109 GCGCTTACCGGATTCACACCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13168  
 Qy 9685 GAGGGGCGGGGTTTCCGGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9744  
 Db 13169 GGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13228  
 Qy 9745 CACCGGCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9804  
 Db 13229 CACGCGCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13276  
 Qy 9805 CGTGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9864  
 Db 13277 ACGACCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13336  
 Qy 9865 CGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9924  
 Db 13337 CCGCTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13383  
 Qy 9925 CCGCGGGGTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 9984  
 Db 13384 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13443  
 Qy 9985 CAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10044  
 Db 13444 ACAGACCGGACGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13492  
 Qy 10045 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10104  
 Db 13493 -----GACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13559  
 Qy 10105 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10164  
 Db 13540 -----CGGGCTTACCCGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13591  
 Qy 10165 CGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10224  
 Db 13592 CCGGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13651  
 Qy 10225 GACGCGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10284  
 Db 13652 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13711  
 Qy 10285 GAGCATTCGGAACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10344  
 Db 13712 CACTCGGCGGACCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13771  
 Qy 10345 ACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10399  
 Db 13772 TCCGCGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13831  
 Qy 10400 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10459  
 Db 13832 ACCGCGGAGACCGGACCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13891  
 Qy 10460 GACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10519  
 Db 13892 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13951  
 Qy 10520 CCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 10579  
 Db 13952 GCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 14009



Db	5648	TG	GT	C	A	G	G	G	A	C	G	C	A	G	T	G	G	G	T	G	G	G	A	T	G	G	G	T	G	G	G	T	C	T	G	G	G	T	T	C	G	A	G	G	T	T	5707			
Qy	3222	C	G	C	C	G	C	G	G	A	T	G	C	A	G	C	G	T	C	C	A	G	A	G	G	G	T	C	T	G	G	C	C	G	T	G	G	T	G	A	C	T	G	T	G	T	3281			
Db	5708	T	G	C	G	C	G	T	C	G	A	T	G	T	G	C	G	C	G	C	T	G	A	G	T	T	C	A	T	G	T	G	A	G	T	G	G	A	T	T	G	C	T	5767						
Qy	3282	G	A	C	A	T	C	T	G	G	C	C	G	G	A	C	G	G	G	G	A	T	G	G	T	T	G	G	A	C	G	G	C	C	A	T	G	T	G	T	G	T	C	A	G	C	3341			
Db	5768	G	A	G	G	T	-----	G	T	G	T	C	G	G	C	G	G	C	G	G	T	T	G	A	C	G	G	T	G	A	T	G	T	G	T	C	A	G	C	5818										
Qy	3342	T	G	T	G	C	T	G	T	C	A	G	T	G	T	C	T	T	T	G	G	T	G	T	C	T	G	T	G	C	T	G	T	G	C	T	C	T	A	C	G	T	A	C	G	A	C	3401		
Db	5819	C	G	T	A	C	T	G	G	C	G	T	G	A	T	G	T	G	T	C	G	T	G	C	C	C	G	G	T	A	C	T	G	G	A	C	G	A	T	G	T	G	A	C	G	T	5878			
Qy	3402	C	A	C	C	G	C	G	T	C	T	T	G	C	C	A	T	T	C	C	A	G	G	C	G	A	G	A	T	C	G	C	G	C	C	G	C	A	T	G	T	G	T	G	G	G	C	G	T	3461
Db	5879	G	G	C	T	G	C	T	G	T	G	G	T	C	A	T	T	C	C	A	G	G	G	A	T	C	G	C	T	G	C	T	G	C	C	A	G	T	G	C	G	C	G	G	G	C	G	T	5938	
Qy	3462	G	A	G	C	T	A	A	G	A	C	C	G	C	G	A	A	C	T	G	T	G	C	T	G	C	G	A	C	G	C	G	C	G	C	T	G	C	-----	G	T	G	T	3518						
Db	5939	G	T	C	G	T	G	A	G	A	T	G	C	G	C	G	T	G	T	G	T	G	C	G	T	C	T	G	C	G	C	G	G	G	T	T	C	A	T	T	G	C	C	G	T	A	C	T	5998	
Qy	3519	C	G	C	C	C	G	G	C	G	A	T	G	C	C	T	C	A	G	T	G	C	C	T	G	C	C	C	C	A	G	A	G	T	G	A	C	G	A	G	T	C	A	T	3578					
Db	5999	G	C	C	G	G	T	C	G	T	G	C	A	T	G	C	G	T	G	C	T	G	C	C	T	G	C	C	G	A	G	T	G	A	C	G	A	G	T	C	A	G	C	C	G	G	C	T	6058	
Qy	3579	T	G	T	A	C	C	G	T	G	C	G	G	C	G	T	T	G	C	G	T	G	C	G	C	G	T	C	A	A	C	G	C	C	C	C	C	C	C	C	C	C	C	C	C	C	3638			
Db	6059	G	G	C	A	G	T	G	C	C	G	-----	G	T	G	A	G	T	G	C	G	C	G	T	C	A	A	C	G	T	C	C	G	C	G	T	C	C	A	G	T	C	C	A	G	T	6112			
Qy	3639	C	G	T	C	C	G	G	G	A	T	G	C	A	G	C	G	T	G	A	C	G	A	G	T	C	T	G	C	T	A	C	T	G	T	G	C	C	C	C	C	C	C	C	C	C	3698			
Db	6113	G	G	T	T	C	C	G	G																																									

QY	4299	CGGACGGCAGAGGTGGAGTTCGCGGTCTTCGGGACGGCGTGCGGCCCGCAGACCTGGAAAC	43358
DB	6669	-----	66668
QY	4359	GGTCGCACCACACTCGCCGTGCCCCCTCCGCGGCCCTGGACACGGTGGTCCCAGCACT	4418
DB	6669	-----ACCCCCACACCCCGCGGACGACACCCAGAGCCCCAC	6706
QY	4419	CTCGCCTGGCACCGCCACCAAACGACCAAGCCCGCATCAACACCTTGGACCTTACCAGGA	4478
DB	6707	CGATGCTTGGCGCTACCGCTCACTTGGANAAGCCCTGACCGAATCTCTCCCGCTCGGCC	6766
QY	4479	AACCTGAAAACCCCTCACTCTCCCGCACCAACCAACCAACCAACCAACCAACCAACCTGGGTCTATCGC	4538
DB	6767	TCACTCATCGGTGCTGCTCTCTGTTGACCCCGGACCAACGAGCGGAGCTCTCTCGA	6826
QY	4539	CATCCCCGNAACCCAGACCCACACCCCAATACCAACATCTTACCAACCTCCACCA	4598
DB	6827	CGGACTGACAACGGTGTGTTCCGAGCGGTGCTCGTTCGCCCGCTTGTAGGTGCCAT	6886
QY	4599	CCAGCGCATCACCCCATCTCCCTCTCAACCAACACACCCACCAACCAACCAACCACT	4658
DB	6887	CGGCGCGCGGTGCGAGTTCGCGNATGTCTTAGCCCTTCATGGAGTACGGGGGA	6946
QY	4659	CCACACACCTTCCAACACACCGCAGAACAAAGCCCCAAAAACACACACCGAGGCCATCAC	4718
DB	6947	GGAAACACACCGTCTCTCGTTCTCGGTCTGTGTCCTTCCACGACGCGGTTCAGGAC	7006
QY	4719	CGGCTGCTCTCTCTCTCTCTCTGACGAGAAACACCCACCCCAACACCCCAACACAC	4778
DB	7007	GTCGATAGCGTCTCTCAGCGGTCTCTCGACATCGCGTTCGCGGCCCGCAGGCTCTGGGC	7066
QY	4779	CACGGCACCCTCTCTCAACCTCACTCACCCAAACCCACACCAACCAACCCACCAAC	4838
DB	7067	GCTG---ACGCGAGGCCGTGGCGCTGTGTTCCGGGGAGACGCGCAGGACGCGGGGGC	7123
QY	4839	CCCCCTGTGTAGCCACCAACCAACGACCAACCAACCAACCAACCAACCAACCAACCA	4898
DB	7124	CCAGTTGTGGGCTTGGACAGTGGCGGCCCTTGAATCTCCGGATATCTGGGGCGGCTT	7183
QY	4899	CCCCACCAAGCCCAACCTTGGGACTCGCCCGGACCAACCTCTCTGMAACACCCACCCA	4958
DB	7184	GATCGATCTGCGGAGACAGCGAGTGTGACGCGGACGCGGAGACCTTCACAGCCCCACA	7243
QY	4959	CACGCGCGGAATCATCGACCTCTCCCAACCCCAACCCCAACCCCAACCCCAACCTCAC	5018
DB	7244	GACCCCGAGA-----GGCTGCGGAGACTCCGAAACCGACGCGGCCCTTGTAGCTTGTGTC	7297
QY	5019	CCAAACCTTCAACCCCAACCAACCAACCAACCTCGCCATCTCGGACCAACCGGCAACCCA	5078
DB	7298	CGCGTCTCTCGCGCGCGACGCGCGAGGACAGGTGCGCGTGGCGCTCGGGGATCTTA	7357
QY	5079	CACCGCGGCTCAACCCCAACCACTCTACCCCAACCAACCAACCAACCAACCAACCCCA	5138
DB	7358	CGGCGCGGCTGTGCGGGCCGCGG-----CAGCGGGCGCGCTCTCTTGGCAGCC	7408
QY	5139	CCAGGAACCAACCTCATCACCGGCGGACCGGGCGCTCGCCACCACTCAACCCCAACCA	5198
DB	7409	GTCGGGACCGGTGTGATCACCGGCGGACATGGGTGGCATCGGACGCGGTCTCGCCGCGAG	7468
QY	5199	CCTCACACCAACCAACCAACCACTCTCTCTCAACCGGAGAACCGGGCCCCCAAC	5258
DB	7469	GCTGGCGGCGAGGGA---GCCGAAAGCCTGTCTCTACGAGCGGTGCGGACCGGAGGC	7525
QY	5259	CCCCACGCAACCACTCAACCAACCTTCAACCAAAAGGATCCACTCAACCTCAC	5318
DB	7526	GC CGGGCGCGCACTCGCCCGAGGAACCTCGAGGACATGCTGCGAGTCTGTGCAGCGC	7585
QY	5319	CACCTGCGACACGACCAACCAACCACTTCAACCAACCTCTCAACCAACCAATCCCCCA	5378
DB	7586	GGCCTGTGAGGTGGCGAGGTGATGGGTCTCGCGGGCTGTCAACGCGGTATCTCGCC---	7642





D	b	9785	CAGTGTGTAACAAAGCGCCCATCTGATCTCTCGAAGCCCCCGGAAGCCCTTCGAAGCCCTCGAAGC	9844
Q	y	7536	AGCACCCGCCGACGACGTTCTCGGGGGGAGACACACC CGCGCGCGAGGGTGACGCGGACGCA	7595
D	b	9845	CACCGAGCCCCCGAAGCCCCCGAAGCCC CGGACGTACCGAGCTCACGAGTCAACCGA	9904
Q	y	7596	CGATGAGGCTGCTGC CGGCGAGTCTCTGGGGTGTGGCCGTGGCTGGTGTGCGGCAAGTCGCA	7655
D	b	9905	AGCCCTCGAAGCCCCCGACCGACCCAGGCGGAGGGTGCGAAGGCTCTCTGGCAGTCCCGA	9964
Q	y	7656	GCCGGCCCTCGGCGCCAGGCCAGGCCCTGACGCGCCACCTCACCGAACCCCGGGCT	7715
D	b	9965	AGAGGACACGCTGCTGTGGGTGTGTGCGGTGGTGGTTCGGGGCGTTCGCGGGTGGT	10024
Q	y	7716	CGACTCTCGCGATGTDCGG-----ATACACCTTCGCCACGCGCCCGCGCGTTCGACCA	7769
D	b	10025	GGTGCGGAGGCTGCGGCCCGGTTCGCGGAGTGTGTGGAGGCGGTGTGTGGGGCTGGC	10084
Q	y	7770	CCGGCCACCTCATGCGCGCGACCGGACACGTTCTCTGCAAGCACTCCAAGCACTGCG	7822
D	b	10085	GGATGTGGCGGTGACGATGCGCGCGCGTTCGCGGTTTGGGTATTGCGGCGGTTGTGTGTC	10144
Q	y	7830	CGCAGGCGAGCCACCCCGCC--GTCA TCACAGCAGCGCCCGCGCGGACGCGGACCG	7888
D	b	10145	TCGGGGTAGGCTGAGCTTCGCCGGCGTTTCGCGGCGGTTTGGCGGGGGTGATCCCGACGC	10204
Q	y	7889	GGGAG-----GCCGCGAGGAAGACCGCATTCATCTGCTCCGACAGGCG	7932
D	b	10205	GGGTGTGGTCACCGGTGCGGTGTGTGACCCGGAGACGGGGTCCGTGTGTGGGGGTGGT	10264
Q	y	7933	ACCCAAAGCCCCGGGCATG GCCCACAGCGCTCTACCA CACCCACCCCGTCTTCGCCGCCGCA	7992
D	b	10265	GTTGGTTTTCCCTGGTCAGGGGACGAGTGGGTGGGGATGGGTGCGGGCTCTCTGGGTC	10324
Q	y	7993	CTCAAAGCAATCTGCACCCACTCTGCAGCCCGCACTCGACCA CCCCTCTCTCCCTCTCTC	8052
D	b	10325	TTCGGAGGTGTTTTCGCGCGTCSGATG--CGGAGTGTGCGCGGCGCTGAGTGTTCATGTG	10382
Q	y	8053	ACCCAAAACACAACAGACAGAGGACGGCGCGCACTGCTCCAGCAGACCCGCTACGCC	8112
D	b	10383	GAGTGGGATTTGCTGGAGGTGTGTGCGGCGGGCCGGGTTGGAGCGGGTGGATGTGTG	10442
Q	y	8113	CAGCCCGCCTCTTCGCTTCAGAGTGGCCCTCCACCGCTCTCTCACCGACGGCTACCA	8172
D	b	10443	CAGCCCGTACGTGGGCGGTGATGGTGTGCTGGCCG--GTACTGGCAGCGATGGGT	10499
Q	y	8173	ATACCCCCCACTACTACGCGGACACTCCCTCGGCGAAATCAACCGCGCGCCACCTCGCC	8232
D	b	10500	GTGAGCGTGTGCTGCGGTGGGTGTCATTTCCAGGGGGAGATCGCTGCTCCACCGTGGCG	10559
Q	y	8233	GGCATCTCACTCACTACCGAGCGCACACGCTCATCAACCAAGCGGCCACCTCAT--G	8289
D	b	10560	GGGGCTTGTGCTGGAGNATGCGGCGGTGTGGTGCCTCTCGGGCGGGGTTGATTGGC	10619
Q	y	8290	CAAAACCATGCCCCCGGCACCATGACCACTCCCTCCACACACCCCGCCACCATACCCAC	8349
D	b	10620	CGGTATCTGSCGGTCTGTGTGCGATGGGCGCTTTCGCTGCTCGCGCGAGTTCGAG	10679
Q	y	8350	CACCTACCGCCACAGMAACGACTCGCGCATCGCGCGCATCAACACCCCGCACTCCCTC	8409
D	b	10680	GCCGGGCTGGCGAAGTGGCCCGGAGTACAGGTAGCGCGCGGTCAACCGTCCGGCGTCCAG	10739
Q	y	8410	GTCA TCAGCGGACCCCGACACCGTCCAACACATCAACACCTCTGCGCAACAACAGGC	8469
D	b	10740	GTGGTTCCGGGATCGGCGGGCGGTGGCGGTTATGTGGCCGTCTGTGCGGGAGGGT	10799
Q	y	8470	ATCAAAACCAAAACCTTCCCGACCAACCGCTTCCACTTCCCCC-----ACACC	8520
D	b	10800	GTGCAGGCTCGGTGATACCGGTGGACTACGCTCTCACTCCCGCATGTGGAGGACCTG	10859
Q	y	8521	AACCCCATCTCAACCAATCTCAACAGCACACCCAAACCTCTACCTTACACCCACCCAC	8580
D	b	10860	AAGGGCGAGTTGAGGGGGTGTGTGTCGGGTATTCGCGCGTATTCGCGCGCGAGTCCGCGGTGCGGGT	10919

QY	8581	ACCCCTCTCATACCGCCAAACCCACCCGAGCAAACTCTCTCAACCCCTCTACTGTGACC	8640
DB	10920	TGTTCCACCGTCCCGGGAGAGAGCGCGGCGAGCGGTTTTTCGATGCGGGGTATTGGTTTC	10979
QY	8641	CAACAAGCCGGAACACCGTTCGACTACGCCACCAACCCAAACCCCTCCACCAACACGGC	8700
DB	10980	CGTAATCTCGGAACCGGGTTTGAGTTCTCCGCGGTGTCGTGGTGTGTTGTTGGAGCAGGGC	11039
QY	8701	GTCAACCACTTACATCGAACTCGGACCCGCAACACCCCTCACACCCCTCACCCACCAAC	8760
DB	11040	CACGTCGGTTTATCGAGGTCACTGCCACCCCGGTACTCGTCCATGTCATTTGAGCAGACG	11099
QY	8761	CTCCCAACCCCCCAACCAACCACTTACCTTACCCACCCCAACCCCAACCAACCCCAAC	8820
DB	11100	---GCCAGCGCCGAGCCGAGTGTCTCATGTCACCGGAACCTCTGCGCGCCAGACGAC	11156
QY	8821	CACCTCTCAACCACTCTGCGAAACCAACCAACCACTTGGCAACCCCACTACACCCAC	8880
DB	11157	AGCCCGACCGCTGTGACCTTCCACCGCCGAGGCTCTGGGCCACCGGCCACCTCAAC	11216
QY	8881	CAGCAAAACCAACCCACACCAACCACTTGCACCTTCCACCTTCCACCTTCCCAACAC	8940
DB	11217	TGGAACCCGCCCTGCCCCAGGTCACTTCAACCACTTCCCACTTCCCACTTCAACCA	11276
QY	8941	CACCACTACTGGCTCGAAAGCACAGAGCCCGGTGCGGCAACGTGTACGAGCCGGAATC	9000
DB	11277	CACCACTACTGGGCGGTGACATCTCCCGCCGAGTCTGCGAGCGGCTGCGGCGCGGTT	11336
QY	9001	GACCCACCC-----GAACACCCCTTACTCGGCGGCACATTTGGAACTTGGCACTGACGGT	9054
DB	11337	GGTATGACCTTGGAGGACCAACCCCTTCTCTCGTGTGCGGGTTTACCCCTGGCCGACCT	11396
QY	9055	GGAGCGCTTCTTGAGGGCGCTTGTCTTTGAGGTGCGATCGTGTGCTGGCTGACCATGSC	9114
DB	11397	GACGGGTGTTTCCCGGGCGGCTGGGGGCTCCGAGCAGCACTGGCTTACGAGCACTGCC	11456
QY	9115	GTCCGGCGCACGTGTCTGTCTGTCGGCGGCACCTTCTCGAACTCGCCCTTTCATCGGGC	9174
DB	11457	GTGTCCGGGTGACGTTGTCTGCCGGTACGGGCTTCTGTGGAGTTTCGGCTGCACGCGGA	11516
QY	9175	ACATAGTGGGTGCGACCGAGTGAATGAGCTGACCTGCACTGCGCCGCTGGTGGTTCTT	9234
DB	11517	GCGCCACCGGCTGCGGGCGGCTGGAAGAGCTGACGCTTGAGGGCGGCTTGGTCTTGCC	11576
QY	9235	GTGGATGGGGTGTAGTCTGCAGGTTGGGGTTGCGGCTGCGGATGGGGAGGGCGGGCT	9294
DB	11577	GCCCGCGGTGTGTGCGGTGCAGATAGGGGTGTGCGCCGCGAGTCTGCGGACGGCGG	11636
QY	9295	TTGGTGAAGTGTATTCGCGGGGTGGGAGTGTCTGT-----GTGGGGGTGGTGGC	9345
DB	11637	AGGGTCGCCATCCATCTGCGCCCGGAAGCCGCGCTCACTCGGCCGAGAGGGCGGAC	11696
QY	9346	TCGGGTGGGTGTGACGTGTATGCTCTGGGGGTGCTGGTTGAGAGCTGCTGCTGGTGGT	9405
DB	11697	TCGGCGGTGTCTGACGCGGCAACGCGAGGGCACGCTCTGTGCGGACCCCGAGCCCCACG	11756
QY	9406	GTGGTGGTGAAGGTCTGCGGGGGGTGTGGCCCGCGGGGTGCGGTGGCGGTGGATGTC	9465
DB	11757	CTTCCGGAACCCGACATGGGGCGCGGGCCCTGGCCGC---CGCCGGGGAACCGTCCAA	11813
QY	9466	GATGGTGTCCGTGACCGTTTGGCTGGGGCTGGTTGTGTTTGGGCGCGGTGTTTTCGGGG	9525
DB	11814	GCCGAGCTTACGACCGTTTCGGGCCCTGGGCTACGAGTACGGTGAAGCGGTTTCGGGGC	11873
QY	9526	CTCGTTCGGGTGTGGCGTGAATGGGGGGAATTTGCTGGCTGAGGTGTGTCTGCCGAGAG	9585
DB	11874	GTGCGCGCGTATGGCGGCGAGCCGACGGCTGCTCGCCGAGGTGCTCTTCCCGCACCGG	11933
QY	9586	GCCTGGGGTGATGCGGCTGGTTTTTGGGCTGCATTCGGGCTTCTGGATGTGTGTGGTCCAG	9645
DB	11934	GCCTCAGACCGGTGCGGCGGTTTCGGTGTGACCCCGCGGCTGCTGTGACGCGGCGCTG	11993



Db 14061 GAGGACGATCTCGGCGCGACGCTGCTCGGCGCGACTGACCGAACTGGCCGCGCTC 14120  
Qy 11797 ATGTTGAGTGGAAACGACACCCAGCATCCGACAGCGGAAGCGCTGATGACGACGAGAAG 11856  
Db 14121 ACCCGCAGGCGGGAACCCCTCGGCGCGGACCGCCCGCTCGATCTGACGAGCGG 14180  
Qy 11857 TTCACATCGGCAACAGAGGCTGAGATTTTCAAATTTTGAACAGACCTCGGCTGTCC 11916  
Db 14181 CTGGAATCCGGAACGACGACGACCTCTTCGCTTCATCGAGGAGCAGCTTTGAGCAGCG 14240  
Qy 11917 TGAAC--CGGACGCTGACACTCCGCGCTATCCGCTGGGCCCTGCTAGGAGTGATGC 11974  
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Qy 11975 AATTGGC-----GAATGAAGCGAAGCTCTGGAATACCTCAAGCGCGTCACTGCGG 12025  
Db 14301 CGGGGGCTCCCCCGGAGGACGCGGCTCAGGAGTATCTGAAGCGGGTGACCGCG 14360  
Qy 12026 ACTTGAACCGCACTCGCGCTGCGCTTATACGAGGTGCTCGAGGTGAGCAGGAGCCGATCG 12085  
Db 14361 AACTGTGCGCAACCGCAAGCGCTCGGCGCGCTGAGGAGCGGCGCGGAACCGATCG 14420  
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Qy 12146 ATCTGTCAAGTCCAGACGAGCGCTATCGGGAGTTCCGACCGACCGTGGATGGAACC 12205  
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Qy 12206 TGGAGAGCTTACGACCGGACCCCGACCGCTCAGGAACCAAGTTACACGCGCAGCGGAG 12265  
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Db 16110 GCGCGACCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 16169  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 17, 2003, 12:54:32 ; Search time 72.1932 Seconds  
(without alignments)  
1618.821 Million cell updates/sec

Title: US-09-914-286-3  
Perfect score: 20829  
Sequence: 1 VORMGGEPRPAAAGEVLGV.....FTSATEAEIKFIDNDLGLS 3972

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8151	39.1	4551	3	US-09-320-878-1
2	8148	39.1	4613	4	US-09-105-537-31
3	8148	39.1	11877	4	US-09-105-537-6
4	7705.5	37.0	4472	2	US-08-804-227C-2
5	7281.5	35.0	5588	4	US-09-036-987A-6
6	7281.5	35.0	5588	4	US-09-370-700-6
7	7255	34.8	4545	2	US-08-804-227C-14
8	7079	34.0	3739	3	US-09-320-878-2
9	7041.5	33.8	3816	4	US-09-428-517-3
10	7017	33.7	3739	4	US-09-105-537-33
11	6941.5	33.3	4550	2	US-08-804-227C-8
12	6941.5	33.3	4550	2	US-08-804-198-2
13	6912.5	33.2	4150	4	US-09-428-517-2
14	6804.5	32.7	3170	4	US-09-036-987A-4
15	6804.5	32.7	3170	4	US-09-370-700-4
16	6736.5	32.3	3724	2	US-08-804-227C-10
17	6736.5	32.3	3724	2	US-08-804-198-4
18	6555	31.5	3729	2	US-08-804-227C-4
19	6447	31.0	4928	4	US-09-036-987A-5
20	6447	31.0	4928	4	US-09-370-700-5
21	6439	30.9	6095	4	US-09-144-085-2
22	6387	30.7	3567	2	US-07-642-734C-4
23	6387	30.7	3567	3	US-08-439-009A-4
24	6383	30.6	5215	4	US-09-105-537-2
25	6360	30.5	3491	2	US-07-642-734C-2
26	6360	30.5	3491	3	US-08-439-009A-2
27	6399.5	30.2	5087	4	US-09-144-085-1

28	6108.5	29.3	3519	4	US-09-428-517-4	Sequence 4, Appli
29	5500	26.4	3170	2	US-07-642-734C-5	Sequence 5, Appli
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31	5031	24.2	7257	3	US-09-335-409-5	Sequence 5, Appli
32	5031	24.2	7257	4	US-09-568-102-5	Sequence 5, Appli
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34	5031	24.2	7257	4	US-09-568-480-5	Sequence 5, Appli
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ALIGNMENTS

RESULT 1  
US-09-320-878-1  
; Sequence 1, Application US/09320878A  
; Patent No. 6117659  
; GENERAL INFORMATION:  
; APPLICANT: ASHLEY, Gary  
; APPLICANT: BETLACH, Melanie C.  
; APPLICANT: BETLACH, Mary C.  
; APPLICANT: MCDANIEL, Robert  
; APPLICANT: TANG, Li  
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 30062202020  
; CURRENT APPLICATION NUMBER: US/09/320,878A  
; CURRENT FILING DATE: 1999-05-27  
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
; EARLIER FILING DATE: 1998-08-28  
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
; EARLIER FILING DATE: 1998-05-06  
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
; EARLIER FILING DATE: 1997-04-30  
; EARLIER APPLICATION NUMBER: 60/119,139  
; EARLIER FILING DATE: 1999-02-08  
; EARLIER APPLICATION NUMBER: 60/100,880  
; EARLIER FILING DATE: 1998-09-22  
; EARLIER APPLICATION NUMBER: 60/087,080  
; EARLIER FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4551  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-320-878-1

Query Match	39.1%;	Score	8151;	DB	3;	Length	4551;
Best Local Similarity	44.8%;	Pred. No.	0;				
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Gap							94;
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Db	558	GLVGVASGV-GRVAFVFGQGTQWAGMGAELLDSSAVFAAAMAECAALSPYVDVNSLEA	616				
QY	75	VLRDSDPAGLDRVDVQPTLFAVMISLAALNRSQVEPCAVLGHSLGIAAAHVGGGLS	134				
Db	617	VVRQAPGAPTLERVDVQVPTFAVMVSLARVWQHGVTPQAVVGHSGQSGIAAAVAGALS	676				
QY	135	LADARVVTLMWSQA-QTTLAGTGVLSVNAATDELLPRIAPWTEDNPARLAVAAVNGPRS	193				
Db	677	LDDAARVVTLRKSTAAHLAKGKMLSLALSDEVLRLAGFD-----GLSVAAVNGPTA	731				





2714 CSSSLTALHLAVRALRSGBCTMALAGGVAMMATPHMFVFSRQRALAPGRSKAFSADAD 2773  
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2774 GFCAEGBVGLLVERLSDAHRNGHRVLA VVRGSAVNQDASNGLTAPNGPSQORVIRQAL 2833  
2378 ANAGLSAGVDVAEAGHTGTTIGDPIEAQALLATYQDRAGEGPLWLSVKSNGHTQAA 2437  
2834 ADARLAPGDI DAVETHGTGTS LGDPIEAQGLQNTYKGERPAERPLAIGSVKSNIGHTQAA 2893  
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2894 AGAAGIKKVLAMRHGELPKTLHADEPSPHVDWANSGLALVTEPIDWPAGTGP-RRAAVS 2952  
2498 SFGVSTNAHVILEEAP-----ADDVP-----GGPPAGEGDAGSDDEAAA 2537  
2953 SFGISGTNAHVLEQAPDAAGEVLGADPEVSETVAMAGTAGTSEVAEGSEASEAPAAP 3012  
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2644 GTQPGMAHGLYHTHPVFAAALNDICTHLDPHLDHPLPQLTQNDNDNDAALLOOTRY 2703  
3124 GSQPCAGRELVDYRHPVFAALDEICAHLDGHLLEPLLDVMPFAEGSAE--AALLDETRY 3181  
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3361 PSYVVRHVGTFRFLDGVRLDLGVRTCLELPGDGLVTAMAADGLADTPADSAGSPVG 3420  
2933 HPHHPQTH-----LLTWL-----AKTTHWHPHYTH-HDNQPHHT----- 2969  
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2970 HLDLPTYPPQHRYWLESTQPCAG---NVSAAGLDPTHEPLLCATLELATDGCALLAGRL 3026  
3481 RVDLPTYSPRRORYWLDA--PAADTAVDTAGLGTADHPLLGAVVSLPDRGGLLTGRL 3538  
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3539 SLRTHPLADHADVGLSVLLPGAAMVELAAHAAESAGLRDVRRELTLEPLVLPHEHGVLEL 3598  
3087 VGVAADGE-----GRLLSVYVARGGSACGGGASGVWTCBASGVLEAAGGVV 3138  
3599 VTVGAPAGPGGESAGDGPVLSLSRLADA-----PAGTAMSCATGLLATDRPPLVA 3653  
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3714 TAPATANGGSAAPYGIHPALLDASLHAIIV---GGL-----VDEPELVVRVPHWGV 3765  
3247 SLHRAGVTGVVRVSAVGRGGGEAVSVVGBEAGVPVAVSRLELRPFVDMQQLRAVSVS 3306  
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3307 AGRRSLSYAVOM-----AEVGPVPVCGO-----A 3330  
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3331 WANHEDEVESGGPVGVVVVLRCPDAGAGGGGGGGGGVGVGVGVGLVGVWGLGLERP 3390  
3878 AALSQDV--AAGAPAPRTVTLAPLP-----AGPADGAGVGTVARTLELLQAWLADEHL 3930  
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3931 AGTRLLLVTRGAVRPEGSAGDDGGEDLSHAAWGLVRTAQTENPGRFGLLDLADASSY 3990  
3446 ---DLDTGAGAGWGVDCGervAAVACGEPQLAVRGERLLAARLKRLESSGVPVPAQRSD 3501  
3991 RTLPSVLSDAGLR-----DEPQLALHDGTIRLARL----- 4020  
3502 TPARESDVPAQRSGGVPAARRSVDVSGREVLPWLSGVSIVTGGTGVGLGNAAVARHLAGVCG 3561  
4021 ---ASVRPETGTAAPA-----LAP-----EGTVLLTGGTGGGLVARHVVGW 4062  
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4063 VRLLLVSRRTDADACADELVHELEALGADYVAACDVADREALTAVLDAIPAEPHTAV 4122  
3622 VHAAGVLDATTIASLTPERLGTVFAAKVDAALLLDELTR--GMELSAFVLFSSAAGLGS 3679  
4123 VHTAGVLSGDTLPSMTTEDVEHVLRPKVDAAPFLDELSTPAYDLAAAFVMPSSAAAVFGG 4182  
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3786 ---TTRTT--TTGGADNGAQLHA-----RLAQOQTHEQQHTTLLALVRSHIATVLGHT 3832  
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3833 TPDTPPDRAFRDLGDFSITAVELNRLSRTTGLPPTLAPDHPNPTTLTHLHTQL--- 3890  
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3891 -QPQPDNA-----VAPVLAELDKLESALSALOKTDS-ASERTVLRLLK 3930  
4423 GASDQDQAGNRNGNENGTTASRSTAEATDALLAQLTRLEGALVLTGLSDAPGSEVLEHLR 4482  
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4483 SLRSVMTGETGTGTASGAPDGAGCAEDRPWAAGDGAGGSEDGAGVDFMNASAEELFG 4542  
3964 FIDND 3968  
4543 LLDQD 4547

## RESULT 2

US-09-105-537-31  
; Sequence 31, Application US/09105537A  
; Patent No. 6265202  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600,438US1  
; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0

104 : SEQ ID NO 31  
105 : LENGTH: 4613  
106 : TYPE: PRT  
107 : ORGANISM: Streptomyces venezuelae  
108 : US-09-105-537-31

Query Match 39.1%; Score 8148; DB 4; Length 4613;  
Best Local Similarity 44.8%; Pred. No. 0;  
Matches 1909; Conservative 463; Mismatches 1307; Indels 586; Gaps 94;

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QY 194 TVVSGAREAVDLVADLTAAQVTRMIPVDVPAHSPMLYALBEVVVSGLLPITPPRSRIP 253  
DB 794 TVVSGDPVQIEELARACEADGVRAVIPVDYASHRSQVEIIESELAELAVLAGLSPOAPRVP 853

QY 254 FHSVVTGGRDLTRELDAAYWYRNMSSTVRFEPAAR-LLLQOGPKTVEVSPHVLTMGLQ 312  
DB 854 FSTLEGAMITEBVLDDGGWYRNLRHRVGFAPAVETLATDEGFTHEVEVSAHPVLTMALP 913

QY 313 ELAPDLGDTTGTADTVIMGTLLRGQGTLDHFLTSLAQ-----LRGHGET 356  
DB 914 -----GTVTGLA-----TLRDNGGQDLVSLAEAWANGLAVDMSPLPSATGHSD 961

QY 357 SATVLS-----ARLTASPT-----QQSLLLDLVRAHTM 387  
DB 962 LPTAFQTERHMLGETEALAPAGEPAVQPAVLRTAAEPAELDRDBQLRVILDKVRAQTA 1021

QY 388 AVLNDGNERTASDAGPSASFHLGFDPSVMGVFELRNLSKATGLRLPVTLIENHTPAAV 447  
DB 1022 QVL-----GYATGGQIEVDRTFREAGCTSLTGVDLRNRINAAGFVRWAPSMIFDFPTFEAL 1077

QY 448 AARLRTAALGHLEDTAPVDPSPSGHGGTAADDPDIAIICMACRFPFGVRSKPDWELAA 507  
DB 1078 AEQLLLVHGEAAANPAGAEPAVAAAG--AVDEPVAIVGMACRLPGGVASPEDLWRLVA 1135

QY 508 SGSDAIGPPTDRGWTEQRHAQDPTQPTGTFYQGGGFLHDAHFDAGFGISPREALAM 567  
DB 1136 GGGDAISEFPQDRGWDVEGLYHPDPHPGTSYVRQGGFTIENVAGFDAAPFGISPREALAM 1195

QY 568 DPQORLLLETSFAFERAGIDPLSVRSRTGVFPAGALSFDYGRMDTASSEGADVEGHI 627  
DB 1196 DPQORLLLETSFAVEDAGIDPLSLRGROGVFTGAMTHEYGPSL-----RDGEGGLDGYL 1251

QY 628 LTGTGCSVLSGRVAYSFGLGEPALTVDTCSSASLVTLHLACOSLRSGECTLALAGGVSW 687  
DB 1252 LTGNTASVMSGRVSYTLGLEGPALTVDTCSSSLVALHLAVQALRGGEVDMALAGGVAM 1311

QY 688 STLGMFIERSRQGLSVDRCKAYSAADGTGNGEGVGMMLVERLSDAVRLGHRVLAVVR 747  
DB 1312 PTPGMFEVFSRQGLAGDRSKAFASADGTSWSEGVGLLVERLSDARRNGHQVLAVVR 1371

QY 748 GSANVDGASNLGTAPNGPAQERVIQALANAGLSVADVDVVEGHGTGTLGDPTBAQAL 807  
DB 1372 GSALNDGASNLGTAPNGSQQRVIRKALADARLTSSDVIDVVEAGTGRGLGDPTBAQAL 1431

QY 808 LATYGO-RAGDRPLMLGSLKSNIGHTMAAGGVGIKVMWALREGVLPRTLHVDPSPQV 866  
DB 1432 IATYGGRRDEQPLRLGSLKSNIGHTQAAAGVSGVVKVMQAMRHGLLPKTLHVDEPSDQI 1491

QY 867 DWSAGAVRLLETAVPWPGDAAGRLRAGVSSFGIGTGNARHILEEAPAAAGCCVAGGVLE 926  
DB 1492 DWSAGAVELLETAVDWPEKQDGLRRAAVSSFGISGNTARHVVLEAPV-----VVE 1542

QY 927 GAPGLAISVAESVAAAPVAVSAPVAESVPVVPVVPVPSARSSEAGLRAQAALQYVAV 986  
DB 1543 GA-----SVPEPSVSGSAGVGGV-----TPWVVSAKSAALDAQIERLAAP-AS 1585

QY 987 RPDVSLADVGA-----GLACGRAVLEHRAVLAADREBELVQGLGALAAAGEPDRVTT 1038  
DB 1586 RDRITDDADAGADAGAVAHVLADGRAQFEHRAVALGAGADDLVQAL-----ADPGLI-R 1639

QY 1039 GHAPGDRGGVVFPFGQGWAGVRLASSPVFAARMQACEEALAPWDMSVVDILR 1098  
DB 1640 GTASG--VGRVAFVFPQGTQWAGMGAEILLDSAVFAAAAECEAAALSPYVWMSLEAVR 1697

QY 1099 RDAGDAVWERADVQVPLFSVMVSLAALWRSYGIEPDAVLGHSGEIAAAHVCAGLSLKD 1158  
DB 1698 QAPGAPTLERVDVQVPTFAVMSLSARVWQHGGVTPQAVVGHSGEIAAAAYAGALPLDD 1757

QY 1159 AAKTVALRSRALAA--VRGRGGMASVPLPAQVEQILIGERWAGRLWVAANGPRSTAVSGD 1217  
DB 1758 AARVVTLSKSIAAHLGAGKGMLSLALNEDAVLERLSD--PDGLSVAANGPTATVWSGD 1815

QY 1218 ABANDVLAAYCAGTGVARRIPVDYASHCPHVOPLREBELLELLGDISPOSGVPESTVE 1277  
DB 1816 PVQIEELAQACKADGFRARIIPVDYASHRSQVEIIESELAQVLAGLSPOAPRVPFSTLE 1875

QY 1278 GTWLDTTTTLDAAYWYRNLRHQPVRFSDAVOALA-DGHRVFEVSPHPTLVPAIETTEDT 1336  
DB 1876 GTWITEPVLDTGYTYWRNLRHRVGFAPAIETLAVDEGFTHFVEVSAHPVLTMLPET---- 1931

QY 1337 AEDVTAIGSLRRGNDTRRFLTALAHHTTGTTGTTTHHHYTHHHPHPTHLIDLPTY 1396  
DB 1932 ---VTGLGTLRREOGQERLVTSLAEAWVNGL--PVAMTSLLPATASRP-----GLPTY 1980

QY 1397 PFQOHYWMLESQPGAGSGGAGSGAGSGAGTAGTAGTAESVEFWDVARQDLTETVAT 1456  
DB 1981 AFQAEYRWLENTPAALATG----- 1999

QY 1457 TLAVPFSAGLDTVPVPAALSAWHRHQDQARINTWYQETWKPLTPTTTHQPHOT-----WL 1511  
DB 2000 -----DDWRVRIWK--RLPAAEGSERTGLSGRWL 2027

QY 1512 TAIPETQTHPHITNLTNLHHGHTPIPLTLNHTHTNPQHLHHTLHTRQQAQNHHTG- 1570  
DB 2028 AVTPE--DHSAAQAAAVLTALVDAGAKVEVLTAG-ADDDREALAARLTAL-----TTGD 2077

QY 1571 AITGLLSLALDETHPHPHPTGTGLNLTLTQHTQTHPTPTPLWYATNTATTHPNDP 1630  
DB 2078 GFTGVVSL-----DGLVPQVAVWQALGDAGIKAPLMSVTQGAHSVGRDPT 2123

QY 1631 LTHPTQAOQTWGLARTTLEHPTHTAGIIDLPTTPTPTHTLOHTQTLTOPHOTQLAIRTT 1690  
DB 2124 PADPDRAMLWGLGRVVALEHFERWAGLDVLPQAPDAAALAHVLTALSGATGEDQIAIRTT 2183

QY 1691 GPHTRRLTPTTLTPTH-QPPTP--TPHGTTLTGTGALATHLTHHTLTHPTOHLHLLTS 1747  
DB 2184 GLHAREL--ARAPLHGRRTDRDQPHGTVLITGTGTGALGSHAARM-AHHGAELHLLVS 2239

QY 1748 RTGPHTPHQAHLTTLOOKGHLITTTCDTSNPDOLOQLLNTIPIQHPLTTVIHTAGILD 1807  
DB 2240 RSGEQAPGATQLTAEALTASGARVTIACDVADPHAMRTLLDPAIETPLTA/VHTAGALD 2299

QY 1808 DATLNLNPTOLNNVLRKAKSAHLHOLTOHTPLTAFVLYSSAAATFGAPQANYAAN 1867  
DB 2300 DGIIVTLTAEQVRRRAHRAKAVGASVLDELTRDLDDAFVLFSSVSTGLIPQGGYAPHN 2359

QY 1868 AYDLALAHHRHTHLPATSIAGWTQWGNGLADSKARAYLDRRRGFRPSPPELATAVTOA 1927  
DB 2360 AYDLALAAARRRATGRSAVSAMGPDGCGGAAGDGVAERLRNHGVGMDPELALALESA 2419

QY 1928 TADTERPVVVIADIDWSK-----IEHTSQTSDLSVA-----AREEFAVQRP 1969  
DB 2420 LGRDETA-ITVADIDWDRFYLAYSSGRPQPLVEELPEVRRRIIDARDSATSGGGSSAQGA 2478



Db .4545 SLRSMVTGETGTCTASCPDAGSAGAEADRPWAAGDAGGSGEDGAGVDFMNASBELFG 4604

Qy 3964 FIDND 3968

Db 4605 LIDQD 4609

## RESULT 3

US-09-105-537-6

; Sequence 6, Application US/09105537A

; Patent No. 6265202

; GENERAL INFORMATION:

; APPLICANT: Sherman, D.H.

; APPLICANT: Liu, H.

; APPLICANT: Xue, Y.

; APPLICANT: Zhao, L.

; TITLE OF INVENTION: DNA encoding methymycin and pikromycin

; FILE REFERENCE: 600.438US1

; CURRENT APPLICATION NUMBER: US/09/105,537A

; CURRENT FILING DATE: 1998-06-26

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 11877

; TYPE: PRT

; ORGANISM: Streptomyces venezuelae

US-09-105-537-6

## Query Match

Best Local Similarity 44.8%; Pred. NO. 0;

Matches 1909; Conservative 463; Mismatches 1307; Indels 586; Gaps 94;

Qy 15 GEVLGVADADGGVVFVFGQGPQWGMRELLDASDVFPRESVRACEAAAFAPVYDWSVEQ 74

Db 956 GLVRGVASGV-GRVAFVFGQGTQWAGMGAELLDSSAVFAAAWAECEAALSFPYDWSLEA 1014

Qy 75 VLKSDPADGLDRDVVQPTLFAVMISLAALWRSQGVPCAVLGHSLGIEIAAHYSGGLS 134

Db 1015 VVROAFGATLERVVVQPTFAVMVSLARVQHGHTVQAVVGHSGHIAAAYAGALS 1074

Qy 135 LADARVTLWSQA-OTTLAGTALVSVAAATPELLPRIPAPWEDNPABLAVAAVNGPRS 193

Db 1075 LDDAARVTLRSKSTAAHLAGKGMLSLASEDAVLRLAGFD-----GLSVAAVNGPTA 1129

Qy 194 TVVSGAREADVLDLTAQVTRMIPVDVPAHSPMLVAIEERVVSGLLPITPRSRIP 253

Db 1130 TVVSGDPVQIEELARACADGVRRVPIVDYASHRSQVEIIESELAELVLAGLSPOQAPRPV 1189

Qy 254 FHSSVTGGRLDTRELDAAWYWRNMSSTVRFEPAAR-LLLQQGPKTFEVMSPHPVLTMGIQ 312

Db 1190 FSTLEGAWITPVLDDGGWYRNLRHVRGFAFVETLATDEGTFHVEVSAHPVLTALP 1249

Qy 313 ELAPDLGDTGTADVTIMGTLRGQGTDLHFTLSLAQ-----LRGHGET 356

Db 1250 -----GTVTGLA-----TLRRDNGQDRLVASLAEAWANGLAVDWSPLLSATGCHSD 1297

Qy 357 SATTVLS-----ARLTALSPT-----QQSLILLDLVRAHTM 387

Db 1298 LPTAFQTRHMLGEIEALAPAGEPAVQPAVLRTAEAPAEILDROBQLRVILDKVRAQTA 1357

Qy 388 AVLNDDGNERTASDAGPSASFALHGFDSVMGVLELNRSLKATGLRPLVTLIPDHTTPAAV 447

Db 1358 QVL-----GYATGGQIEVDTRFEAGCTSLTGVDLNRINAAFGVMAWPSMIFDFTPEAL 1413

Qy 448 AARLRTAALGHLEDDPAVPDPSPSGHGTTAADDPIAIIIGMACRFPFGVRSKPDWELAA 507

Db 1414 ABQLLVHVEGEAAANPAGAEAPFAAAG--AVDEPVAIVGMACRLPGGVASPEDLWRLVA 1471

Qy 508 SGCDALGPPTDRGWPTEQRHAQDPTQCTFFYQGGFLHDAHPDAGFPGISPRENLAM 567

Db 1472 GGGDALLSEFPQDRGWDVEGLHPDPEHPTGTSYVROGGFTENVAGDFAAFPGISPREALM 1531

Qy 568 DPQORLLLETSWEAFERAGIDPLSVRSRTGTGFAGALSFPDYGPRMDTASSEGAADVEGHI 627

1532 DPQORLLLETSWEAVEDAGIDPTSLRGQVGVFTGANTHEYGPSL-----RDGEGLDGYL 1587

Qy 628 LTGTTGSLVSGRIAYSFLGEGPAITVDTGCSASIVTLHLACQSIRSGECTLALAGVSYM 687

Db 1588 LTGNTASVMSGRVSYTLGLEGPALTVDITACSSSLVALHLAVQALRKGEVDMALAGGVAM 1647

Qy 688 STLGMPIEFISRORGLSVDRCKKAYSAADGTGCGVGMLLVERLSDAVRLGHRVLAVVR 747

Db 1648 PTPGMFVFSRORGLAGDGRSKAPFAASADGTSWSEGVLLVERLSDARNHQVLA VR 1707

Qy 748 GSAVNQDQASNGLTAPNGPAQERVIRQALANAGLSVADVVDVVEGHGTGTTGLDPIEAQAL 807

Db 1708 GSAVNQDQASNGLTAPNGPSQQRVIRRALADARLTTSDDVDVVEAHGTGTRGLDPIEAQAL 1767

Qy 808 LATYQO-RAGDRPLWLSLSKSNIGHTMAAGVGGVIMVMALREGVLPTLIHVDKPSQV 866

Db 1768 LATYQOGRDDEQPLRLGSLKSNIGHTQAAAGSVGIMVQAMRHGLLPKTLHVDKPSQV 1827

Qy 867 DWSAGAVRLLTAVPWPQDAAGRLRRAGVSSFGIGTNAHVILBEAPAAAGGCVAGGGVLE 926

Db 1828 DWSAGAVRLLTAVDWPKEQDGLRRAAVSSFGISGTNAHVILBEAPV-----VVE 1878

Qy 927 GAPGLAISVAESVAAPVAVSAPVAVSPVPPVPPVPSARSEAGLRAQAEALRQYVAV 986

Db 1879 GA-----SWVEPSVGSAGVGGV-----TPWVVSASAKAALDAQIERLAAF-AS 1921

Qy 987 RPDVSLADVGA-----GLACRAVLEHRAVLAADREELVQGLGALAAAGEPDRVTT 1038

Db 1922 RDRDADADAGAVDAGAVAVLADGRAQFHEHRAVALGAGADDILVQAL-----ADPDGLI-R 1975

Qy 1039 GHAPCGDGGVVFPFGQGWAGMGRLLASSPVFARRMQACEALAPWVDWSVVDILR 1098

Db 1976 GTASG--VGRVAFVFGQGTQWAGMGAELLDSSAVFAAAMAECEAALSFPYDWSLEA VR 2033

Qy 1099 RDAGDAVVERADVQVPLFVMSVLAALWRSYGIETPDVGLHSGQIEIAAHYCGALSXK 1158

Db 2034 QAPGAPTLEVDVQVPTFAVMVSLARVQHGHTVQAVVGHSGHIAAAYAGALS PLDD 2093

Qy 1159 AKTVALSRALAA--VRGGMASVPLPAQVEQLIGRWAGRLVWAAVNGPRSTAVSGD 1217

Db 2094 AARVTLRSKSTAAHLAGKGMLSLASEDAVLRLSD--FDGLSVAAVNGPTATVVSQD 2151

Qy 1218 ABADDEVLAYCAGTGVARRIPVDYASHCPVQPLRELELLELLDIPSPGVPFSTVE 1277

Db 2152 PVQIELAQACKADGFRARIIPVDYASHRSQVEIIESELAQVLGSLSPQAPRVPFSTLE 2211

Qy 1278 GTWLDTTDLDAAYWYRNHLQPVRFSDAVQALA-DDGHRVFEVSPHPTLVPAIEDTDT 1336

Db 2212 GTWITEPVLDDGTWYRNLRHVRGFAFVETLATDEGTFHVEVSAHPVLTMTLPT 2267

Qy 1337 AEDVTAIGSLRGDNDTRFLTAHAHTTGTGTTWHHTHHHTHHHTHHHTHHHTHHHT 1396

Db 2268 ---VTGLGTLRREOGQERLVTSLAEAVNGVL--PVAVTSLLPATASRP-----GLPTY 2316

Qy 1397 PFQOHVWLESQPCGAGSGAGAGSGAGSGAGTAGTAGTAEVSRFMDAVARQDLTVAT 1456

Db 2317 AFQERYWLENTPAALATG----- 2335

Qy 1457 TLAVPSPAGLDTVPVPAALSAWHRHQDQARINTWYQETWKPLTPTTTHPHOT-----WL 1511

Db 2336 -----DDWRVYIDWK--RLPAAEGSERTGLSGRWL 2363

Qy 1512 TAIPETQTHHHHTHILNLHHHGTPIPLTNHHTHPQHLLHHTHHHTHHHTHHHTHHHT 1570

Db 2364 AVTPE--DHSQAQAAVALDAGAKVEVLTAG-ADDDREALAARLTAL-----TTGD 2413

Qy 1571 AITGLLSLLALDETHPHHPTPTCTLLNLTLTQHTQTHPTPLWYATNTATTTTHPNP 1630

Db 2414 GFTGVVSL-----DGLVQVAVWQALGDAGIKAPLWSVTOGAVSVGLDT 2459

Qy 1631 LTHPTAQOTWGLARTLLEHPTHTAGIIDLPTPTPTHTLQHLTOTLTPHPTHTQALARTT 1690

Db 2460 PADPDRAMLWGLGRVVALEHPERKAGLVLDLPADQDAAALAHULVTALSGATGEDQIAIRTT 2519  
 Qy 1691 GTHRRRLTPTTLTPTH-QPPTP--TPHGTTLITGTCALATHLTHLTHLTHQPTQHLLLS 1747  
 Db 2520 GLHAREL--ARAPLHGRRTDQWQPHGTVLITGTTGALGSHAARMW-AHHGAHLLLYS 2575  
 Qy 1748 RTGPHPTPHQHLTQLOQKGIHITITTCDSNPDLQOQLLNTTTPPOHPLTTVIHTAGILD 1807  
 Db 2576 RSCEQAPGATQTAELTASGARVTIAACVDADPHAMRTLLDAIPAEPTPLTAVVHTAGALD 2635  
 Qy 1808 DATLTLNLTQNLNNVLRKAKSHALLHQLTOHTPLTAFVLVSSAAATFGAPGOANYAAN 1867  
 Db 2636 DGIVDLTAEQVRAHRAKAVAGSVLDLRTDLDAFVLSSVSTLGIPOGNTAPHN 2695  
 Qy 1868 AYLDALHRRHHTLHLLPATSIAMGTWQNGLADSKARAYLDRRGFRPMSPELATAAVTQA 1927  
 Db 2696 AYLDALAARRRATGRSAVSAMGPMWGGGMAAGDGAERLRNHNHGVPCMPDELALALESA 2755  
 Qy 1928 IADTERPVVVIADINSK-----IEHTSQTSLVSA-----ARREPAVQRP 1969  
 Db 2756 LGRDETA-ITVADIDWDRFLAYSSGRPOPLVEELPEVRRIIDARDSATSGQGSSAOGA 2814  
 Qy 1970 TTPAELHKLTAHOTSADORAALLLEVRDHVAALRHADPKAIAPDOSERALGFDLSITAVE 2029  
 Db 2815 NPLAE--RLAAAPGERTIELGLVRAQAAAALVRMSPEDVAADRFAKDOIIGFDSLAGVE 2871  
 Qy 2030 FRNLLIKATGLRPLVSLVFDHPTPAKLAHLOQLRG-----TAABSAPSAAAVTAEASV 2084  
 Db 2872 LRNLTRATGLQLPATLVFDHPTPLALVSLRSEFLGDEETADARSAAALPATVGAGAGA 2931  
 Qy 2085 -----TPIALVGMACRP PGVTSADDPWDLISSQDAIGGPTDRGWLDLTYLDDPP 2137  
 Db 2932 GAGTDADDPIAIVAMSCRYPGDIRSPEDLWRMLSEGGEGITPPTDRGWLDLTYLDDPP 2991  
 Qy 2138 DHPGTCYTRNGFLYDAGHFDABFFGISPREALAMPQORLLLETAWETIEHAGINPHTL 2197  
 Db 2992 DALGRAVREGFLHDAAEADABFFGVSPREALAMPQORMLLTSWEAFERAGIEPASL 3051  
 Qy 2198 HGPTGVTGTGNTQDYALRVHNAQSGTDGFPALGTAGSVISGRISYTFGPEGPAVSVDTA 2257  
 Db 3052 RGSSTGVFGLSYQDYAARVPNAPRGVEGYLLTSTPVSASGRIATVTFLEGPAITVDTA 3111  
 Qy 2258 CSSLVALHUALCOALRAGECSMALAGVTVWSSPGAFVFPFSRORGLAAGHCHKAFSAAD 2317  
 Db 3112 CSSLTALHLAVALRSAGECTMALAGVAMATPHMFVFPFSRORALAPDCRSKAFSADAD 3171  
 Qy 2318 GTCMGEGVGMVLVRLSDAHNRHVLAVVRGSVAVNODGASNGLTAPNGSPQORVIRQAL 2377  
 Db 3172 GFGAAGVGVLVRLSDAHNRHVLAVVRGSVAVNODGASNGLTAPNGSPQORVIRQAL 3231  
 Qy 2378 ANAGLSAGVDVAEAREHGTGTTLGDPIEAQALLATYQODRAGEPLMGLSVKSNVGHQA 2437  
 Db 3232 ADARLAPGDDIDAVEHGTGTSGLDPIEAQGLQATYKERPAPRPAERPLAIGSVKSNIGHTQA 3291  
 Qy 2438 AGVAGVIMVMAURHGLLPTLHVDSPSHVMSAGAVQLLTTPVMPWGEGBRLRAGVS 2497  
 Db 3292 AGAAGIKMVLAMRHGTLPTLHADBPSPHVDWANSGLAVTPEIDWPACTGP-RRAAVS 3350  
 Qy 2498 SFGVSGTNAHVILEEAP-----ADDVP-----CGPPAGECDAGSDDEAAA 2537  
 Db 3351 SFGISGTNAHVILEEAPDAAGEVVLGADPEVSETVAMAGTAGTSEVAEGSEASEAPAP 3410  
 Qy 2538 GS-----PGVMPVLVSAKSOPALRAQAALHAHLTDHPGLDLA-----DVGTYLTH 2583  
 Db 3411 GSREASLPGLHPVLVSAKDEQSLRGQAALHAWLSE-PAADLSDADGAPRLRDVGTYLAT 3469  
 Qy 2584 ARAVFHRATLIADRDITFLQALQAAGEPHPAVTHSSAPGTTGTGEAGKTAFTCSQ 2643  
 Db 3470 SRTAFARAAVTAARDGDFLDGLATLAQGTSARVHLDTARDCT-----TAFLETCQ 3521  
 Qy 2644 GTORPGMAHGLYHYPVFAAALNDICTHLDPLHDHPLPLLTQNDNDNEAALLQOTRY 2703  
 Db 3522 GSQRPAGRELYDRHPVFAARLDEICAHLDGHLLEPLLDVYMAEAGSAE--AALLDETRY 3579

Qy 2704 AQPALFAQVALHRLLTDGYHITPHYAGHSIGBITAAHLAGILTLTDATLITQORATLM 2763  
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 Db 3639 QSLPAGGAMLAQAAAEDEIRVWLETEERYAGRLDVAANVNGPEAAVLSDADAAREAEAYW 3698  
 Qy 2820 QOQGIKTKTLPNHAFFSPHTNPIQLHQHQTTLTYHPHPTPLITANT-----PPQLLT 2875  
 Db 3699 SGLGRTRALRVSHAFPHSAHMDGLDGPRAVLTEVFPFRPSLTVVSNVTGLAAGPDLCD 3758  
 Qy 2876 PHYWTQARNTVDYATTTQTLHQHGVTVYIELGPONTLTTLTHNLPNPPTTLT---LT 2932  
 Db 3759 PEYVVRHVRGTFRFDGVRVRLDGLVTCLELGPDLTAMAAADGLADTADPASAAGSPVG 3818  
 Qy 2933 HPHHPHPTH-----LLTNL-----AKTTHHPHYTH-HDNQPHHTH----- 2969  
 Db 3819 SPAGSPADSAAGALRPRLVALLRRKSETETVADALGRAHAHGTGPDWHAFAGSGAH 3878  
 Qy 2970 HLDLPTYFQHHHYWLESTQPCAG---NVSAAGLDPTHEPLLGATLELATDGGALLAGRL 3026  
 Db 3879 RVDLPTYFRRDRYWLDA--PAADTAVDTAGLGTADHPLLGAVVSLPDRDGLLTLTGLR 3936  
 Qy 3027 SLRSHPLADHAGVGTVLLSGATFLELALHAGTYVYCDRVDDELTHAPLVVPDGVSVQ 3086  
 Db 3937 SLRTHPLADHAGVGLLPGAAWVELAAHAAESAGLRDVRLELTLEPLVLPEHGGVELR 3996  
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 Db 3997 VTVGAPAGEPGGESAGDGAARPVLSRLADA-----PAGTAMWSCHTGLLATDRPELPA 4051  
 Qy 3139 DGLAGVWPRGAVVDVDRDLRAGACVLCVPSGLRVAVWRDGGDLIAECLP----- 3193  
 Db 4052 PDRANWPPQGAABEVPLDGLYERLDONGLAFLPLFQGLNAVWRYEGEVFADTALPATWA 4111  
 Qy 3194 -----EEAWGDAAG--FGLHPALLDGVVQPLSVLLPGGTGCGEGAGFGGVRVPAVWG 3246  
 Db 4112 TAPATANGGSAAPYGIHPALLDASLHAIIV--GGL-----VDEPELVRVPWHSGV 4163  
 Qy 3247 SLHRAGVTGRVVRVAVGREGGREGAVVVVDEAGVPVAVDRLELRPMDQLRAVSVS 3306  
 Db 4164 TVHAAGAAAARVRLAS---AGTDAVLSLTDGEGRLVSVBELTLRPVTADQAAASRVG 4219  
 Qy 3307 ACRRGSLYAVQV-----AEVGPVPVCGO-----A 3330  
 Db 4220 -----GLMHRVAVRPYALASSGEQDPHATSYGPTAVLGKDELKVAALAESAGVEVGLY 4275  
 Qy 3331 WAWHEDVSGSGGPGVGVVVLRCPPDAGAGGGGGGGGGVGVGVGVGVGVGVGVGVGVGV 3390  
 Db 4276 AALSQDV--AAGAPAPRTVLAPLP-----AGPADGGAEGVRCVTARTLELLQAWLADEHL 4328  
 Qy 3391 AGSRLVVYTRGAV-----VAGPEDGPDVVVGVASVWGLVRSQAQAEHDPFRVLLDLDTDGT- 3445  
 Db 4329 ACTRLLLVTRGAVRDPGEGSADGGEDLSHAAWGLVRTAQTENFGRFGLLDLADASSY 4388  
 Qy 3446 ----DLDTGAGAGWGDGGRVAAVACGEPQLAVRGERLLAARLKREBSSGDVPAQRSGD 3501  
 Db 4389 RTLPSVLSDAGR-----DEPQALHDGTIRLARL----- 4418  
 Qy 3502 TRARRSDVPAQRSGGVPARRSVDSGREVLPLMLSGSVLVTGCTGVGLAAVAARHLAGVCG 3561  
 Db 4419 ----ASVRPETGTAAPA-----LAP---EGTVLLTGTGGLGLVARHVVGENG 4460  
 Qy 3562 VRDLLLLVSRGPDAPGABGLRAELALGAEBVIRVACDVGGERVRLLEGVGAGCPDLTV 3621  
 Db 4461 VRRLLLVSRGGTDPAGADEL VHELEALGADSVAAACDVADREALTAVLDALPAEHLPTAV 4520  
 Qy 3622 VHAAGVLDADATTASLTTPERLGTVFAAKVDAALLDLDELTR--GMELSAFVLPSSAAGILGS 3679  
 Db 4521 VHTAGVLSGTLPSMTTEDVEHVRPKVDAAFLDELDTSTPAYDLAAAFVWFSSAAAVFGG 4580





Qy	1037	TTGHA----	PGDRGGVVFP	PGCGGWAGVRL	LASSPVFARMQACSEALAPWVDWS	1092
Db	1590	VTVAVDPETSGGGGVVLVPFGQGTQWVGNGAGLLGSSEVFASMSRECARALS	VHVEMD	1649		
Qy	1093	VVDTLRRDAGDAVMERADVQPVLFSVMVSLAALWRSYGI	EPDAVLGHSGOGEATAAHVCG	1152		
Db	1650	LLEV-----SGAGUERVDVQVPTWAMVMSLARWQMGWDVAAVVGHSOGETAATVAG	1706			
Qy	1153	ALSUKDAAKTVALSRALAA--VRGRGGMASVPLPAQOEVEQLIGERMAGRILWVAANGPRS	1211			
Db	1707	ALSLEDAAAVVALRAGLIGRYLAGRGAMAAPLPAGEVEAGLA-KWPG-VEVAANGPAS	1764			
Qy	1212	TAVSGDAEAVDEULAYCAGCTGVRARRIPVDYASHCPHQVPIRBELLELLGDISPSQSGVP	1271			
Db	1765	TWVSGDRRAVAGYVAVCAEGVQARLI	PVDYASHSRIVEDELKGBELRVLSGIRPRSPRPV	1824		
Qy	1272	PFSTVEGTWLDTTTTLDAAYMYNHLHQPVRSDAQALADDGHRVFPVEVSHPHTLVPAIED	1331			
Db	1825	VCSTVABEGPCEPVFDAGYFRPNLRNVFSAVVGGLLBEGHRRFIEVSAHPVLVHAIEQ	1884			
Qy	1332	TTEDTABDVTAIGSLRGDNDRFLTALARHTTGITPTWHHHVTTHHTTPHPTHIL	1391			
Db	1885	TAEAADRSVHATGTLRRQDOSPHLLTS-----TAEAMAHGATLTWDPALPPGHL	1934			
Qy	1392	-DLPTYFOHQHYWLESSQPGAGSGSAGAGSGAGSGAGTAGGTAEVESRFWDVAROD	1450			
Db	1935	TTLPTYPFNHHYWLDTTP-----	1953			
Qy	1451	LETVAITLAVPPSGLOTVVPALSAWRHQHDQBARINTWTYOETWKDKLTIPTTHQHQQ--	1508			
Db	1954	-TTPATTTQSPDA-----	MRVYTWKALTESSVPRHSIG	1988		
Qy	1509	TWLIAIPEOTOPHHPIHNILTNLHHGIT---PIPLTNHNTNPQHLHHTLHHTROQA	1564			
Db	1989	RCLLVAPT-TDGELLDOGLTYVLSERGASVANLEVPICARRA-----EVAELLKPSMESA	2042			
Qy	1565	QNHTTGAITGLLSLLALDETDPHPHHPTPTGTLNLNLTLQTQHTQH--PPTPLMYATTNAT	1623			
Db	2043	GEENT-TVWSLLGLV-----PST-DAVRTSIALLQAVSDIGVPAARVWALTERRAV	2090			
Qy	1624	TTENDPLTHPTQAOQTWGLARTLLEPHPTHTAGIIDLP-----TTPPTHTLOHLT	1673			
Db	2091	AVVEGB-TPQDAGAQLMGFCGRVAALEPDIWGGLIDLPETAELTRTPETSQPTPERLP	2149			
Qy	1674	QT-----LTQPHQTOIAIRTTGTGTHRRLTPPTLTPTHQPTPTPHGTTLIIG	1721			
Db	2150	QTPNRALLEAAVAVLAGDGEDQVAVRASGLYGRVSRAAAAGA--ASWQPSGTVLIIG	2206			
Qy	1722	GTGALATHLTHLTHPTQOHLTSTRGPTPHAQHLTTLQOQKGIIHLTITTCDSINPD	1781			
Db	2207	GWGAIGRRLLARRLAA--EGAERLVLTSSRRGPAPCAEAELAEBELRGHCCEVVHAACDVAERD	2265			
Qy	1782	QLOQLLNTIIPPOHPLTTVIHTAGILDATLTNLTPQLNVLRAKAHSAHLHLQLTQHTP	1841			
Db	2266	ALAAVLTAYP--NAVFHTAGILDDAVIDTLSPESFETVRGAKVCGABELLHQLTADIK	2321			
Qy	1842	-LTAFLVLYSAAATFGAGQANYAAAAAYDALAAHHRHTHLLPATSTJAWCTWMOGNGLADS	1900			
Db	2322	GLDAFLVLFSSVTGWGNAGQYAAAAANAALDALERRRAAGLPAITSVAVWMGGGGMA-A	2380			
Qy	1901	DKARAYLDRGRGFPMSPELATAAVTOAIADTERPVVYADIOWSKIE-----HTSQSD	1954			
Db	2381	GAGEESLSRGLRAMDPDAADVALLGAMGRND-VCVTIVDVDWERFAPATNATRPGLFLD	2439			
Qy	1955	LVSAAAREPAV-----QRPTPPABELHKTLAQHTSADQRAALLELVRDHVAAVILRHADPKA	2010			
Db	2440	TVPEAREALTAAGTTSATPDGAPELARRLSMLNETRLKLVELVTEAAAFVLRHPNTDA	2499			
Qy	2011	IAPQSFRALGFDSLTAVERNILLIKATGLRLVSVLFDHPDTPAKLAVHLONOLRCT---	2067			
Db	2500	IGABRPFKSGFDSLTSLEUNRNUNACTGUKLPATVIIFDHPSPTALARLLDLLDLTGAGAP	2559			
Qy	2068	--AAESAPSAAAVTAEASVTPEPIAVGMACRFPFGCVTSADDFWDLTSSEODAIGGFPTOR	2125			

Db 3608 RVAIHSAPEAAVHSAAGSDSAGVWTRHGEGTILVDPPEPTPPDADWARAWPPAGE-RVEP 3666  
Qy 3156 DGVRDLRAGACVLPVFESGLRAVWDGDLAEVCLPBEANGDAGFGHLPALLDGVVQ 3215  
Db 3667 AELYERFAGLYEYBAGFAGVRAVWQPDALLAEVLLPDRASTGAGRFVGHPLDAAQ 3726  
Qy 3216 PLSVLLPGG-TGFEAGGAGGEGVRVPAVGVVSLHAGVTGVRVRSVAVGRGGREAVSV 3274  
Db 3727 P---WLAGLLEVPEDA-----VLLPFAMQGVSLYATGAGALVRILTAKAGD-----AVSL 3774  
Qy 3275 VUGDEAGVPVAVDRLELRPDMQQLRA-VVSAGARRGSLIYAVQ-----WAE 3320  
Db 3775 QAAITSGAAVLSLGAIVMRPLARRKLDVLLGTGTDAGER-SLYRVEWQPRLLPAGPPRSWAV 3833  
Qy 3321 VGP-----VPVCGQAWHEDVGSGGPV---PGVVVLRCPDAGAG-----3360  
Db 3834 LGPDADRLAGTGPLGD-----QPDGGPTALYPEVRLR--KALAAAGAPRPEAVLVP 3882  
Qy 3361 --GGGGGGGGGVEVVGVLGVVQVGLERFAGSLVVVTRGAVVAGPEDPVDVVVGAS 3418  
Db 3883 VLSGAGATPESVQTTERTCILTALQDMLDAEELVDTPLVITRGAVAAVFGBEIGDLACAG 3942  
Qy 3419 VMLVRSQAQHPDRFVLLDLDTDGTLDTGAGAGVGDGGRVAAVACGEPQLAVRGE 3478  
Db 3943 VMLVRSARSEHPRFALVDTD-----GHPDDORTAL-----PLALRAV 3980  
Qy 3479 RLLAARLKLESGDVPAPRSQDTRA---RRSDVPAQRSGGVPARSDVDSGREVLPMLS 3535  
Db 3981 -----LDGAGQL-SURAGTARTPVLLRAGTPEEQG--PA-----FDP 4015  
Qy 3536 GGSVLVTGTVGLGAAVAVRHLAGVCGVRDLVLSRRGPDAPGAEGRLAEALGAEVRIV 3595  
Db 4016 AGTVLVTGATGLRLARHLAAEHGVRHLLLSRCGRAEGADELAELAGLEAPCPA 4075  
Qy 3596 ACVGBRERVRLEGVGACPLTGVVHAAGVLDATIASLTPERLGTVFAAKVDAALL 3655  
Db 4076 ACDAADREALARVLASVPADRPPLTGTVIHAAGVLDGTLDTALTPERTGTVMRPKADAALL 4135  
Qy 3656 DELTRCMEISAFVLFSSAGILGSGAGVYAAANAALDALAYRRRAAGLPGVSLAWGLWE 3715  
Db 4136 HELTRTSPUSVFAVFGAAGILGRPGQANYAANTFLDALAQHRRRAHGLPAVSLAWGLWG 4195  
Qy 3716 EASGTMGLHAGTDHRIIRSGLHPMSTPDALALFDAALA--LDRPVLLPADLRPA-----3768  
Db 4196 GATGTMGLHSGTDLRRMRSGIAPMTHDQGLALFDALAAAEPLVPMLDLAALVRE 4255  
Qy 3769 -----PPLPPLLQDILLPATRR-RTTRTTTGGAD---NGAQHARLAGQTHQOHTLL 3818  
Db 4256 RAEHGPDAVFGPLLGLLPAARAVQAAAPVRGAPAPAGGEGTAERLAGLGEARLEIV 4315  
Qy 3819 ALVRSHIATVLGHTTTPDPRAPDLGFDLSITAVELRNLSRTTGLRLPTTLAFDHPN 3878  
Db 4316 RLVRAEVSGVLGSGDPAVEGPRPKDLGFDLSITAVELRNRLGAATGLRLPTALVDRPT 4375  
Qy 3879 PTTLTHLHTLQPOQPD--NAVAPVLAELDKLSEALSALDKTDSASE-----RVTLRKLKL 3932  
Db 4376 SQVAEYLAELAGPRDGDGTAAPAEGLAALAAVGALEADDRLRDVRLRLTELAAAL 4435  
Qy 3933 MLRWNAPOHPTAESADDDKFTSATEABIPKFIINDL 3969  
Db 4436 TPQGRNPSAPAPAPSDRLERLDSANDDDLFAFIEEQ 4472

## RESULT 5

US-09-036-987A-6  
; Sequence 6, Application US/09036987A  
; Patent No. 6143526  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H.  
; APPLICANT: Broughton, Mary C.  
; APPLICANT: Crawford, Kathryn P.  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Merlo, Donald J.

; APPLICANT: Treadway, Patti J.  
; APPLICANT: Turner, Jan R.  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; TITLE OF INVENTION: Production  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dow Agrosciences LLC Patent Department  
; STREET: 9330 Zionsville Road  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: USA  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/036,987A  
; FILING DATE: 09-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stuart, Donald R.  
; REGISTRATION NUMBER: 28,479  
; REFERENCE/DOCKET NUMBER: 50,608  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (317)337-4816  
; TELEFAX: (317)337-4847  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5588 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-036-987A-6

Query Match 35.0%; Score 7281.5; DB 4; Length 5588;  
Best Local Similarity 36.1%; Pred. No. 0;  
Matches 1821; Conservative 490; Mismatches 1349; Indels 1389; Gaps 86;

Qy 12 PAAGEVLGVGADEADGGVVVFPGQGPMPGMRGLLDASDFRESVRACEAFAFAPYDWS 71  
Db 546 PAANVVQGAAD-CKGKVAFFVPGQSHWQGMARELSSESPVFRKRLAECAATAFVYDWS 604  
Qy 72 VEQVLRDSDPARGLDVRVQVQPTLPANMISLAALWRSQGVPCAVLHSLGLGIAAHVSG 131  
Db 605 LLGLVLRGDPDAPALDRDDVIQLALFAMVSLAELWRSQGVPEAPVYVGHSGEIAAHVAG 664  
Qy 132 GLSLADAARVVVTLWSQAQTTLAGTALVSVVAATPDDELPRIAPMTEDNPARLAAVANGP 191  
Db 665 ALSLTDVARIITAAACDVAISLTGKGLAIALPESAVVVRITAGLPE-----LTVAANGP 719  
Qy 192 RSTVVGAREAVADILVADLTAAQVTRMI PVDVPAHSPMLYAEIERSVVSGLLPITPRPSR 251  
Db 720 GSTVVGSEPSALERLQTELTAENVQTRRVGIDYASHSPQIAQVQGRLLDRLGSEVSEPAE 779  
Qy 252 IPFSSVTGRLDTRLDAAWYRNMSSTVPEPAARLLLOQPKTFVEMSPHPLVTWGL 311  
Db 780 IAFYSTVTGERTDTGRDLADYQNLRFQVFRFQQTVAEMADQGYRFFVEVSPHPLTAGI 839  
Qy 312 QELAPDLGTTGTADT--VIMGTLRRGGTDLHDHFTLSLA--QLRG-----352  
Db 840 QE-----TLEADAGGVVGSLLRGGGRRRLTSLAEQVRLGVNWEQVFLNTGAR 892  
Qy 353 -----352  
Db 893 RVPLTPYFQRYWLESAEYDAGDLGSLLSAEHPLLGAAVTLADAGGLLTGKLSVK 952  
Qy 353 -----352  
Db 953 TQPLADHVVGAILLPCTAFVEMILRAADQVGCGLIELSLTTPVLVLPATGAVQVIAV 1012

QY 353 ----- 352  
Db 1013 GGPDEAGRRSVRHSCRDDAVPQDSWTKATGTLTSSDHQDQGGPDGIWPPNDVAVPL 1072  
QY 353 ----- HGR- ----- 355  
Db 1073 DSFYARAABERGDFGPAFQGLQAANKRGDEIFAEVGLPTAHREDAGRFGIHPALLDAALQ 1132  
QY 356 ----- TSATTVLS- ----- 363  
Db 1133 ALGAABEDPDGWLFPFAMQGVSLKATGALSRLVHLVPAGANAVSVFTTDTTGOAVLSIDS 1192  
QY 364 ----- 363  
Db 1193 LVLRQISDKOLAAARAMEHESLFRVDWKRIISPGAAKFVSWAVIGNDELARACGSLGTEL 1252  
QY 364 ----- 363  
Db 1253 HPDLTGLADPPDVVVPCGASQDLDVASEARAAQRMLDLIQDWLAARFAGSLVVV 1312  
QY 364 ----- 363  
Db 1313 TCGAAGSTGPAEGVSDLVHAASWGLLSAQSENPDRLFVLDVDCGTAESWRALAAAVRSGER 1372  
QY 364 ----- 363  
Db 1373 QLALRAGEVVRPRLARCVAEADSRI PVPGADGTVLISGGTGLGLVARHLVAERGVRL 1432  
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Db 1433 VLAGRGWSAPGVTDLVDELVLGAAVEVASCVDGDRQAQLDRLLTTISAEFFLURGVVHAA 1492  
QY 364 ----- 363  
Db 1493 GALADGVVESLTPHVAKVFGPKAGAWHLHLLTDLDSLFFVLFSFSGVAGAACQGY 1552  
QY 364 ----- 363  
Db 1553 AANAFLDGLAQHRRTAGLPAVSLAWGLWEQPSGMTGALDAAGRSRIARTNPPMSAPDGL 1612  
QY 364 ----- 363  
Db 1613 RLFEAFRVPGBSLLVPVHVLDNALRAADAGGVPALLRDLVPAPVRRSAVNESADVNGL 1672  
QY 364 -ARLTALSPQQSLLLDLVRHAHTMAVLNDGNGERTASDAGPSASFAHLGFDSDVMGVELR 422  
Db 1673 VGRRLRDLQDETQLLGLVREHVSAVLGHSG- - -AVEVGADRAFRDLGFDLSLGVFR 1728  
QY 423 NRLSKATGLRLPVTLPDHTTPAAVARLRTAALGHLDEDTAPVPSPSGHGTTAAADDP 482  
Db 1729 NRLGGVGLVRLPATAVFDYPTPRALVRLDKLIGGYEAPT-PAPAAVA- - -AVTADDP 1783  
QY 483 IATIGHMACRPPGVRSPKOLWELAAAGGDAIGPPTDRGWPTQRHAQDPTQGTFFPQ 542  
Db 1784 VJLVGMCRTPGGVSSPEELVRLVAGLDVAEFPPDRGMDQAGLFDPPDDRIGTSYVCE 1843  
QY 543 GGFLLHDAHFDAFFGFSIPREALAMPQORLLLETWEAFERAGIDPLSVRGSRTGVFAG 602  
Db 1844 GGFLLRDAEFDAFFGFSIPREALAMPQORLLLETWEAFERAGIDPLSVRGSRTGVFAG 1903  
QY 603 ALSFDYGPMDTASSGAADEVGHIITGTTGVSLSGRIAYSGLEGPAITVDTCASLV 662  
Db 1904 LMHHYCARFITRAPEG- - -FEGYLGNGSAGGVSGRVAYSFGFEPAVTVDTCASSLV 1960  
QY 663 TLHLACOSLRSGCTALAGGVSMSTLGMFIFBSRQGLSVDRCKAYSAADGTGWGE 722  
Db 1961 ALHLAQOARSGECDLALAGGVMTATPGMFVFSRQGLAADGRCKSPAAAADGTGWGE 2020  
QY 723 GUGMLLVERLSDAVRLGHRVLA VVRGSVAVNQDGASNGLTAPNGPAQERVIRQALANAGLS 782  
Db 2021 GAGLVLLERLSDARRNGHAVLA VVRGSVAVNQDGASNGLTAPNGPSQORVITQALASAGLS 2080  
QY 783 VADVVDVEHGCTGTLTGDPDIEAQALLATYQ- - -RAGDRPLWLGLSKNIGHTMAAGVGV 841

Db 2081 VSDVDAVEAHGTGTLGDPDIEAQALLATYQOGRDSDRPLWLGSVKSNIQHTQAAAGVAGV 2140  
QY 842 IKWMALREGVLPRTLHVDKPSVDWSAGAVRLLEATEAVPMPGDAAAGRLRRRAGVSSFGIG 901  
Db 2141 IKWMAMRHGQLPATLHVDDEPTSEVDWSAGDVQLTENTPWFONS- - -HPRRVGVSSFGIS 2198  
QY 902 GTNAHVILBEEAPAAAGCVAGGVLEGAPGLAISVAESVAAAPVAVASVPAESVVPVVPV 961  
Db 2199 GTNAHVILEQA- - -SKTPDETADKSGPDSSEST-VDLPA-V 2233  
QY 962 PVPVSARSBAEGLRAQAEALRQYVAVRPOVSLADVAGLACGRVLEHRAVLAADREELV 1021  
Db 2234 PLIVSGRTPAALSAQASALLSYLGERGDIISTLDAAFSLASSRAALEERAVVIGADRETL 2293  
QY 1022 QCLGALAAAGEPDRRTVTTGHAPGGDRGGVVFPFGGOGWAGMGRVLLLAGSPVPFARRMQAC 1081  
Db 2294 SGLEALASREASGVVSGSPVS- - -GGVGFVAGGGQWLMGRGLYSVPFVA- - -DAP 2347  
QY 1082 EBALAP- - -WYDVMSVVDILRRDAGDAVWERADVVPVLFSVMVSLAALWRSYIEPDA 1136  
Db 2348 DEACAGLDHAGLQGVDRDVVFGSDG-SLLDRTLWAQSLGFALQVGLLSLLGSGWVRPGV 2406  
QY 1137 VLCHSQGETAAAHVCGALSCLKDAAKTVALRSALAAVRCRGCMASVPLPAQVEQOLIGR 1196  
Db 2407 VLGHSVGEFAAAVAAAGVLSLPDAARMVAGRARLMQALPSGGAMLA VAAAGEQOLRLLADR 2466  
QY 1197 WAGRLWAAVNGPRSTAVSGDAEAVDEVLAYCAGTGVARRIPVDYVASHCPHVQURBEL 1256  
Db 2467 VDG-AGIAAVNAPESVVLSGDREVLDIAGALDGGQIRWRRLRVSHAHSYRMDPMLQBF 2525  
QY 1257 LELLGDISPQSGVPPFFSTVEGTWLTDTTTLDA- - -WYRNHLQHPVRFSDAVALADDGHR 1314  
Db 2526 ASIARSDVRRGDLPVWSTLTGE-LDTAGVMATPEYVVRQVREPVRFADGVRVLAQOGVA 2584  
QY 1315 VFVVSPPHLLVPALDITTEDTTDAEDVTAGLSRGGNDTRRELTAALHHTTGTGTPTW 1374  
Db 2585 TIFELGPDATLSALI PD-CHSWADQAMPIMLURKORTETETVVAAVARAHTRGV- - -PVEV 2641  
QY 1375 HHVYHHHTHPHPTHLDLPTYPFOHVMLESSQPGAGSGS- - - 1417  
Db 2642 SAYPAGTGAR- - -RVELPTTAFQRQYWLSTSDYDVTGIGLAAAEHPLIGAVVALAD 2696  
QY 1418 - - -AGAGSG- - - 1423  
Db 2697 GDGWLITGRLSVGTHPWLQAHRVGLGVVVPGTAILMALHAGARLGCDCRVEELTLETPLV 2756  
QY 1424 - - -AGSGRAGTAG- - -TAEVESRFPWDAVARQDLE- - - 1452  
Db 2757 VPERAAGAGSRGPAGGTTVSIETABERVRTNDIAIEIQLLVNAPDEGGRRRVLSYRPAAG 2816  
QY 1453 - - -TVATT- - -LAVP- - -PSAGLDTVPAL- - -S 1474  
Db 2817 SRGGWTRHATGELVVGTTGGRVAVPDWSAGAESIALDEFYVALAGNGPEYGPLFOGLOA 2876  
QY 1475 AWHRHQHQDART- - -NTW- - - 1489  
Db 2877 AMRRGDEVLAETAPPAEADAMASGYLLDPALLDAALQASALGDRPEQGGAWLPSPFTGVE 2936  
QY 1490 - - -TV 1491  
Db 2937 LSAPAGTISRVRLETRRRPDAISVAVMDESGRLLASIDSRLRSVSSGQLANRDAVRDALP 2996  
QY 1492 QSTWKLPLTLPHTPHOTWLIAPETOTHHPHITNLTNLHH- - -GITPILTLNHTHN 1549  
Db 2997 EYTWEPVATQST-EPGR-WAL- - -LGDATACCKODLILATUDASADRCADLAALAEKLDSSALV 3053  
QY 1550 POHLHHTLHHTRQQQNHTTGAI TGLLSLLALDETPHHPHPTGTCTLLNLTLTQHTQT 1609  
Db 3054 PDVV- - -VYCAGEQADPGTGAA- - -ALAEQOQ- - -TLALLQAWLAEPRL- - - 3093  
QY 1610 HPPTPLMWATTNATTHHPNDPLTHPTQAOQTWGLARTTLEHPTHTAGIIDLPTT- - -P 1664

3094 -AEARLVVVTCRAVTTAPSDGASELAHAPLWGLLRAAQVENPQGVF-LADVDGTAEWMRA 3151  
Db  
1665 THTLQHLQTLQPHHQTLAIRTGTHTRRLTPTTLTPTHTQPTTPTHTGTLTGNG 1724  
Qy  
3152 LPSALGSM-----EPQALURKGAAPRAPLASVAGQIDVPVAVDPTVLSGGTG 3202  
Db  
1725 ALATHLTHLTHOPTQHLLLSRTGPHTPHQAHLTQLOQKQIHLITITCTDTSNDQIQ 1784  
Qy  
3203 LLGAVARHLVTERGVRLVLCRGGWDAPGITELVGLNGLGAVDVVACDVADRALE 3262  
Db  
1785 QLLNTTIPPOHPLTVIHTAGILDATLNLTPQLANNVLRKAKSHLHLQHUTQHTPLTA 1844  
Qy  
3263 SLIAAPVAFBFFLCGVVHAAGALADVIESLSPDDVCAVFGPACAGANNLHELTRDLSF 3322  
Db  
1845 FVLSSAATFCGAPGOANYAANAYLDALAHRRHHLHPATSTANGTW-OGNGLADSKA 1903  
Qy  
3323 FALFSSLSGVAGAPGOGNYAANAFDALAHYRSOGLPAVSLAWLWEPQSGMTET--- 3379  
Db  
1904 RAYLDRGRFPMSPELAT---AAVTOAIADTERPYVVIADIDWSKIETHTSQTSDLVSAAR 1960  
Qy  
3380 LSEVDRSRTARANPPLSTKEGLELFDAGLADRAAVPAKLDRTPLEAQRSGSL----- 3434  
Db  
1961 EREPAVQRPPTPAELHKTIAHOTSADQRAALLLELVRDHVAALRHADPKAIAPDQSFRAL 2020  
Qy  
3435 ---PALLTALVPPIRNRNRASGTETADEGTLGCVVREHAAAVLGYSSAADVGVERAFDL 3491  
Db  
2021 GFDSLTAVEFRNLLIKATGLRPLVSLVDFHPTPAKLAHLQNLQRLCTAAESAPSAV-T 2079  
Qy  
3492 GDSLSGVLELRNLGVLGRVLPATAVFDYPTPRALARFHOEL---ADEIATTPAPVT 3548  
Db  
2080 AEASVTEP--IAIVGMACRFPFGVTSADDFWDLISSEQDAIAGFPDTRGDWDLTDYDPP 2137  
Qy  
3549 TRAPVAEDDLVALVGMCRFPQGVSSPEELMRLVAGGVDAVADFPADRGWDLAGLFDPP 3608  
Db  
2138 DHPGTCTYRNGFLYDAGHFDABFFGISPREALAMPQORLLELTAWETIEHAGNPHYL 2197  
Qy  
3609 ERAGKTYVREGAFLTDADRDFAGFFGISPREALAMPQORLLELTAWETIEHAGNPHYL 2197  
Db  
2198 HGTPTGVFTGNGQDVALR-VHNAQOSTDGFALTGTAGSVISGRISYTFEGEGPAVSDT 2256  
Qy  
3669 RGSRTGVFAGLMVHDYGAAPASRAPEGFEYGLNGSAGSVASGRISYTFEGEGPAVSDT 3728  
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2257 ACSSSLVALHLAQALRAGECSMALAGVTVMSSPGAFVEFSRQRLGAADGHCKAFSA 2316  
Qy  
3729 ACSSSLVALHLAQSLRSGECDLAAGVTVMSSTPCTFVEFSRQRLGAPDGRCKFAESA 3788  
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2317 DGTGMEGEGVMLLVERLSDAHRNGHRLVAVRGSANQDGSANGLTAPNGPSQORVROA 2376  
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3789 DGTGMEGEGAGLVLLERLSDARENGHRLVAVRGSANQDGSANGLTAPNGPSQORVROA 3848  
Db  
2377 LANAGLSAGDVDAVEAHGTGTLGDPTEAQALLATYGDORAGEGPLWGLSVKSNVHTQA 2436  
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3849 LASAGLSVDVDAVEAHGTGTLGDPTEAQALLATYGDORAGEGPLWGLSVKSNVHTQA 3908  
Db  
2437 AAGVAGVIKVMNALRHLLPRLTHVDEPSPHVDWAGAVQLLTETVPWPGEGRRLRAGV 2496  
Qy  
3909 AAGVAGVIKVMNAMRHGQLPRLTHVDAPSSQVDWAGRVQLLTETVPW-DSGRPCRCV 3967  
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2497 SSGVSGTNAHVILEAPADDDVPGPPAGEG-AGSDDDEAAGSPGVWPLVSAKSQPAL 2555  
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3968 SSGFSGTNAHVILEOS-----TQMDQAAEPDSSPLVDVPVWVWVSGKTPAL 4017  
Db  
2556 RAOAQLHAHLTDHPCGLDLADVGYTLAHARAVFDHRATLI AADRTFLQALCALAGEPH 2615  
Qy  
4018 SAQAATLATYLDONVDVSPDLVGISLAVTRSLDERAVVIGSDRDTLLSGLNALAAG--- 4074  
Db  
2616 PAVIHSSAPGGTGEAAGKTAFCISGQGTQBPFGMAHGLYHTHPVFAALNDICTHLDPH 2675  
Qy  
4075 ----HEAAGVTPGVIGERTGVFAGQGGQWLGMRRLYSFEPAFAGAFDEACAEALDAN 4130  
Db  
2676 LDHP--LLPILLTONDNDEAALLQOTRYAQAPALFAFOVALHRLITDGYHTHPHYAGH 2733  
Qy  
4131 LGREVGVRDVFSGDE-----SLDRTLWAQSGLFALQVGLWELL-GTWGVRPSVVLGH 4183  
Db

2734 SLGEITAAHLAAGILTLDTATLITORATLTMOTMP- GTMTTLHTTTPHHITHTAHENDL 2792  
Qy  
4184 SVGELAAAFNAGVLSMAEAAARLVAGARLMQALPSGAMLAVSATEARVGLDGVDRV 4243  
Db  
2793 AIAAINTPTSLVISGTPHTVQHITTLTCCOQGIKTKLPNHPAFSPHTNPIQLHQHQHQ 2852  
Qy  
4244 GVAANVAPGSVVLSDRDVLDGIAGRLDQGIIRSRWLRSVSHAFSHRMDPMLAEFAELAR 4303  
Db  
2853 TLTYHPHTPLITANT---PPDQLLTPHYWTOQARNTVDYATTTTQTLHQHGVITYIELG 2908  
Qy  
4304 SVDYRSPRLPIVSTLTGNLDDGVGNATPEYVWRQVREFVADGVQALVDQGVDTIVELG 4363  
Db  
2909 PONTLTTLTHLNPPTTT-LTLTHPHHPQTHLLTNLAKTTTTHWPHHYTHDNQPH 2967  
Qy  
4364 PDGALSSLVQCBVAESGRATGIPVRRDRDEVRTVLDALAQ-----HT 4407  
Db  
2968 H-----THLDLPTYPFHHPHYWLESTQPCAGNVSAAGLDPTPHPLGATL 3012  
Qy  
4408 RGVAVDWSGFFAGTRATQVLDPTVAFQRYWLEPSD--SGDVTGVLGTGAEPHLLGAVV 4465  
Db  
3013 ELATDGGALLAGRLSLRSHPLADHAGVTLLSGATFLELALHAGTVVGCORVDELTLH 3072  
Qy  
4466 PVAGDEVLTLGRLSVGTHPLAEHRVLGEVVPVGTALLLEMAWRAGSOVGCERVELTLE 4525  
Db  
3073 APLVVPVGVSVQVGAADGEGRLVSVVARGSSACGGGSGGVWTCASGVLVBA 3132  
Qy  
4526 APLVLPFERGAQAQVAVGAPDEAGRRSLQYSGAD-----EDGWRRTASGLAQAN 4578  
Db  
3133 AGVVVDVGLAGVWPPRGAVAVDVGDVDRDLRAGACVLPFVSGLRVAVWRDGGDLAEVCL 3192  
Qy  
4579 A---VPPADSTAWPPDGAGQVDLAEFYERLAERGLTYGVFQGLRAAHRHGGDI PAELA- 4634  
Db  
3193 PEEAWGDAAGLHPALLDGVVQPLSVLLPGTGFEGCAGGEGVYRVAWVGCVSLHRAG 3252  
Qy  
4635 ---GSPDASGFIHPALLDAALHAMAL-----GASPDSEARLPFSMRGAOLYRAE 4681  
Db  
3253 VTGVVRVSVAVRGGGREAASVVVGDGAGVPVAVDRLELRPVDMDGOLRAVSVSAGRGS 3312  
Qy  
4682 GAALVRLSPGSG---AVSLTVDTGRRVAVAESLSTRPVSTDTQGA---GRGDQER 4734  
Db  
3313 LYAVQW---AEVGPVPCQAWA-----WHEDVGESE-----GGPV 3345  
Qy  
4735 LLHVEWVRSASAGMSLTSCAVVGLGEPEWHAALKTTGVQVESHADLASLATEVAKRGA 4794  
Db  
3346 PQVWVLRCPDAGAGGGGGGGGGGVEV-----VGVVGVVQVWGLGERPAGSRLVV 3398  
Qy  
4795 PCAVTPCPRPRA-----MOELPTAARRATQOAMAMLOQLADDRFVSTRLLIL 4843  
Db  
3399 TRGAVVAGPDPVVDVVGASVWGLVRSQAQAEHPDRFVLDDTDGTDLDTGAGAGWGD 3458  
Qy  
4844 THRVA SAVAGEDVLDLVHAPLWGLVRSQAQAEHPDRFALIDMDDERASQT----- 4892  
Db  
3459 GGRVAAVACGEPQLAVRGERLLAARLKRLESSESGDVPQAQRSGDTRARRSDVPAQRSGVP 3518  
Qy  
4893 --ALAEALTAGEAQLAVRSGVVLPRLCQ----- 4919  
Db  
3519 ARRSVDVSGREVLPWLSGSGVLVTGCTGVLGAAVAVHLAGVCCVRDILLVSRGGPAPGA 3578  
Qy  
4920 ---VKVSGGAFRW-DEGTVLVTGGTGGGLLALHRLVSAHGVRHLLLASRRGLAAPGA 4974  
Db  
3579 EGLRAELAAAGAEVRI VACDGERREVRVRLLEGVPAGCPLTCVVHAAAGVLDATTASITP 3638  
Qy  
4975 DELVAELQAGADVAVVACDSADRDSLARLVASVPAENPLRVVHAAVGLDDGVLMSP 5034  
Db  
3639 ERLGTVFAAKYDAALLDELTRGMELSAFVLFSSAAGILSGAGQGNAAAAALDALAYR 3698  
Qy  
5035 ERLDAVLPKYDAAWYLHELTRGLSFAVLFSSVAGLFGGAGQSNYAAGNAFLDALAHC 5094  
Db  
3699 PRAAGLPVSLAWGLWEASGHTGLAGTDRHRIIRSGLHPMSTDALADALADALDRP 3758  
Qy  
5095 RQAQGLPALSLASGLWASIDGMAGDLAAADVERLSRAGIGLPSLPGGLADVAAGSDEP 5154  
Db









Db 603 LEVV---SGGAGLERVDVQVPTWAVMVSLARYQAMGVDAVAAVGHSGSCEIAAATVAGA 659  
QY 133 LSLADAAARVVLNS-QAOTTLTLAGTALVSVAATPDELLPRIAPWTEDNPARLAAVAANGP 191  
Db 660 LSLADAAARVVALRAGLIGRYLAGRAGMAAIVPLPAGEVEAGLAKW-----PGVEAAVANGP 714  
QY 192 RSTVSGAREAVADLVADLTAAQVTRMIIPVDVPAHSPLMAYJE---ERVUSGLLPITR 248  
Db 715 ASTVSGDRARAGYAVACQAGVQARLIPVDVASHSRHVEDDKGELERVLSC---IRPR 771  
QY 249 PSRIPEHSSVTGRLDTRIEDAAYWYRNMSSTVRFPAPARLLIQOQPKTFVENSHPVLVT 308  
Db 772 SPRVPVCSITVAGQPCPEFVDAGYWFNRNLNRNRFVSFAVGVGLLEEGHRRFIEVSAHPVLV 831  
QY 309 MGLOELAPDLGDTTGTADTVI---MGTLRGQGTLDHPLTSLAQIRGHGET-----356  
Db 832 HAIETQ-----TAEAADRSVHATGTLRRQDDSPHRLTSTABAWAHGATLTWDPALPPG 884  
QY 357 SATTV-----LSARLTALSPTOOQ-SLLLDLVRA 384  
Db 885 HLTLPTYPNNHHYMLDTIDGGGGDDATOESKESGPLTRELRLGPSQKQLGFLLDLVC 944  
QY 385 HTMAVLNDCNERTASDAGSASFALHGFDSVMGVELNRNLSKATGLRLPVTILIFDHTTP 444  
Db 945 HTAVVLGLD---TAAEVDPLSFKKQIQSGMTGVELNRNLTETGLALPTTLVLVDRPTP 1000  
QY 445 AVAARLRITAA-----GHLEDDTAIPVDPSPSGHGGTAAADDPI 483  
Db 1001 RALAQLFHTLLEDGSPSGSVLAPAKQSFEAGGPGVLSSAAVGVSDA---RGGSRDDDDPI 1057  
QY 484 AITGMACRPPGGVRSKPOLWELAAASGDAIGPPTDRGWPTEQHOAQDPTQPCTFYPOGS 543  
Db 1058 AIVGVGRLPGGVDSRAALWELLESADALSSPTDRGMDLGLYDEPGTPCKTYVREG 1117  
QY 544 GFLHDAHFADGFFGISPREALAMPQORLLLSWEAFERAGIDPLSVGRSGTGVFAGA 603  
Db 1118 GFLHSAAEFDAEFFGISPREATAMPQORLLLEASWEALEDAGVLPESLRGGDAGVFVGA 1177  
QY 604 LSFDPGRMDTASSEGADVEGHILGTGTGSVLSGRIAYSFLEGPATIVDTGCSASLYT 663  
Db 1178 TAPEYGPRL-----HEGADGYEGYLLTGTASVAGRIAYTLGTGGPALTVDTCSSSLVA 1233  
QY 664 LHLACOSLSRGECTALAGVSVNMTLGMPIEFSRORGLSVDCRCKAYASAAADGTGCMGEG 723  
Db 1234 LHLAVALRRGECGLALAGATVNSGPMFVEFSRORGLAPDGRCPMFPFSADADGTAWSEG 1293  
QY 724 VGMLLVERLSDAVRLGHRVLAVRGSVAVNQDGASNGLTAPNGPAQERVIQOALANAGLSV 783  
Db 1294 VAVLALERLSDARRAGHRVLGVVRGSVAVNQDGASNGLTAPNRSQAQGVIRAAALADAGLAP 1353  
QY 784 ADVVDVEGHTGTGLDPTIAQALLATYG-ORAGDRPLWGLSKNSI GHTMAAAGVGVY 842  
Db 1354 GDYDAVEAGHTGTALGDPIEASALLATYGRERYGD-PLWGLSKSVNVTQAAAGAAGVV 1412  
QY 843 KMYMALREGVLPRTLHVDPSPQVDASAGAVRLLTTEAVWPBGDAACRLRAGVSSPGIGS 902  
Db 1413 KMLALEHGLTLPRLHADRPSTHVDWSSSGTVALLAEARRWP-RRDRPRRAAVSSPGISG 1471  
QY 903 TNAHVILEAPAAAGCGVAGGVLEGAPGLAISVAESVAAFPVAVSAPVAVSVPVPPVPP 962  
Db 1472 TNAHLIIEAPE-----WVEDIDGVAAPDRGTADAA-----APSP 1506  
QY 963 VFPVSARSEAGLRAQAEALRQYVAVRDPVSLADVGAGLACGRAVLEHRAVVLAAADRELVO 1022  
Db 1507 LLSARSSEGRALQAQAVRLGEYVE-RVGADPRDVAYSLASTRTLFEHRAVVPVPCGGRELVA 1565  
QY 1023 GLCALAAGEPDRVTTHGAPGDRGGVVFVPCQGGQWAGMGRVLLIASSPVARRMQACE 1082  
Db 1566 ALGGPAGRVSGVRSGRAV---PGGVGLFTQGGQWGMGRGLYAGGGVFA---EVLV 1619  
QY 1083 EALAPW-----VDMVSDILRRDAG---DA-----VWERADVV 1112

Db 1620 EYLSMVGEVGRSLRDVMPFGDVV---DAGAGADAGAGAGVSGSGSVGGILLGRTEPA 1676  
QY 1113 QPVLFSVMVSLAALWRSYGIPEDAVLGHSGQEGIAAAHVCAGLSLKDAAKTVALRSALAA 1172  
Db 1677 QPALFALFALFALFALFALFALFALFALFALFALFALFALFALFALFALFALFALFALF 1736  
QY 1173 VNRGCGMASVPLPAQEVFQLI---GERWAGRLWVAANGPRSTAVSGDAEADEVLAYCA 1229  
Db 1737 LPVGGGMSVSGASVSVGVVEGLGE-WVS---VAANGPRSVLSDGVGVLESVVASLM 1792  
QY 1230 GTGVARARIPVDYASHCHPHVQPLREE---LLELL---GDISPQSPGVPPFSTVEGTWLD 1284  
Db 1793 GGVGECRLDVSHGFHSHVLMEDVLFGEFRGVESLEFRVRP---GVVVVSGVSGVSG 1849  
QY 1285 TL-DAAYWRNLHQPVRSDAVALADDDHVRVFEVSDHPTLVPAIEDTETEDTADVTAI 1343  
Db 1850 ELGDPGYWRHAREAVRFADGVGVRLGVGLTVLEVGHVGLT-GMAGECLGAGDDVVVV 1908  
QY 1344 GSLRGDNDTRRFLTALAHHTTGTGPTTHHHYTHHHHTHPHPTHLDLPTYPFOHQHY 1403  
Db 1909 PMRRGRAEREFEAALATVFRDAGLDATALHTGS-----TGRRIDLPTYPFQDRY 1961  
QY 1404 WLESQPGAGSGSGAGSGAGS-----GRAGTAGTGAESREFWDAVARQDLETVAITLAV 1460  
Db 1962 WLDPVKRTAVTGVEPAGSPADARATERGRSTTAG-----1994  
QY 1461 PPSAGLDTVPALSAWHRHQHDARINTWTYQETWKPLTL-----PTTHQPHQHTWLI 1514  
Db 1995 -----IRYRVAMQPAVVDNRGNPGPAGHV-----LLLA 2021  
QY 1515 PETQTHPHITNLTNLHHHGITPIPLTNLHHTHPQLHHTHHTHHTHHTHHTHHTHHTH 1574  
Db 2022 PDEDT-----1599  
QY 1575 LLSLLALDETPHHPHPT---PTGT-----LLN-----2090  
Db 2031 LAPALARELAVRGAHVTVAVSVGTGREAGDGLLRAAGDGAARSTRVLWLAPEAPDA 2090  
QY 1600 LTLTQHTQHTPPLTWATTNATTHPNDPDLTHPTQATWGLARTLLEHHTHTAGIID 1659  
Db 2091 VALVOALGEAVEAPLWITREAAVRP-DETPSVGGQALWGLGQVAALELGRRRGGLAD 2149  
QY 1660 LPTTPTPTLQHLTQTLQPHQTQLAIRTTCTHTTTRLTPTTL-----TPTHOPPTPT 1712  
Db 2150 LFGSASPAVLRFFVCALL-AGGENQFAVRPSGVHVRVPVAPVPPASARTVTPATAV 2208  
QY 1713 -----PHGTTLITGGTGALATHLTHLTHHTHHTHHTHHTHHTHHTHHTHHTHHTH 1754  
Db 2209 GEDARNDTSDVVVPDDRWSGGTVLITGGTGALGAQVARRL-ARSGAARLLLVRGRGA 2267  
QY 1755 HAQLHTTLOQKGIHLTITTCDSNPDQLOLLNTIPQHPPLTTVIHTAGILDDATLNL 1814  
Db 2268 GVGELVEELTALGSEVAVEACDVADRDLAALLAGLPEERPLVAVLHAAGVLDGVDLS 2327  
QY 1815 TPTOLNNVLRKAKHSAHLHOLTQHTPLTAFVLYSSAAATFGAPQOYAAANAYLDALA 1874  
Db 2328 TSDRDVAVLRDKVTAARHDELDTADLPDADFVLPSSI VGVWNGGQOYVAAANALDALA 2387  
QY 1875 HRRHHTHLPATSIANGTWQGNGLSDSKARAYLDRRGFRPMSPELA-----T 1921  
Db 2388 QRRRARGARAAASIAANGPWAGMAGSATAKSF-ERDGVVTDLPERALDVLDDVVGAGGTS 2446  
QY 1922 RAVTQAIADTERPYVVIADIDW-----SKTEHSTQSDLSAAR-----EREPAVO 1967  
Db 2447 AAGTHAAGESS---LLVADVDMETVFGSRVTRRTWSLFDGVSAAARSAGHAADRAALT 2503  
QY 1968 RPTPPAEHLKHTLAHQ-----TSADQRAALLELRVHVAALVRHADPKAIAPD 2014  
Db 2504 PCTRFGDAGPCGGQDGGEGRPWLSVGPSPAERRALLTLVRSEANGILRHASADAVDE 2563  
QY 2015 QSFRALGFDSTLAVEFNRLLIKATGLRPLVSLVDPHTPAKLAHVHQLNQLRGTAAESAPS 2074  
Db 2564 LAFRSAGFDSLTVLELRNRLTAATGLNLTNTLLFDHPTPLSLASHLHDELFGPDSEAPBA 2623



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APPLICANT: MCDANIEL, Robert
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TYPE: PRT
ORGANISM: Streptomyces venezuelae
US-09-320-878-2

Query Match      34.0%; Score 7079; DB 3; Length 3739;
Best Local Similarity 42.5%; Pred. No. 0;
Matches 1681; Conservative 391; Mismatches 1171; Indels 712; Gaps 81;

QY 477 AAADDDIAIGMACRPPGGVRSKDLWELAAAGDGAIGPPFTRDGMWPTQRHAQDPTQPG 536
DB 32 AKAGEFVAIVGMACRLPGGVASPEDLWRLVAGEDAISFPQDRGWDVGLDPPNEATG 91

QY 537 TFPQGGGLHDAHFDAGFFGISPREALAMDPOQLLETWEAPERAGIDPLSVRGRS 596
DB 92 KSYAREAGFLYEAGEFDADFFGISPREALAMDPOQLLETWEAPERAGIDPAATARGTS 151

QY 597 TGVFAGNLSFDVGPMDTASGEAADVEGHILTTGTVLSGRIAYSGLEGPAITVDTG 656
DB 152 VGVFTGMVHYATRL-TDVPEG---IEGLYGTGNSGVSAGRVAVTLGLEGPVAVDTA 207

QY 657 CSASVLTLLHACQSLRSGETLALAGCVSVMTGLCMFIBFSRQGLSVDRCKKAYSAAD 716
DB 208 CSSSLVALHLAVQALRKGEVDALAGVTVMTSTPSTFVFSRQGLAPDGRSKSFSTAD 267

QY 717 GTGWSGEGVGMILVERLSDAVRLGHRVLAVRGSVAVNQDGASGLTAPNGPAQERVTRQAL 776
DB 268 GTSWSEGVGVLLVERLSDAVRLGHRILAVVRGTAVNQDGASSGLTAPNGPSQQRVIRRAL 327

QY 777 ANAGLSVADVVDVVEGHGTGTTLDGPTEAQAALLATYQG-RAGDRPLWLSGSKNIGHTMAA 835
DB 328 ADARLTTSDVDVVEAHGTGRLGDPTEAQAVALTYQGGDRGEOPLRLGSLKNIGHTQAA 387

QY 836 AGVGGVIVKVMALREGVLPRTLHVDPKPSQVDWSAGAVRLLTEAVPWPQDAAAGRLRAGV 895
DB 388 AGVSGVIVKVMQAMHGVLPKTLHVERPTQVDWSAGAVELLTEAMDWPKDGGGLRAAV 447

QY 896 SSGIGIGTNAHVILEAPAGCGVAGGVLEGAPGLAISVASSAAAPVAVSAPVAVSVPV 955
DB 448 SSGVSGTNAHVIVLEAPA-----AETPASEATPA 478

QY 956 PVPVP-----VPPVPSARSAGLRAOAEALROYVAVRDPVSLADVGA---GLACGRAVLEH 1008
DB 479 VEPSVAGVLPVLSVAKTTPAALDAQIGRLAAP-ASQGRTDADPGAVARVLAGGRAEFHEH 537

QY 1009 RAVVLAADREELVQGLGA---LAAGEPDRRTVTGHPAGCDRGGVVFPVFPQCGQWAGMGV 1065
DB 538 RAVVLGTGDDFAALTAPEGLIRGTP-----SDVGRVAVFPVFPQGTQWAGMGA 586

QY 1066 RLLASGFPVARRMQACEALAPWDSVVDIILRRDAGDAVWERADVQVPLFSVMVSLAA 1125
DB 587 ELLDVSKEFAAAMAECEALSRYVDWSLEAVVRQAFGAPTLEKRVVDVQVPTFAVMVSLAK 646
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1126 LWRSYGIBPDVAVLGHSGEIAAAHVCGALSCLKDAAKTVALRSALAA--VRGCGMASVPL 1184
DB 647 VMOHGVTPQAVVGHSGEIAAAHVAGALFLDDAARVVTLRSKSTAAHLAGGGMISAL 706
QY 1185 ----PAQVEVEQIGERWAGRLWVAAVNGPRSTAVSGDAEAVDEVILAYCAGTGVARRIPV 1240
DB 707 SEEATRQRIENLHG-----LSIAAVNGPTATVSGDPTQIQELAAQACEADGVARRIIPV 760
QY 1241 DYASHCPHVQPIREELLEGDISPOPSGVFPFSTVEGTWLDTTTLDAAVYRNHLHQVPR 1300
DB 761 DYASHSAHVETIESELAELVLAGLSPTPEVPFSTLEGAWITEPVLDTGTWYRNLRHVG 820
QY 1301 RSDAVQALA-DDGHRVFEVSPHPTLPAIEDTETDTEADVTAGSLRRGDDNTRRFLTA 1359
DB 821 FAPAVETIATDEGFTPIEVSAPVLTWLTPE-----VTGLTLRRQGGQRLVTS 873
QY 1360 LAHTHTTGIG-----TPTTWHHHYTHHHHPHPTHLDLPTYPFHQHWLWLESSQPGAG 1413
DB 874 LAEAWTNGLTIDWAPVLTATGH-----HPELPTAFAORRHVWLHDSPAVQG 920
QY 1414 SGSGAGAGSGAGSGRAGTAGTAESREFWDAVARODLETVAATLAVPPSAGLDTVPAL 1473
DB 921 SVQ----- 923
QY 1474 SAWHRHQDQARINTWYQETWKPLTLPTTHOP---HQTWLIATPETOTHHPHITNLTN 1530
DB 924 -----DSWRYRIDWKRLAVADASERAGLSGRWLWVVEDRS--AEAAPVLA 968
QY 1531 LHHGITPIPLTNHTNTPQHLLHHTHTRQQAQNHHTGATGLLSLLALDETTPHPHP 1590
DB 969 LSGAGADPVQLDV-----SPLGDRQRLAATLGEALAAAGGAVGVLSLLAWDESAPGHP 1023
QY 1591 HTPPT-GTLLNLTLTQTHPTPLWATNTATTHHPNDPLTHPTQATWGLARTLLE 1649
DB 1024 APFTRGATLTLVQALEADAGVAAELWCVTGAVSVGRADHVTSPAQVMWGMGRVALE 1083
QY 1650 HPTHTAGIIDLPTTPTHTLQHLTQTLQPHHOTQLAIRTTGTHRRRLTPTTLTTHOPP 1709
DB 1084 HPERWGGHIDLPDSADRAALDRMTVLAGGTGEDOVAVRASGLLARRLVASL-PAHGT 1142
QY 1710 TP--TPHGTTLTGCTGALATHLTHLTHHTHPTQHLHLSRTGPH---TPHAQH----- 1758
DB 1143 SPWQADGTVLVTGAEEPAEAAARLARDGAGHLLHTTPSGSEAGETSAAEDSGLA 1202
QY 1759 -LTTLQOQKQHLTITTCOTSNPDQOLQQLNTIIPQHPLTTVIHTAGLDDATLNLPT 1817
DB 1203 GLVAELADLGAATVVTCTDLTDAEAAARLLAGVSDAHLPLSAVLHLPPTVDSPLAATDAD 1262
QY 1818 QLNNVLRKAKSAHLLHOLTQHTPLT-----AFVLYSSAAATFGAPQANAAAAYLDA 1872
DB 1263 ALARVVTAKATAALHDLRLREAAAGGPPVPLVLFSSVAALWAGGAGQAYAGTAFDA 1322
QY 1873 LAHHRHTHLLPATSTAWGTWONGLADSKARAYLDRGPRPMSPELATAVTOAI--AD 1930
DB 1323 LAGQHRADGPTVTSVAMSPWEGSRVTEGATGER-LRRLGLRELAATALTALDHALGHD 1381
QY 1931 TERPVVVIADIDWSKIE---HTSQTSDLVSAAREPAP--QRPTPPAE---LHKTILAHQ 1982
DB 1382 TA---VTIADVWSSFAFGFTTAREPTLADLPEARARLDEQQSTTAADDTVLSELGAL 1438
QY 1983 TSADORAALLELRDVAALRHADPKAIPDOSFRALGFDLSLTAVERFNLLIKATGLRL 2042
DB 1439 TCAGEQRQRMQELVREHLAVLNHPSPEAVDTGRAFRDLGFSLTAVELNRNLKNATGLAL 1498
QY 2043 PVSIVDFDHTPAKLAVHLQNLQRTAESAAPSAAAVTAESV-TEPIAVGMACRPPGCV 2101
DB 1499 PATLVDFYPTPRTLAEFLAEILG---EQAGAGEQLPVDGGVDDPEVAIVGMACRLPGCV 1555
QY 2102 TSADDFWDLISSEQDAIGGFTDRGWLDLTYDDPDHPGTCYTRNGGFLYDAGHFDADF 2161
DB 1556 ASPEDLWRLVAGGEDAISGFPQDRGWGVEGLYDDPDPAASGRTYCRAGGLDEAGEFDAF 1615
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Qy	2162	FGISPREALAMDPOORLLELTETAMETIIEHAGINPHUHLHGTTGVTPTGNTGNYQDYALURVHNAG	2222
Db	1616	FGISPREALAMDPOORLLELTETAMETIIEHAGINPHUHLHGTTGVTPTGNTGNYQDYALURVHNAG	1675
Qy	2222	QSTDGFALJTGAGSVISGRISYTFEGFEGPAVSVDVDTACSSSLVALHLACQALRAGECSMAL	2281
Db	1676	EDLEGYVGTGNAASIMSGRVSYTLGLEGPVTVTDVDTACSSSLVALHLAVQALRKECGCLAL	1735
Qy	2282	AGGVTVNSSPGAFVFEFSRQRGLAADHCKAFSAAADGTGMGEGVGMLLVERLSDAHRNGH	2341
Db	1736	AGGVTVNSTPTTFVFEFSRQRGLAEDGRSKAFASASADGFGPAEGVGMLLVERLSDAHRNGH	1795
Qy	2342	RVLAVRGSVAVNQDASNGLTAPNGPSQORVIRLOALNAGLSAGDVDAVEAHGTGTTGLD	2401
Db	1796	RVLAVRGSVAVNQDASNGLTAPNGPSQORVIRRALADARLTTADVDVVEAHGTGTTGLD	1855
Qy	2402	PIEAQALLATVYGODRAGEGPELWLGVSXKSNVCHTQAAAGVAGVTKMVMALRHGLLPRTLHV	2461
Db	1956	PIEAQALIATYQGRDTEQPLURLGSLKSNIGHTQAAAGVSGIITKMVMQRHGVLPKTLHV	1915
Qy	2462	DEPSPHVDWSAGAVQLLTETVPWP--GGEGRLLRAGSVSGFVSGTGNHVIILEEAPAD--DVP	2519
Db	1916	DRPSDQIDWSAGTVYELLTEAMDMWRKQEGGLRRAAVSSFGISGTNAHIVLEEAPVDEBAP	1975
Qy	2520	GGPPAGSGDDDEAAAGSFGVWPMVLVSAKSPALRAQAAQLHAHUTDHPGLDLAD---	2576
Db	1976	A-----DEPSVG--GVVPMVLVSARKTPAALDAQIGRL--AAPASQGRDAAADPGA	2020
Qy	2577	VGTYLAHARAVFDHRAATLIAADRDTFLQALQALAAEGFHPAVIHSAPGG--TGTGEAAG	2634
Db	2021	VARVLAGRAQFHEHRAVLTGQDDLAAL-----AAPEGLVRGVASGVG	2065
Qy	2635	KTAFICSGQGTQRPGMAHGLYHTHPVFAAALNDICTHLDPHLDPLPLTLNDNDNEDA	2694
Db	2066	RVAVFPGQGTOWAGMGANELLDVSKFEPAAWAECEALAPYDWSLEAVRQ-----APG	2120
Qy	2695	AALLQOTRYAQPALFAFOVALHRLLLTDGYHITPHYHYAGHSLGETTAHAHLAGILTLTDATT	2754
Db	2121	APTLEIRVDVVQPVTFEAMVSLAK--VMQHGGVTPQAVVGVSGEITAAAVYAGALSLLDAAAR	2179
Qy	2755	LITQBATLM--QTMPPGCTMTTLHTTPHHITHHLTAHENDLIAAINPTPSLVSIGTPHTV	2812
Db	2180	VVTLRSKSIHAHLAQCGGMLSLASEAAVVERLAGFDG--LSVAAVNGFTATVVGSGDPTQI	2238
Qy	2813	QHITTLCCQOQIKTKTLPTNHAFSHPNTPINLQHQHTQTLTVHPHPTPLITA-----N	2867
Db	2239	QELAAQACEADGVRAIIPVDYASHASARVETIESELADVLAGLSPTQVQFVFTLEGAWI	2298
Qy	2868	TPPDQLLTPHYWTOQARTVDYATTTQTL--HQHGVTYIIELGPDNTLTTLTHNLPNPPT	2926
Db	2299	TEP--ALDGGVYRNLRHRVGFAPAVETLATDEGFTHFVEVSAHPVLTMA---LPETVT	2352
Qy	2927	TTTLTTPHHPHPTHLTLNLAKT-----TTTTWHPHYTHDNQPHTHLTLDTLPTPQHH	2981
Db	2353	GLGTLRR--DRNGQHRLLTSLAEAWANGLTVDW-----ASLPTTTTHPDLPYAFQTE	2404
Qy	2982	HYMLESQPCAGNVSAAGLDPTBHPHLLGATLELATDGCALLAGLSLRSHHPMLADHAVGG	3041
Db	2405	RYWPQDPLSAAGDITSLAGLNAEHPHLLGAVALADSOGCLTSGSLURTHPMLADHAVAG	2464
Qy	3042	TVLLSGATFLLEALHAGTYCGDRVDEBLTLHAPLVVPVDDGVSVQVGAADAGEGRRLVS	3101
Db	2465	TVLLPGTAFVELAFRAGDQVGCDDLVEBLTLDAPLVLPRRGAVRQLSVGASDESGRRTFG	2524
Qy	3102	VYARGSGACGGGASGGWVWTHCHASGVLEAAAGVVVDGLAGV-----WPRGVAIVDVD	3156
Db	2525	LYAHPEDAPG-----EAEWTRHATGVLAARA-----DRTAPVADPEAWPPGAEPEVDVD	2573
Qy	3157	GVDRLAGACVCLGPFVPSGLRAVMRDCGDLLEAVCLPEEAWG--DAECFGHLHPALLDGVQ	3215
Db	2574	GLYERFPAANGYGYGLFCQVGRVWRRGDEVPADVALPAEVAGAEARFGLHPLALLDAAVQ	2633
Qy	3216	PLSVLLPGCTGCFGSGAGFGBGVVPVAVMGVGSVLLHRAGVTGVRVRSVAVRGGGCREAVSVV	3275









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Db 1499 PATLVFDYPTFRTLABFLAAILG---EQAGAGEQLPVDGVDDEPVAIVGMACRLPGGV 1555
Qy 2102 TSADDWDLISSBQDAIGPPTDRGMDLDTLYDPDPDPCTCYTRNGGFLYDAGHDEAP 2161
Db 1556 ASPEDLWRLVAGEDAISGFPQDRGMDVEGLYDPDPDASRTYCRAGGFDEAGEFDADF 1615
Qy 2162 FGISPREALAMPQORLLLETAWETIEHAGINPHTLHGTPYFTGTNGQDYALRVHNAG 2221
Db 1616 FGISPREALAMPQORLLLETSEAVEADAGIDPSTLQOQGVGFAGTNGPHYEPPLRNATA 1675
Qy 2222 QSTDGALCTAGSVISGRISYTFGEGRAVSVDTACSSSLVALHLACQALRAGESMAL 2281
Db 1676 EDLEGVGTGNAASINGRVSXYTLGLEGPAYVDTTACSSSLVALHLAVQALRKEGCGLAL 1735
Qy 2282 AGGVTVMSPPGAFVFSRORGLAADGCKAFSAADCTGMGEGVGLMLVERLSDAURNGH 2341
Db 1736 AGGVTVMSPTTTFVFSRORGLAEDGRSAFASADGFGPAEGVGLMLVERLSDAURNGH 1795
Qy 2342 RVLAVRGSANVDGASNGLTAPNGPSQQRVIRQALANAGLSAGDVDAVEAHGCTGTLGD 2401
Db 1796 RVLAVRGSANVDGASNGLTAPNGPSQQRVIRRALADARLTADVDVVEAHGCTGRLGD 1855
Qy 2402 PTEAQUALATYGODRAGEGLMHLGVSXNVGHTQAAAGVAGVIXMWMALRHGLLPTLHV 2461
Db 1856 PTEAQUALATYGODRTEQPLRLGSLKSNIGHTQAAAGVSGIIMVQAMRHGVLPTLHV 1915
Qy 2462 DEPSPHVDVSAGAVOLLTETVWP - GEGRLRAGVSSFGVSGTNAHVILEAPAD - DVP 2519
Db 1916 DRPSDQIDMSAGTEVILLTEAMDPKQEGGLRRAVSSFGISGTNAHVILEAPVDEBAP 1975
Qy 2520 GGPAGEGDAGSDEAAAGSPGVMPLVSAKSQPALRAQAALHAHLTDHPGLDLAD --- 2576
Db 1976 A-----DEPSVG - GVPVPLVSAKTPAALDAQIGRL - AAFASQGRDTAADPGA 2020
Qy 2577 VGYTLAHARAVPHRATLIAADRDTPLOALQALAGEPHPAVHSSAPG - TGTGEAAG 2634
Db 2021 VARVLAGGAQFHRVALVAGTGQDDLAAL-----AAPEGLVRGVASGVG 2065
Qy 2635 KTAFCISGQGTQRPQMAHGLYHTHPVFAAALNDICTHLDPHLPLLLTQNDNEDA 2694
Db 2066 RVAFVFPQGTQWAGHGAELLDVSKFEFAAMACEAALAPYDWSLEAVRQ-----APG 2120
Qy 2695 AALLQOTRYAQPALFAFQVALHRLLTGYHITPHYAGHSLGEBITAAHLAGILTLTDATT 2754
Db 2121 APTLERVDVVPVTFVAVMVSIAK - VMQHGVTFQAVVGHSGQGEIAAAYVAGALSLODAAR 2179
Qy 2755 LITQATLM--QTMPTGTMTLTHTPHHITHHLTAHENDLAIAAINTPTSLVSGTPTHV 2812
Db 2180 VVTLRSKISGAHLAGOGGMLSLALSEAAVVERLAGFDG - LSVAAVNGPTATVVSQDPTQI 2238
Qy 2813 QHITTLCOQOQIKTKLPTNHPHSPHTNPILNQLHQHTQTLTYHPHPTPLITA-----N 2867
Db 2239 QELAQACEADGVARAIIPVDYASHSAHVETIESELADVLAGLSFQTPQVPPFFSLSGAMI 2298
Qy 2868 TPDQDLTHPHYTQOQARNTVDYATTTQTL - HORGVTTYIELGPDNTLTLTHNLNPNPT 2926
Db 2299 TEB - ALDGGYWRNLRRHRVGPAVETLATDSEFTHFVEVSAHPVLTWA-----LPETVT 2352
Qy 2927 TLTTLTHPHHPOTHLLTNLAKT-----TTTHPHPHYTHHDNOPHTHLLDTPYFQHH 2981
Db 2353 GLGTLRR - DNGGQHRLTTSIAEWANGLTVDM-----ASLLPTTTTHPDLPTVAFQTE 2404
Qy 2982 HYWLESTQPCAGNVSAAGLDPTSHPLLGATLELATDGGALLAGRLSIRSHPLWADHAVGG 3041
Db 2405 RYWPQDLSNAGDITISAGLGAEBHPLUGRAVALADSDGCLLTGSLRTHPLWADHAVAG 2464
Qy 3042 TVLLSGATFLELALHAGTYVGCDDRVDELTHAPLVVPDGGVSVQVGAADGEGRLVS 3101
Db 2465 TVLLPGTAFVELAFRAGDQVGCCLVEELTLDAPLVLPFRGAVRVQLSVGASDESGRTFC 2524
Qy 3102 VYAGGSACGGGASGVWTCASGVILVEAAAGVVVDGLAGV-----WPPRGAVAVDVD 3156

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Db 2525 LYAHPEADAPG-----EAEWTRHATGVLAARA-----DRTPVADPEAWPPGABEPVDVD 2573
Qy 3157 GYVRDLRAGACCVLPGVFSGLRAVWRDGGDLLEAECVLPBEEAWG - DAAGFGLHLPALLDGVVQ 3215
Db 2574 GLYERFANGYCYGGLPFGVRCVWRGDEVFADVALPAEVAGAGARFGLHLPALLDAAVQ 2633
Qy 3216 PLUSVILLPGGTGFGGAGFGGEGVVRVPAVMGCVSLHRLAGVTGVRVRVSAGVGGGREGREAVSV 3275
Db 2634 -----AAGAGRGVRGRHAAAVRLER-----DLLYAVGATALRVRLAP-----AGPDTVSVS 2679
Qy 3276 VGDEAGVPVASVDRLELRPDMGOLRAVSAGRRGSLYAVQW-----AEVGPVPVC 3327
Db 2680 AADSSQOPVFAADSLTVPDPAQAAAFSDPT - LDALHLEWTAWDGAQAALPGAVVLG 2737
Qy 3328 GQA-----WAMHEDVGES-----GGGPVPGVVVLRCPDAGAGGGGGGGGG 3368
Db 2738 GDADGLAALRAGGTEVLSFPDLTDLVEAVDRGETPAPATVLVACPAAGP-----DGPE 2791
Qy 3369 GYGEVVGVGVVQVQWGLGLERFAGRLVVVTRGAVVAGPEDGVPVVGASVMGLVRSQA 3428
Db 2792 HVREALHGSALMQAWLADERPTDGLRLVLTTRDAVAARSGLRSTGQAAVMGLGRSAQT 2851
Qy 3429 EHPDRPVLIDL-----DTDTGTDLTGACAGHGV-----GGRVAAVVACGEPQAV 3475
Db 2852 ESGPFRVLLDLAGEARTAGDATAGDGLTTGDTATVGTSGDAALGSALATALSGEPQAL 2911
Qy 3476 RGERLLAARLKE-----LES-----SGD - 3493
Db 2912 ROGALLVPLARAANAAPAADGLAADGLAALPLPAAPALWRLEPGTDSLESLETAAPGDA 2971
Qy 3494 ETLAPEPLGPGQVRIAIRATGLNFRDVLIALGMYPDPALMGTEGAGVVTATPGVTHLAP 3495
Db 2972 ETLAPEPLGPGQVRIAIRATGLNFRDVLIALGMYPDPALMGTEGAGVVTATPGVTHLAP 3031
Qy 3496 AQR-----SGDTAARSDVPA-----3511
Db 3032 GDRVMGLLSGAYAPVVVADARTVARMPEGTFAQASVPVFLTAVYALRDLADVKPGR 3091
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Db 3092 LLVHSAAGGVGMAAVQLARHWGVEVHGTASHGKWDALRALGLDDAHIASRTLDPESA 3151
Qy 3519 -----ARRSDVS-----3526
Db 3152 AASGAGMDVWLSLAREPVDASRLGLGPGRFVEMGKTDVRDAERVAADHPGVGYRAF 3211
Qy 3527 -----GREVLPHLS 3535
Db 3212 LGEAGPERIGEMLAEBVIALFEDGVLRHLPTVTWVRRARDAFRHVSQARHTGKVLTMPS 3271
Qy 3536 G-----GSVLVTGCTGVGLAAVARHLAGVCGVRDLLLLVSRGPDAPGAEGRLAEALGA 3591
Db 3272 GLDPGTVLUTGCTGALGGIVARHVVGWGVVRLLLVSRGGTDPAGAGELVHELEALGAD 3331
Qy 3592 VRIVACDVGERRREVRLLEGVPAGCPLTGVVHAAGVLDATTIASLTPERLGTVFAAKVDA 3651
Db 3332 VSAACDADREALTAVLDSIPAEPHPLTAVVHTAGVLSGTLPSMTAEDEHVHLRPKVD 3391
Qy 3652 ALLLDELTR--GMELSAFVLPSAAGILGSAGCGVYAAANAALDALAYRRRAAGLPGVSL 3709
Db 3392 AFLLDLSTPTGYDIAAFVYMFSSAAVFGAGQAGYAAANATLDALAMRRRTAGLPA 3451
Qy 3710 ANGLEEASGMTGHLAGTDHRRIRSGLHPMTDPDALALDPAALDRPVLPLPADLRPAP 3769
Db 3452 GMGLMAETSMTGGSLSDTDRSLRSGATPMOSELTLSLLDAMRRDDPALVPIALDVAA 3511
Qy 3770 -----PLPPLLOL-----LPATRRRTTRTTTTTGGG - DNGAQLHARLAGOTHEQ 3812
Db 3512 LRAQQRDGMGLA PLLSGLTRGSRVGGAPVQRR-----AAAGGAGEADTDLGGRLAAMT 3567
Qy 3813 QHTTLALVRSHIATVILGHTTTPDTPDRAPDGLDPDSLTAVELNRNRLSRTTGLRLPTTL 3872
Db 3568 RVAHLRLDLVRTHVATVILGHGTPSRVDERAFRDTGPDLSLTAVELNRNRLNAATGLRLPATL 3627

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Db 3837 RPVTIGRADAPQ-----PLXRVDMQPVGQGTASGAQGWTVLGOAAETVAQAAHAD 3889
QY 3337 VG-----ESGGPVPVGVVLRCPDAGAGG-----GGGGGGGVEVGVV 3378
Db 3890 LTAIRTAVAAGTFVPLRVVSVVDTRLDEGPVLDAEARAARAGDGDWDDPLRVALGRGL 3949
QY 3379 GUVQVGLGERFAGSLVVVTRCAVAGPDPVDDVVVGASVMSGLVRSQAQAEHPDRVLID 3438
Db 3950 TLVREWEDEBLADSLVLRITRGAAGPQDVP-DLITGAALWGLLSAQSEVPDRFTLID 4008
QY 3439 LDDTDTGDLDTGAGAGWGDGGRVAAVACG--EPQLAVRGERLLAARLKRLLESSGDVPA 3496
Db 4009 VDDSPES-----RAALPRALGSAERQLALRTGDLAPALVPMATR--PA 4050
QY 3497 QRSQDTRARRSDVPAQRSGGVPARRSVDSGRVLPWLSGGSVLVITGGTGVLGAAVARHL 3556
Db 4051 ETTPTATAVASATTQTQVTPAPDDPAADA-----VFDPAQTVLITGGTGALGRRVASHL 4104
QY 3557 AGVCGVRDLLLLVSRGPDAPAGBLRAELAAALCAEVRIIVACDVGERREVRVRLLEGVPACG 3616
Db 4105 ARRYGVHRMLLVSRGPDAPAGPLERELAGLVGTATFLACDLDTEAVRKAAVAVPSDH 4164
QY 3617 PLTGVVHAAGVLDATIASLTPERLGTVFAAKVDAALLLDLDELTRGMELSAFVLSAAGI 3676
Db 4165 PLTGVVHTAGVLDGALTGITRQRLDTVLRPKADAVENLHEATLDRPLRAFVLFSAAAGL 4224
QY 3677 LGSAGQGNVAAANAALDALAYRRRAAGLPCVSLAWGLWBEASQWTHLGTDRHRIIRSG 3736
Db 4225 LGRPGQASAAAANAVLDALAGARRAAGLPAVSLAWGLWDEQTMAGGLDEMALRVLRDGG 4284
QY 3737 LHEMSTPDALALDFAALDOR-----PVLL-----PADLRPAPPLPPLLQDILLPAT 3782
Db 4285 IAMPPEQGLELLDLALTGHRDGPVAVVPLLLDGAALRTAKERGAHTWSPLRLALPPAA 4344
QY 3783 RRRTRTTTGG-----ADNGAQLHARLAGOT---HEQQTTLTALVRSHTA 3826
Db 4345 LRR-----SGGAGAPAAADRHCKEADPGA---GRLAGVVALEAERSAAVLELVTEQVA 4395
QY 3827 TVLGHPTPTDTPDRAFRDLGFSLTAVELRNELSTTGLRLPTTLAFOHPNPTTLTHL 3886
Db 4396 EVLGYASAAIEPERFPEIGVDLSAAVELRNLSRLVGLRLPTTLFSFDHPTPKDMAQHI 4455
QY 3887 HTLOQPQPNAPVLAELD---KLSALSALDKTDSASERVTLRLKSLMLRNAPQH-- 3941
Db 4456 DGQL-PRPAGA-SPADAALLEGICGLARAVALLGTGDARAEVREQLVGLLAALDPPCPTG 4513
QY 3942 ---PTAESADD-----DEKFTSATEAEIFKPIDNDL 3969
Db 4514 TRAPGVPSGADGAEPVTDRLDEATDDEIFAFLEQL 4550
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## RESULT 12

```
US-08-804-198-2
; Sequence 2, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
; APPLICANT: Burgett, Stanley G.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rao, Nagaraja R.
; APPLICANT: Richardson, Mark A.
; APPLICANT: Rostek, Paul R., Jr.
; TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL R. CANTRELL 1138
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4550 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-198-2
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Query Match 33.3%; Score 6941.5; DB 2; Length 4550;  
Best Local Similarity 41.0%; Pred. No. 0;  
Matches 1760; Conservative 450; Mismatches 1496; Indels 591; Gaps 101;

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QY 13 AAGEVLG---VADEADGGVVFVPGQGPQWPCMGRELLDASDVFRSVRACEAPAPYVD 69
Db 505 AAGRVSQGVSRGAVPGGVVLTGCGAQWVGNGRGLVAGGCVFAEVLDEVLSMGEVDG 564
QY 70 WSEVQVLRDSDPAG-----LDRVDVVQPTLFAVMISLAAL 105
Db 565 RSLRDMFGDVEDVDAGADAGAGAGVSGSGVGLGRTERFAQPALFALEVALFRA 624
QY 106 WRSQVEPCAVLCHSLGEIAAAHVSGLSLADAAARVTLWSQAQTTLAGTALVSVAATP 165
Db 625 LEARGVEVSVVLGHVSVEVAAAYVAGVLSLGDVAVLWARGLMGGLPVGGGKWSVGASE 684
QY 166 D---ELLPRIAPTWEDNPARLAAVAVNGPRSTVWSGAREAVADLVADLTAAQVTRMIPV 222
Db 685 SVVRGVVEGLGEM-----VSVAAVNGPRSVVLSGDVGLSVVASLMDGVECRLDV 737
QY 223 DYPAPSLPMYAI--BER-VVSGLLPITPRPSRIPHSSVTGRLDPTREL-DAAYVNRNMS 278
Db 738 SHGFHSVLMEPVLEGRFVGSLEFRVRPG-VVVVSVSGVSGVSGELGDPGCVVVRHAR 796
QY 279 STVREPAARLLQQGPKTFVEMSPHVLTMGLQELAPDLGTTGTADTVIMGLRRGOG 338
Db 797 EAVRFADGVGVVRGLVGTVLVEVGHVLT-GMAGECLGAGD-----DVVVVPAMRRGRA 850
QY 339 TLDFHFLTSLAQL--RGHG-----ETSAT-----TVLSARLTALSPQQOQLLID-- 380
Db 851 EREVFEALATVTRDAGLDATALHTGSTRIDLPYFPQRTHWSPALSPVTDAGA 910
QY 381 -----LVRHAHTMAVLNDGG 394
Db 911 GVTATDAVGHVSVPDPESTEGTSHRDTDDDEASGPEPMSPEDAVRLVRESTAAVLGHDD 970
QY 395 NERTASDAGPSASFAHLGSDSVNGVELNRNLSKATGLRLPVTLIIFDHTTAAVAARLRTA 454
Db 971 PGEVALD-----RTFTSQGMDSVTAVELCDLLKGASGLPLAATLVLYDLPTRPRAVHIVA 1026
QY 455 ALGHLDE-----DTAPVPDPSGHHGTAADDPALIIIGMACFPFGVGRPKDLWELA 506
Db 1027 AGCPKDSVAGGPGVLSAAVGV-S-DARSGSRDDDDPIALVGVCRLLPGGVDSRAALWELL 1085
QY 507 ASGSDAIGFPPTDRGWPTQRHAQDPTQGTYPQGGFLHDAHFDAGFFGISPREALA 566
Db 1086 ESGADAISFFPTDRGWLDGLYDPEGTPGKTVYREGFLHSAABFADAEFFGISPREATA 1145
QY 567 MDPOQRLLLETWEAFERAGIDPLSVRGSRTOVFAGALSFDYGPMDTASSGAADVEGH 626
Db 1146 MDPOQRLLLEASWEALDAGVLPESLRGGDAGVFGVATAPYEGPRL-----HEGADGYEGY 1201
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Db 3205 GVFAEVLDEVLVVG-EVDGSRSLRVNMFADADSV-LGGLIGRTFPAQPALFALEVALFRA 3262  
Qy 2719 LTDGYHITHYAGHSGETAAHLAGILTLTATTLITQATLMQTMP-PGTMTHLHT 2777  
Db 3263 L-EARGVEVSVLGHVSVEVAAYAGVLSGLDAVRLWARGLMGLPVGGMWVGAS 3321  
Qy 2778 PHHITHLTAHENDLAIANTSLVISGTHVQHTTLTCCQOQIKTKTLPNTNAPHS 2837  
Db 3322 ESVVGVGEGLGEMWSVAANGPRSVLSGDUVGLSVVVVTLMGDGVCCRLLDVSHGPHS 3381  
Qy 2838 PHTNPILNQLHQHTQTLTYHPHTPLITAN-----TPPDQLTPHYWTQQAQNTVDYAT 2891  
Db 3382 VLMEPLVGEPRGVVSEFGRVPGVWVSGVSGVGVGSGELGDPGVWVRHAREAVRFAD 3441  
Qy 2892 TTQTLHQHGVTTVIELGPDNTLTTLTHNLNPNPTTLTTLTHPHHPOTHLLTNLAKT-- 2949  
Db 3442 GVGVRGLGVTLVGVPHGLTGMAGQCLEAGDDVVVPMRGRPEREVFEALATVF 3501  
Qy 2950 -----TTTWHPHYTHHDNQPHTHLDLPTYPFQHYYHYLESTQPGAGNVSA--G 2999  
Db 3502 TRDAGLDATLH-----TGSTGRRIDLPTYPFQHNRYWATGVTGATGTSAAARFG 3552  
Qy 3000 LDTEPHLIGATLELATDGCALLAGRLSLRSHPWADHAGVGVVLSLGSATFELALHAGT 3059  
Db 3553 LEWKDHPFLSGATPIAGSGALLTGRVGLAAHPWADHAIISGTVLLPGTAIADLLRAVE 3612  
Qy 3060 YVGCDDVDELTHAPLVVVDGVSQVGVAAADGGRRLVSVYARGSGACGGGASG-- 3117  
Db 3613 EVGAGGVEELTHPELPLPERGGLHVQVLVEADEQGRRAVAARP-----EGPGRDGBE 3668  
Qy 3118 GWTCHASGVLVEAAGGVVVDGLAGVWPPRGAVAVDVGDRDLRAGAGCVLGPVFSGLR 3177  
Db 3669 QEWTRHAEGVLTSTETAPDMGMWAGAWPPGGAEPIDVEELYDAFADGVGYGPATALS 3728  
Qy 3178 AVNRDGGDLIAEVLCPPEEAWGDA--GFGHLPALLDGVVQPLSV--LLP--GGTGFGGAG 3232  
Db 3729 GWRGLDELFAEVRPAGAGTGTGDFGVHPALFDAALHPWRAGGLLPDTGGTTW----- 3783  
Qy 3233 FGSVVRVPAVMGVSLHRAAGTVTVRVSVAVGRRGGRVAVVVGDEAGVPVASVDRL 3292  
Db 3784 -----APFSWQIALHTTGAETLVRVL--APAAGGTESAFSVOAADPAGTPVLTDLALL 3836  
Qy 3293 RPVDMGQLRAVSVSAGRRSLYAVOWAEVGPVPCQAWAW-----HED 3336  
Db 3837 RPTVLGRADAPQ-----PLYRVDMPQVQGTEASGAGTWTVLGQAAAEVTAQPAAHAD 3889  
Qy 3337 VG-----BSGGPVPVGVVLRCPDAGAGG-----GGGGGGGVGVGVVGV 3378  
Db 3890 LTALRTAVAAAGTVPVRLVVPVSPVTRLDGPPVLADAEARAGAGDGDWDDPLRVALGRGL 3949  
Qy 3379 GVVQGLGLERFAGSLVVVTRGAVVAGPEDGPDVVGVASVGLVSAQAEHPDRFVLDD 3438  
Db 3950 TLVREWEDELRADSLRVLVTRGAVAGPDVP-DUTGAALMGLLSAQSEYPPDRFTLLD 4008  
Qy 3439 LQDTQTLDTGAGAGWVDGGRVAAVACG--EPQLAVRGERLLAARLKRLLESSGDVPA 3496  
Db 4009 VDDSPES-----RAALPRALGSAERQALRTGDVLAPALVPMAIR--PA 4050  
Qy 3497 QRSGDTRARRSDVPAQRSGVPARRSVDSVGRVLPWLSGGSVLVTGGTGVIGAAVARHL 3556  
Db 4051 ETTPTATAVASATQTQVTAAPADPPAADA-----VFDPAQTVLITGGTCALGRVRVASHL 4104  
Qy 3557 AGVCGVRDILLVSRRGPDAPGAGRLAEALAEVRIIVACDVGERREVRLLGVPACC 3616  
Db 4105 ARRYGVRRHMLVSRRGPDAPAGPLERELAGLVGTATFLACDLTDEAVRKAAVAVPSDH 4164  
Qy 3617 PLTVGVHAAAGVLDATIASLTPERLCTVFAAKVDAALLDDELTRGMELSAFVFSAAGI 3676  
Db 4165 PLTVGVHTAGVLDGALTGTRQLDVLRLPRKADAVRNLEATLDRPLRAFVLSAAAGL 4224  
Qy 3677 LGSAGCGNTAANAALDALAYRRRAAGLPGVSLANGLWEEASGMTGHLGTHRRRIIRSG 3736  
Db 4225 LGRPGQASVAAAANAVLDLAGARRAAGLPAVSLANGLWDEQTMAGGLDEMALRVLRRDG 4284

Qy 3737 LHPMTSPDALAFDAALADR-----PVLL-----PADLRPAPPPLPQLDILLPAT 3782  
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Qy 3783 RRRTRTTTGTG-----ADNGAQULHARLAGOT---HEQQHTTLLALVRSHIA 3826  
Db 4345 LRR-----SGCAGAPAAADRHRGKEADPGA---GRLAGMVALEAAERSAAVLELVTEQVA 4395  
Qy 3827 TVLGHHTTPTTIPDRAFRDLGFDLSITAVELNRNLSRTTGLRLPTTLAEPHNPPTTLTHHL 3886  
Db 4396 EYLGVSAAAEIPEPRFEIGVDSLAARELNRNLSRLVGLRLPTTLSPDHPPTPKMAQHI 4455  
Qy 3887 HTLOPOPDNAVAPVLAELD---KLESALSALDKTDSASERTVLRKLSMLRWNAPOH-- 3941  
Db 4456 DQQL--PRPAGA--SPADALEGIGDLARAVALLGTGDARAEVREQLVGLLAALDPPGRTG 4513  
Qy 3942 ---PTAESADD-----DEKFTSATEABIFKIDNDL 3969  
Db 4514 TAAPGVPSGADGAEPVTVDRLDEATDDDEIFAFLDEQL 4550

## RESULT 13

US-09-428-517-2  
; Sequence 2, Application US/09428517  
; Patent No. 6251636  
; GENERAL INFORMATION:  
; APPLICANT: Betlach, Mary C.  
; APPLICANT: Shah, Sanjay Krishnakant  
; APPLICANT: McDaniel, Robert  
; APPLICANT: Tang, Li  
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 30062-20029.00  
; CURRENT APPLICATION NUMBER: US/09/428,517  
; CURRENT FILING DATE: 1999-10-28  
; EARLIER APPLICATION NUMBER: 60/120,254  
; EARLIER FILING DATE: 1999-02-16  
; EARLIER APPLICATION NUMBER: 60/106,100  
; EARLIER FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4150  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant  
; OTHER INFORMATION: Oleandolide PKS  
US-09-428-517-2

Query Match 33.2%; Score 6912.5; DB 4; Length 4150;  
Best Local Similarity 40.9%; Pred. No. 0;  
Matches 1685; Conservative 447; Mismatches 1328; Indels 655; Gaps 89;  
Qy 8 BEPRPAAGEVLGVADEAD-GGVVFVFPQGPQGPQMGRELLDASDVRESV-RACE- --- 61  
Db 541 ENGLPAPQVLLGRTTTPPEGLAFLFSGGSOQPGKXELHQVFPGRDALDEVCAELDT 600  
Qy 62 ---AFAFPVDMVSVEQVL---RSDPADGLDRVVDVQPTLFAVMISLAALMRSQGVPC 115  
Db 601 HLGRLLGPEAGPLRDMVFAERGTASHALLSETHYTAALFALETALFRLVQWGLKPDH 660  
Qy 116 VLGHSLGETAAHVSGGSLADAAARVVTLSQAQTTAGTGTALVSVAATPDPELLPRIAPW 175  
Db 661 LAGHSVGEIAAAHAGIIDLSDAELVATRGALMRSPLCGGVNLSVQAPES- ----VAPL 716  
Qy 176 TEDNPARLAAVAVNGPRSTVWSGAREAVADLVADITAAQVTRMRI PVDVPHASPLMYALE 235  
Db 717 LLGREAHVGLAANGPDAVVVSGERGHVAAIEQLRDRGRKSRVLRVSHAFHSPLEPVL 776  
Qy 236 ERVVGGLPITPRPSRIIPFHSVVTGRLDTRRL-DAAYWYRNMSSTVRFEPAPARLLQOG 294  
Db 777 BEFAEAVAGLTFRAPRTTTLVSNLTGAPVDDRTMATPAYWVRHVREAVRFGDGIRALGKLG 836



2837 LADAGLAPADVVEAHGTRGLDPIEAQALLATYGQRTSGRPWMLGSVKSNIGHTQA 2896  
2437 AAGVAGVVKWMAIRGLLPRTHLVDEPSPHVDWSAGAVOLLTETVPWEGGEBRLRAGV 2496  
2897 AAGVAGVVKWMAIRGLLPRTHLVDEPSPHVDWSAGAVOLLTETVPWEGGEBRLRAGV 2955  
2497 SFGVSGTNAHVITLBEAPADDDVPGPPAGEGDAGSDDEAAAGSPGWMLVSAKSQPALR 2556  
2956 SFGVSGTNAHVITLBEAPADDDVPGPPAGEGDAGSDDEAAAGSPGWMLVSAKSQPALR 3002  
2557 AQAQALHAHLTHDPGLDLDADVGTYLHAHARAVDFHRAATLFAADRTDPLQALQALAAAGEPH 2616  
3003 AQAARLAHVSS--TGAGVVDVGVMSLVAITRSVFEHRAVMTGLDLSMAGSLAGFAAGVVP 3061  
2617 AVTHSSAPGCTGEAAG--KTAFCISGQGTQRPMAHGLYHYPVFAALNDICTHLDHP 2675  
3062 GVVSGVAP-----AEGRRVVFVFPQGSQWVMAAGLLDACVFAEAVAECAAVLDRL 3114  
2676 LDHPLPLLTQNDNDNEDAAALLQOTRYAOPALFAFOVALHRLTLDGYHITHYVAGHSL 2735  
3115 TGWSLVEVLRGGE-----AVLGRVDVVQPALWAVMWSLARTWR--YGVVEPAVAVGHSQ 3166  
2736 GEITAAHLAHLTLDATLITQRA--TLMQTPMPGTMTLTTPHHITHHLTAHENDLAI 2794  
3167 GEIAAACVAGGLSLADGARVWLRSRAIARIAGGGGMSVGLSAERVRTMLDTYGGRSV 3226  
2795 AINTPTSLVISTPHTVQHIITLCOQGIKTKLPTNHAHPSHTNPLNQLHQHTQL 2854  
3227 AAVNGPSSVWSGDAQALDELLAGCEREGVRARRVVDYASHAQMQLRDELLEALADV 3286  
2855 TYHPHTPL--ITANTPPDQLTTPHYTQOARNTVDYATTQTTLHQHGVTVYIELGPDN 2911  
3287 TQDSSVPFSTVADWLTOTDADAGYFTNURVETVFOEAGVGLVQAQMGAPVECSHP 3346  
2912 TLTTLTHNLPL--NPPTTLTTLTHPHHPQTHLLTNLAKTTTTHPHHYTH--HNOQHT 2967  
3347 VLVPGITETLTDADAVALLSLRDEGGLDRFLTSIAEAFVQGVVVDWTHAFEGRPR- 3405  
2968 HTHLDLPTVPFQHHVHLESTOPGAGNVSAAGLDPTHEPLLGLATLELATDGGALLAGRLS 3027  
3406 --FVLDLTYAFORQRYLH----- 3422  
3028 LRSHPLADHAVGGTVLLSGATFLELALHAGTVGCDRVDLTHAPLVVPVDDGGVSVQV 3087  
3423 -----EFPLOEPVD----- 3431  
3088 GVAADGEGRRILSVYARGSGACGGGSGGVWMTCHASGLVVEAAAGGVVVDGLAGWVP 3147  
3432 --EAWDAE--FWSVVERG----- 3445  
3148 RGAVAVDVGDRDLRAGACVLPVPSGLRAVWR-----DGGDLAEVCLPBEAWGDAQF 3203  
3446 -----DATAVSDLLSTDAEALHTVLPLALSS--WRRRVEHRL-----QDMRYRVEW 3490  
3204 GLHPALLDGVQPLSVLLPGGTGFGAGFGEVVRVPAVMGVSGLHRAAGTVGRVRSVAV 3263  
3491 KPFPALDEV-----LGGWLVFVVRGLADD-----GVV-ARVVAATV 3527  
3264 GRGGREAVSVVVGDEAGVPVAVSDRLRLPVDMLQRAVSVSAGR--RGSLYAVQW--- 3318  
3528 ARGG--EVSIV-----ELDTPRDPORRAYAEAVAGRGVSVFSLSDDR 3569  
3319 --AEVGPVP-----VCOQAWHEDVGESGGVPVGVVLRCPDAGAGGGGGGGGG 3369  
3570 RHSEHSVWPAGLAASIVLAQALV--DLGRVGEPP----- 3601  
3370 VGEWVGVLGVQWGLERFAGSLVVYTRGAVAGPDPGV--DVVGASVWGLVRSQA 3427  
3602 -----RLNLVTRGAVAGPDSAGVVIDPVOAQWNGRVLG 3637  
3428 AEHPDRFVLLDLDTDGTDLDTGAGAGWGVGDSRVAAVVACG--EPQLAVRGERLLAARLK 3486

3638 LEHPBLW-----GGLVDLPVGVDBEVCRRFFVGVVASAGFQDQAVRGSGVMVRLV 3688  
3487 RLESSGDVPAQRSQDTRARRSDVPAQRSQVPAERSVDVSGREVLPWLSGGSVLVTTGGTG 3546  
3689 RAVVDGG-----GGG-----WRPRGTVLVTGGUG 3712  
3547 VLGAARVHLACVCGVRDLILVSRRGPDAPAGAEGLRAELAL--GAERVIVACDVGERRV 3605  
3713 GLCAHTARLVG--CGADHVLVSRGGAPGAGDLVRELEGLGARVSVRACDVADVAL 3771  
3606 VLLGEGVAGCPLTGVVHAAGVLDATIASLTPERLGTVFAAKVDAALLDLBELTGMELS 3665  
3772 RALLSDL--GEPVTAFFHAAGVPOSTPLAEISVQEAADVMAAKVAGAVNLGSLVDPCCGLE 3829  
3666 AVELSSAAGILGSAQGNVYAAANALDALAVRRRAAGLPGVSLANGLWEEASGWTGHLA 3725  
3830 AVELSSNAGVWVGSGQAVYAAANAFDALAVRRRGVGLPATSVANGMW--AGEGMAS--V 3886  
3726 GTDHRRIIRSGLHPMTDPAALFADALADLPVLLPADL-----RPAPPLPP 3773  
3887 GGAARELSRGRVAMPPEAVAVMADAVORGEAFVAVADVDERFVTGFSASRPR----P 3942  
3774 LQDLPATRRRTTTTTG-----GADNGAQLHARLAGQTHEQHTTLLAV 3821  
3943 LITSL-----PEVRAVVEGQVQGRGQGLGVGEESSGWLKRLSGLSRVQEEELVELV 3996  
3822 RSHIATVGHHTPTDTPDRAFDLGFDSLTAVELNBLRSTGLRLPTLAFDHPNPT 3881  
3997 RAQAAVVLGHGSAQDVPAPRAFKELGFDLSLTAVELNGLAAATGRLPATMAFDHTATA 4056  
3882 LTHLHTOLOPQDNPVAVPLAELEKLSALSALDKTDSASERVTLRLKSLMRW---N 3937  
4057 TARFLOSELVGS--DDPLTMRSAIDQLETGLALLESDEARSEITKRLNILLPRFGSGS 4115  
3938 APQHPTAESADDEKFTSATEAEIFKFDINDIGLS 3972  
4116 SRGREGQDAGEHQVEDATIDELFEVLDNELGNS 4150

## RESULT 14

US-09-036-987A-4  
; Sequence 4, Application US/09036987A  
; Patent No. 6143526  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H.  
; APPLICANT: Broughton, Mary C.  
; APPLICANT: Crawford, Kathryn P.  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Merlo, Donald J.  
; APPLICANT: Treadway, Patti J.  
; APPLICANT: Turner, Jan R.  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dow Agrosciences LLC Patent Department  
; STREET: 9330 Zionsville Road  
; CITY: Indianapolis  
; STATE: Indiana  
; COUNTRY: USA  
; ZIP: 46268  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/036,987A  
; FILING DATE: 09-MAR-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stuart, Donald R.

REGISTRATION NUMBER: 28,479  
REFERENCE/DOCKET NUMBER: 50,608  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317)337-4816  
TELEFAX: (317)337-4847  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3170 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-036-987A-4

Query Match 32.7%; Score 6804.5; DB 4; Length 3170;

Best Local Similarity 44.3%; Pred. No. 0;  
Matches 1581; Conservative 380; Mismatches 1115; Indels 493; Gaps 68;

473 HGGTAAADDPALIGMACRPGVRSKDLWEIAASGDAIGPPTDRGHPTQRHAODP 532  
26 HEAESGEREPALVAMGCRYPGGVQDPGLWKLVASGGDAIGBFPADRGMHLDLYDDP 85  
533 TOPGTCTYPPGGGFLDHAHFDAGFFGISPREALAMDPOORLLLETSWEAFERAGIDPLSV 592  
86 DQPGTCYTRHGGFLHDAGEFDAGFFDISPREALAMDPOORLLLEISWEIVESAGMDPRSL 145  
593 RGRGTGVFAGALSFYDGRMDTASSEGAADVEGHILTTGTVSLSGRIAYSFGLGPAIT 652  
146 RGSRTGVFAGLMEGY----DTGAHRAGEGVEGLTGNAGSVASGRVAVAFGEPAVT 201  
653 VDFGCSASLVLHLACOSLRSGECTLALAGCVSMVLTGLMFIERSQRLSGVDRCKAYS 712  
202 VDTACSSSLVALHLACOSLRQSGCDLALAGGVTVMTSPERFVFSRQGLAPDGRCKSFA 261  
713 AAADGTGWMGEGVGLVRLERLSDAVRLGHRVLAUVRGSAVNDGASNGLTAPNGPAOERVI 772  
262 AAADGTGMBEGAGLVLLERLSDARRGHRVLAUVRGSAVNDGASNGLTAPNGLAQERVI 321  
773 RQLANAGLSVADVVDVVEGHGTGTTLDGPTEAQAALLATYQQ-RAGDRPLWGLSKNIGH 831  
322 QQVLTAGLSASDVDAVEAHGTGTRGLDGPTEAQAALLATYAAQODRDRPLWGLSVKSNIGH 381  
832 TMAAGGVGVIKVMALREGVLRTLVHDKPSQVDMVSAGAVRLLTEAVPWPGDAAGRLR 891  
382 TQAAAGVAGVIKVMAMRHGELPRTLHVDFNPSHVDMVSAGAVRLLTENIRWPGTGT---R 438  
892 RAGVSSFGIGCTNAHVILEBAPAAAGCGVAGGVLGAPGLAISVAESVAAPVAVSAE 951  
439 RAGVSSFGVSGTNAHVILEHDP-----LAVTENE-----E 468  
952 SVVPVVPVVPVPSARSEAGLRAQAEALRQYVAVRDPVSLADVAGLAGRAVLGHRVAV 1011  
469 AAQSPAPGIVPMALSGRSSALRAQAERLRE-LCEQTDPDPVDVGFSLAATRTAWEHRAV 527  
1012 VLAADREELVQGLGALAAEGPDRVTTGHPAGCDRGVVFVFGQGGQHWGMVRLIASS 1071  
528 VLGRDSATLRSGLGVVASGEPADVVEGSLDGE---VVFVFGQGGQHWGMVRLIASS 584  
1072 PVFARMQACEALAPWDMVSVVDILRRDAGDAVWERADVQVPLFSVMVSLAALWRSYG 1131  
585 PTFARHMDCATALRYVDVSLVLRGAENSPPLDRVDVLQPASFAVMVSLAEVWRSYG 644  
1132 IEPDAVLHSGQSIEAAHVCGLSLKDAKTVLALSRALAAVRRGGMASVPLPAQVEQ 1191  
645 VRPAAVVHSGSIEAAACAGVLPLEDAARLVALRSALKGLSGRGMASLACPADEVA 704  
1192 LIGERWAGRLWAAVNGPRSTAVSGDAEAVDEVLAVCAGTGVTARRIPVDYASHCHPHVQ 1251  
705 LFAGS-GRLEVAANINGPRSVVWSGLAEVDELLAECAEKDMFARRIPVDYASHSAHVE 763  
1252 LREELLELLGDISQPSPGVFPFSTVEGTLDTTTLDAAVYRNLHOPVRFSDAVQALADD 1311  
764 VRSPVLAAGVRRHRRGQVPMWSTVIGDWVDPARLDGEYWRNLRQVPRFEHAVQGLVER 823

QY 1312 GHRVFEVVEVSPHPTLPVPAIEDTTEDTADVDTAIGSLRRGNDTRRFLTALAHTTTGIGTP 1371  
DB 824 GFLGFIEMSAHPVLTAVEETGAESATAVAAGTGLRRDGGRLRLHSLAEAVR--GAT 881  
QY 1372 TTWHHHYTHHHHPHPTHLDLPYFQHQHWLESSQPCAGSGSAGAGSAGSAGSAGT 1431  
DB 882 VDMAVAF-----GGAGRRLDLPYFQHQWLDK-----GAASDSARAVSDP 924  
QY 1432 AGGTAEVESRFDVARQOLETVATTAVPPSAGLDTVPVPPALSAMHRHOHQARINTWTY 1491  
DB 925 AAGW-----FWQAVARQDLKSVSDALDLDADAPLSATLPALSVWHRQERERVLADGWRY 978  
QY 1492 QETWKPRLTPTTHQPHQTWLIPIPETQTHPHITNLNLHHGHTPIPIPLTNLHHTNPQ 1551  
DB 979 RVDWVRVAPQPVRRTRTETWLLVVPVGGIEEALVERLTDALNTRGISTGLRLDVPAAATSGE 1038  
QY 1552 HLHHTLHHTTQQAQNHHTTCAITGLLSLLALDETPHHPHHTTGTLLNLTLTQTHTQTHP 1611  
DB 1039 ----LATELRAAAGDGFVKAI---LSLTALDERPHECKDVPSGIALLLNLKALGEADL 1091  
QY 1612 PTLVWVATTNATTTTENDPLTHTPTQATWGLARTTLLLEHPTHTAGIIDLPTTPTHTLOH 1671  
DB 1092 RLPLWTITRGAVKAGPADRLRLPMQAWGLRGAALHPERWGGILDLPLSDGLDGLVLR 1151  
QY 1672 LTQTLTQPHHQTOLAIRTTGTHTRRLTPTTLTPTHTPPTP--TPHGTTLITGTTGALATH 1729  
DB 1152 LGEALLTGLAEQOLAIRQSGVLARLVP--APANQPAGRKWRPRGSALITGGLGAVGAQ 1208  
QY 1730 LTHLTHTHQTHOHLTLTSTGHTPHAOHLTTLOOQKGLHLLTITTCDSNPDOLOQLLNT 1789  
DB 1209 VARWL-AETGAERIIVLTSSRQQAAGAAEELRGAQVSIACDVTDRAEMSAALL-- 1265  
QY 1790 IPPOHPLTVIHTAGTLDLDDATLNTLPTTOLNNVLRKASHLHLHLLTQHTPLTAPVLXS 1849  
DB 1266 --AEFDVAVFHAAGVGRLLPLAETDQNGLAIECAKVRGAQVLDLCLDSTDLDAFVLS 1323  
QY 1850 SAAATFGAPQQAANYAAAAYDALAHRRHHLHPATSIANGTWQGNGLADSKARAYLDR 1909  
DB 1324 SGAVMVGCGGQAGYGAANAFDGLAEORRARGLPATSIWGWAGGMAWG-AAGEHLRR 1382  
QY 1910 RGRFMSPELATAVTAATADTERPVYVIADTDSWKIEHT-----SQTSDLSVAAREE 1963  
DB 1383 RGIRPM-PAASAILALQEVLDQDCTVSIADVDMDFVPTFAATRATRLFDEVPAAKAM 1441  
QY 1964 PAVQRPPTP--AELKHKLTAHOTSAQORAAALVELVRDHVAALRHADPKAIPDQSPFALG 2021  
DB 1442 PA-NGPAEPCGSPFARNLAELPEAQRHRLVLCQAQVATVLCGRREVBQPERAFALG 1500  
QY 2022 FDSLTAVEPRNLLIKATGLRLEPVSFVFDHPTPAKLAHLQNLQRTAAESAFSAAVTAE 2081  
DB 1501 FDSLMAVDLNRLLTTATGLRLPTTTFVDPNPAALAAHLLBELVGDVAGAAVTAASAPAS 1560  
QY 2082 ASVTPIALVGMACHPCPGVTSADDFWDLISSEQDAIGFPDTRGDWDLDTLVDPPDPHPC 2141  
DB 1561 ---DEPIATVAMSCRFPFGGAHSPEDLWRLVAAAGTEVIGFPPSDRGWDAGSLVDPDASRPG 1617  
QY 2142 TCVTNRGGLYDAGHFDAAEFPGISPREALAMPQORLLLETAWETIEHAGINPHTLHGT 2201  
DB 1618 TTYARMAGLYDAGEFDALFGLISPREALAMPQORLVLEIAWEALERAGIDPLSLKGG 1677  
QY 2202 TGVFTGTNGQDYALRVHNAQSGTDGFALTGTAGSVISGRISYTFEGEPASVDTACSSS 2261  
DB 1678 VGTIYGASRGVATDVQFPPEAEVLLTGTSSVLSGRVAVSFGFEGPAVTVDTACSSS 1737  
QY 2262 LVALLHACQALRAGSCSMALAGVTVMSPGAIFVFSRQRLGAADHCKAFSAADGTGW 2321  
DB 1738 LVALLHACQSLRSGCDLALAGSVTMSPTFENFVFSRQRLGAPDGRCKSFAESADGTGW 1797  
QY 2322 GEGVGMILLVERLSDAHRNGHRVLAUVRGSAVNDGASNGLTAPNGPSQORVIRQALANAG 2381  
DB 1798 GEGAGLLULERLSDAHRNGHRVLAUVRGSAVNDGASNGLAAPNGPSQORVIRQALANAA 1857  
QY 2382 LSAGVDVDAVEAHGTGTTLDGPTEAQAALLATYQQDRAGEPLWGLSVKSNVGHVQTQAAAGVA 2441



1858 LSASDVDAVEAHGTGTGLDPIEAQALITATYQARERDRPMLTGLSVKSNIGHTQAAAGVA 1917  
2442 GVTKMAMALRHGLLPRTHLWDESPHVDMSAGAVOLLITETVPPGEGRLRRAGVSPGV 2501  
1918 GVTKMAMRHGLQFASLHADEPTSEVDMSSGAVLLAEQVWPESD-RVRRVGVSSFGI 1976  
2502 SGTNAHVILBEAPADDPGPPAGEGAGDAGDDAAAGSPGWPMLVSAKSOPALRAQAQA 2561  
1977 SGTNAHVILBEAT-----NAPDSTAEKTESGTVDI PVVPMVSGKTTDSLRGAER 2030  
2562 LHAHLTDHPGLDLADVGTYTLAARAVFDHRATLTAADRTTFLQALQALAAAGEPHPAVHS 2621  
2031 VLSQVESRPEQSLDVAISLASGRAALDERAVVLGADRGELVAGLAAAGQASGVI-- 2088  
2622 SAPGCTGGEAGKTAICSGOGTQPCMAHGLYHHPVFAAALNDICHTLHDPLH--DHP 2679  
2089 -----SGT-RASARFVGFGGQGLMGGRALYSKFPVFAAFDEACAELEAHLGEDRR 2142  
2680 LLPLLTONDNEDAAALLOQTRYAQAPALFAFOVALHRLITDGVHITPHYVYAGHSLGEIT 2739  
2143 VRDVFGSD-----AQLDQTLWAQSLFALQAGLLGLL-GSWGVRPDMVWGSHVGEA 2195  
2740 AAHLAGLITDATTTLTORATLMQTMP-PGTMTTLHTTTPHHTLTAHENDLAAIAIN 2798  
2196 AFAAAGVLSLRDAARLVAARLMOALPSDCMLAAVAGEDLVRPLLAGEESVVAALN 2255  
2799 TPTSLVTSCTPHVQHTTLCQOGIKTKTLPNNHAFSPHTPILNQLHQHTQTLYHP 2858  
2256 AGSVVLSGDRVLASVGRLTRELVRTRLSHAFSHRMDPMLGEFAQIAESAFFGK 2315  
2859 PHTPLITANT-----PPDQLTPTHYTOQARTVDYATTTCTLHQHGVTVTVIELGPDNTLT 2914  
2316 PTTPLVSTLTGELDRAEMSTPGVWRQAREPVRFDGVQALAAQAGITVVELGPGTLA 2375  
2915 TLTHNLNPNP-----TTTLTLTHPHHPHTLNLAKTTTWHPHHYTHDNPHTHT- 2969  
2376 ALVRECATEDRVRGISSIPLMRERDETRSVMTALA-----HLHTR 2417  
2970 -----HLDPPTYFPQHHYHLESTQPGA-----GNVSA-----AGLDPTY 3004  
2418 GGEVDMAQFAGTARQLELPTAFQORHYWIESSARPARDRADIGEVAFQFWTAVDQGD 2477  
3005 HPLIGATLELATDGG-----ALLAGRLSRHPMLADHAVGTVLLSGATELEA 3054  
2478 LATLVAALDGLADDDTCASLSVLPALSSWRSGLRNS-----LVDSCRYRIS 2525  
3055 LHAGTVGCDRDELTLHAPLVVPDGVSVQVGAADGEGRRLSVYVARGSGACGGG 3114  
2526 WHSSREVPAPKISGTWL---LVVP-----GAADDG---LVALT---SSLVGGG 2565  
3115 ASGVVWCHASGVLVEAAGVVVDGLAGVWPPRGAVAVDVGVRDLRAGAGCVLPVFS 3174  
2566 AE-----VVRIGLSEEDPHR-----EDVAORALNALTDAGL--- 2597  
3175 GLRAVRDGDLLAEVCLPEAWGDAAGFGLHALLDGVVQPLSVLLPGGTGFGGAGFG 3234  
2598 -----GGVLSLGLDE---SPAGFSCLP-----TGF----- 2621  
3235 EGVVRPAVWGVSLHAGVTGVRVRVSAVGRGGGREAUSVYVVGDEAGVPVAVDRLELRP 3294  
2622 -----ALTVQL----- 2627  
3295 VDMGOLRAVSVSAGRGSLSYAVOWAEVGPVPVCGQAWAHMEDVGESGGGPVGVVLRCP 3354  
2628 -----LRAL-----RKADVEAPFWA----- 2642  
3355 DAGAGGGGGGGGGGVGVGVVGVVGVVQVWGLGLERFAGSLRVVVYTRGAVVAGPEDGPDV 3414  
2643 -----VTRGGVAL---EDVRVSP 2657  
3415 VGSVWGLVRSQAQHPDRF-VLLDLDTDTGTDLTDTGAGAGWGVGDGRVAVVA-CGEPQ 3472

2658 EQALVWGLLRVAGLEHPEFWGGLIDLPSPDMDRL-----CARLAGVLADGGEDQ 2706  
3473 LAVRGERLLAARUKRLESSGDVPAQRSGDTRARRSDVPAQRSGVPPARRSDVSGREVLP 3532  
2707 VAIRRGGVFRURERAGSG-----AGSV----- 2730  
3533 WLSGGSVLVGTGTGVLGAARVAVRHLAGVCGVRDLLLLVSRGPDAPAGAEGLRAELAAALGAEV 3592  
2731 WRPRGTVLVGTGTGGLGAHVARWLAG-AGAEHVULTSRGADAPGAGELRAELEALGARV 2789  
3593 RIVACDVGRERVRVRLLEGVPAGCPLTGVVHAAGVLDATIASTLTPERLGTVPAAKVDAA 3652  
2790 SIIVPCDVADRDAVAGVLAGIGGECPLTAVVHAAGVGEAGDVVEMGLADFAAIVLSAKVRGA 2849  
3653 LLLDELTRCMELSAFVLFSSAAGILGSGAGVYAAANAALDALAYRRAAGLPGVSLAMG 3712  
2850 ANLDELADSELDFAVFMFSSVSGVWGAGGAGYAAANAYLDALAEORRARGLVGTAVAMG 2909  
3713 LMEEASGMTCHLAGTDRHRIIRSGLHPMSTPDALALFDAAALDRPVLPAIDL---RPAP 3769  
2910 PW-AGDGMA---AGETGAQLHRWGLASMEPSAALLALQALDDETSLLVVADVDMWAFAP 2965  
3770 PLP-----PLLOQLPATRRRTTITTCGANGAOLHARLAGQTHEOQHTTLALVRSH 3824  
2966 AFTSARRRPLL-DTIDEARAALETTGEQAGTKPKVELTQRLAGLSKRDADAVIDLVRAE 3024  
3825 IATVLGHTTTPDTPDPAFRDGLGSLTAVELNRRLSRTGLRPTTLAFDHPNPPTLTH 3884  
3025 TAAVLRDDATLAPSRPFQELGFDLSMAVELNRRLNTATGQLPASTIFDPYNAESLSR 3084  
3885 HLHTQLQOPDNVAVPVLAECLKLSALSALDKTDSASERVTLRLKSLMLRN-APQHPT 3943  
3085 HLCALFLP-TEITVDSALAEALDRIEQOLSWLTGCEAFARDRIATRLALHEKWNAAEVPT 3143  
3944 ABSADDEKFTSATEABEIFKPIDNDLGLS 3972  
3144 ---GADVLTSDSATHEIFEIDNELDLS 3170

## RESULT 15

US-09-370-700-4  
; Sequence 4, Application US/09370700  
; Patent No. 6274350  
; GENERAL INFORMATION:  
; APPLICANT: Baltz, Richard H  
; APPLICANT: Broughton, Mary C  
; APPLICANT: Crawford, Kathryn P  
; APPLICANT: Madduri, Krishnamurthy  
; APPLICANT: Treadway, Patti J  
; APPLICANT: Turner, Jan R  
; APPLICANT: Waldron, Clive  
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide  
; FILE REFERENCE: 50489 DIV1  
; CURRENT APPLICATION NUMBER: US/09/370,700  
; CURRENT FILING DATE: 1999-08-09  
; EARLIER APPLICATION NUMBER: US 09/36987  
; EARLIER FILING DATE: 1998-03-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 3170  
; TYPE: PRT  
; ORGANISM: Saccharopolyspora spinosa  
US-09-370-700-4

Query Match 32.7%; Score 6804.5; DB 4; Length 3170;  
Best Local Similarity 44.3%; Pred. No. 0;  
Matches 1581; Conservative 380; Mismatches 1115; Indels 493; Gaps 68;  
QY 473 HGTAAADDPPIAIGHACFPFGVSPKDLWELASGGDAIGFFPTDRGWPTQRHAQDP 532  
DB 26 HEBSGEREPIAIVAGCMGCRYPGVQDPGLWKLVASGGDAIGFFPADRGHLDLDDPDP 85

Qy	533	TQBGTYPOGGGFLHDAHPDAGFGISPREALAMPQORLLLETSCWEPERAGIDPLSV	592	Db	1092	RIPLWTITRGAVKAGPADRLRPMQOAWGLGRVAALEHPERWGLLIDLPDSDGDLVLR	1151
Db	86	DOFGCTYTRGGFLDAGEFDISPREALAMPQORLLLETSCWEPERAGIDPLSV	145	Qy	1672	LTQTLTQPHQHTQALRTTGTHTRLTPTTLTTPHQPTP---TPHGTTLITGCTGALATH	1729
Qy	593	RGSRGTGVEGALSFDFGPRMDTASSGAAADVEGHILTTGTVSLGRIAYSGLEGPAIT	652	Db	1152	LGEALTNGLAEQDLAIQSGVLAARLVP---APANQAGRWPRGSRALITGGLGAVGAQ	1208
Db	146	RGSRGTGVFAGLMEGY-----DTGAHAGBEGVEGLTGNAGSVASGRVAFYAFBGPVAT	201	Qy	1730	LTHHTLTHQPTQHLTLTSTGPHTPHAOHLTTQLOOKQIHLTITTCDTNSNPOLQOULT	1789
Qy	653	VDTGCSASLVLHLACQSLRSGECTIALAGGVVMTLGMFIERSQRLSGVDRCKAYS	712	Db	1209	VARWL--AETGABRIVLTSSRRGNQAAAELEALRALGAQVSIACDVTVDRAEMSALL--	1265
Db	202	VDTACSSSLVALHLACQSLRQGCDELALAGGVVMTSTPERFVEFSRQGLAPDGRCKSPA	261	Qy	1790	IPQPHLTVITHAGILDDATLTNLTPQLNNVLAKAHSAHLHLQHTQHTLTPLTAPVLS	1849
Qy	713	AAADGTGWEGBGVNMLVERLSDAVRLGHRVLAVRGSAVNDQASNGLTAPNGPAQERVI	772	Db	1266	--AETFDVTAVFAHAGVGRLLPLAETDQNGLAIECAAKVRGAQVLDLDELCDSTDLAPVLS	1323
Db	262	AAADGTGWEGBGVNMLVERLSDAVRLGHRVLAVRGSAVNDQASNGLTAPNGPAQERVI	321	Qy	1850	SAATFTGAPGQANYAAANAYLDALAHRRHTHLPATSIANGTWQNGGLADSKARAYLDR	1909
Qy	773	QALANAGLSVADVVVEGHGTGTTGLDPTIEAALLATYGO--RAGDRPLWGLSKSNIGH	831	Db	1324	SGAGVWGGGQOAYGAANAPLDTLAEQRRARGLPATSIWGSWAGGMDAG--AAGEHLRR	1382
Db	322	QVLTSGAGLSASDVDAVEAHGTGTRLGDPIEAQALTAAYQDQDRDRPLWGLSVKSNIGH	381	Qy	1910	RGFRMSPELATAVTAQAIADTERPVVVIADIDMSKIEHT-----SOTSDLVSAARE	1963
Qy	832	TMAAGVGVYKVMALREGVLPRTLHVDPKPSQVDWSAGAVRLLTEAVPWPQDAAAGRLR	891	Db	1383	RGIREM--PAASAILALQEVLDQDETCVSIADVMDRFVPTFAATRATRLFDVPAARKAM	1441
Db	382	TQAAAGVAGVYKVMAMRHGELPRTLHVDPNSHVDWSAGAVRLLTENIRWPGTGT--R	438	Qy	1964	PAVQPTPP--AELHKTILAHQTSADQRAALLLEVRDHVNAVLRHADPKAIAPDQSFRAIG	2021
Qy	892	RAGVSSFGIGTNAHVILEEAPAGGCVAGGVLECAPGLAISVAESSAAPVAVSAPVAE	951	Db	1442	PA--NGPABEGGSPFARNLAELPEAQRHRELVDLCAQVATVLGHGSRREEVQPERAFRAIG	1500
Db	439	RAGVSSFGVSGTNAHVILEHDP-----LAVTENE-----E	468	Qy	2022	FDSLTAVERPNLLIKATGLRLPVSLVFDPHTPAKLAHLONOLRGTAABSAAPSAAAVTAB	2081
Qy	952	SVPVPVPVPVPSVARSSEAGLBAQAEALROYAVRDPVSLADYVGLACGRAVLEHRAV	1011	Db	1501	FDSLMAVDURNLTATATGLRLPTTVFYPNPALAAHLLELVDGVASAAVTAASAPAS	1560
Db	469	AAQSPAGVIVFWALSGRSSSTALRAQAEURLR--LCEQTDPPDVVDVGFSLAATRTAWEHRAV	527	Qy	2082	ASVTBPIAIVGNACRPPGGVTSADDFWDLISSEQDAIGGFPPTDRGMDLDTLDPDPHPG	2141
Qy	1012	VLAADREELVQGLGALAAAGPDRVTTGHAPGDRGVVFPVFGQGGQWAGMVRLLASS	1071	Db	1561	---DEPIAIVAMSCRFPGGAHSPEDLWRLVAAGTEVIGEFPSPDRGMDABGLYDPAASRPG	1617
Db	528	VLGRDSATLRSGLGVVASGEPAVDVVEGSLDGE---VVFVFGQWQWAGMVAVDLLDAS	584	Qy	2142	TCYTRNGGLYDAGHFDABFPFGISPREALAMPQORLLLETSCWEPERAGIDPLSGKSG	1677
Qy	1072	PVFAHMQACEALAPWDMVSVVDILRRDAGDAVWERADVQVPLFSVMVSLAALWRSYG	1131	Db	1618	TTYARMAGFLYDAGBFDADLFGISPREALAMPQORLLLETSCWEPERAGIDPLSGKSG	1677
Db	585	PTFAHMQACEALAPWDMVSVVDILRRDAGDAVWERADVQVPLFSVMVSLAALWRSYG	644	Qy	2202	TCVFTGTNGODVALRVHNAQSTGDFALTGTAGTSVGRISYTPFEGEPASVVDTCSSS	2261
Qy	1132	IEPDVHLGSHQSGIAAHVCGALSLLDAKTAVALRSRALLAAVGRGMSVPLPAQEVQ	1191	Db	1678	VTYTGASGRGYATDVQPEPEAGVLLTGTSSVLSGRVAYSFEGEGEPAVTVDTACSSS	1737
Db	645	VRPAAVHGSQSGIAAACAGVPLDDEARLVALRSRALKGLSGRGMASLACPADEVA	704	Qy	2262	LVALHLAQUALRAGECSMALAGGVTVMSSPGAFVFEFSRQGLAADGHCKAFSAADGTGW	2321
Qy	1192	LIGERWAGRLWAAVNGPRSTAVSGDAEAVDEVLAVCAGTVARRIPVDYASHCHVOP	1251	Db	1738	LVALHLACQSLRSGECDELALAGGVTVMTPEMFVFEFSRQGLAADGHCKAFSAADGTGW	1797
Db	705	LFAGS--GGRLEVAANGPRSVVSGLEAVDELLAECAEKMDARRIPVDYASHSHVAV	763	Qy	2322	GGVGMVLLVERLSDAHRNHRVLAVRGSAVNDQASNGLTAPNGPSQORVIRQALANAG	2381
Qy	1252	LRBELLELGDISPQSGVPFFSTVEGTWLDTTTLDAAYWYRNLHQVFRFSDAVQALADD	1311	Db	1798	GGCAGLLILLERLSDAHRNHRVLAVRGSAVNDQASNGLTAPNGPSQORVIRQALANAA	1857
Db	764	VRSPVLAAGVVRHRDQGVPMWSTVIGDWVDPARLDGEYWRNLQPVRFHVAQGLVER	823	Qy	2382	LSAGDVDAVEAHGTGTRLGDPIEAQALTAATYQOARERDRPLWGLSVKSNVGHGTAAAGVA	2441
Qy	1312	GHRVFEVSPHPTLVPVPAIEDTDAEDVTAIGSLRGONDTRFLTALAHHTTGTGP	1371	Db	1858	LSASDVDAVEAHGTGTRLGDPIEAQALTAATYQOARERDRPLWGLSVKSNVGHGTAAAGVA	1917
Db	824	GFGLFIEMSAHPVLLTAVETGAESETAAVAGVTLRRDGLRRLHLSLAAYVR--GAT	881	Qy	2442	GVYKVMALRHGILLPRTLHVDPSPHVDMSAGAVOLLTETVPWPGEGEGLRAGVSSFGV	2501
Qy	1372	TTWHHTYTHHTPHPHPTLHDLPTYPQOHVWLESSQPCAGSGSAGSAGSAGSAGT	1431	Db	1918	GVYKVMAMRHQQLPASLHAEDEPTSEVDWSSGAVLLAEQVWPESD--RVRRVGVSSFGI	1976
Db	882	VDWAVAF-----GGAGRRLLDPTYPQORVWLDK-----GAASDEARAVSDP	924	Qy	2502	SGTNAHVILEEAPADDVPGGPAGSGDAGSDDEAAGSGVGVWPLVSAKSPALLRAQAQA	2561
Qy	1432	AGCTAEVESFWDVAQADLETVATTAVLPPSAGLDTVPVPAALSAHRRHQDQARINTWY	1491	Db	1977	SGTNAHVILEEQAT-----NAPDSTAETDKTESGSTVDIPVVPVWLVSGTKTDSLRCQABR	2030
Db	925	AAGW-----FWQAVARQDLKSDALDLADAPLSATLPAALSVHRRQERERVLADGWRY	978	Qy	2562	LHAHLTDHPLGLDLADVGTYTLAHARAVFDHRAVTLIADRDPTFLQALQALAAAGEPHPAVHS	2621
Qy	1492	QETWKPDLTPTTHQPHQHTWALIPETQTHPHHTNLTNLHHGHTPIPIPLNHTHTNPQ	1551	Db	2031	VLSQVESREPEQSLVDVAYSLASGRALDERAVVLGADRGELVAGLAALAAAGEASGVI--	2088
Db	979	RVDWVRVAPQVVRTRTETLWVPPGGEIEEALVERLTDALNTRGISTLRLDVPFAATSGE	1038	Qy	2622	SAPGGTGTCEAAKGTAFICSGQGTQORPGMAHGLYHITHPVFAAALNDICTHLPHL--DHP	2679
Qy	1552	HLHHTLHHTTQQAQNHHTTGAITGLLSLLALDETPHHPHPTGTLNLTNLTLTQTHQTHP	1611	Db	2089	-----SGT--RASARGFVPSGGQWGLGMGRALYSKFPVFAAAFDEACAELENHGEDRR	2142
Db	1039	-----LATELRAADGDVKA1-----LSLTAUDERPHPECKDQVPSGILLNVLKALGEADL	1091	Qy	2680	LLPLTLTQNDNDNEDAAALLQOTRYAQPALFAPQVALHRLTLTDGYHTHTPHYHAGHSIGEIT	2739
Qy	1612	PTPLWVATTNATTTNPDNPLTHPTQATQWGLARTLTLEHPTHTAGIIDLPTTPTPTLQH	1671				

Db 2143 VRDVFGSD-----AQLDQTLMAOSGLFALOAGLGLL-GSWGVRPVDVVMGHVSGELA 2195  
Qy 2740 AALHAGLTLTDATTLTORATLMOTMP-PGTWTLTHLTHLTAHENDLAATAIN 2798  
Db 2196 AAFAGVLSURDAARLARARLMOALPDSGAMLAVAAGEDLVRLPLLAGREESVVAALN 2255  
Qy 2799 TPTSLVISGTPHTVQHITLUCOOGIKTKLPTNHAFSPHTPIPLNQLHQHTQTITYHP 2858  
Db 2256 APGSVLSGDEVLASIVGLRTELVRTRLRVSHAFSHRMDPMLGEFAQIAESAFCG 2315  
Qy 2859 PHTPLITANT-----PPDQLTPHYTQOARTVDYATTTQTLHQGVTVVIELGPONTLT 2914  
Db 2316 PTTPLVSLTCELDRAAEMSTPGVVRQAREPVRFAADGVQALAAOQIGTVVIELGPDGTLA 2375  
Qy 2915 TLTHNLNPP-----TTLTLTHPHHPQTHLTLNLAKTITTTWPHHYTHHDNQPHHT- 2969  
Db 2376 ALVRECATEDRVRIRISSIPMRREDTRSVMTALA-----HLHTR 2417  
Qy 2970 -----HLDLTPFPFQHHYWLSTOPGA-----GNVSA-----AGLDPTE 3004  
Db 2418 GGEVDMQAFAGTGARGLELPTAFQHQHYWIESSARPARDRADIGEVAEQFWTAVDQGD 2477  
Qy 3005 HPLLGATLELATGG-----ALLAGRLSIRSHPMHADHAGVTLLSGATFLELA 3054  
Db 2478 LATLVAALDLGADDDTCASLSVLPALSSWRSGRLNRS-----LVDSCRYRIS 2525  
Qy 3055 LHAGTVGCDRVDLTLHAPLVVPDGGVSVQVGAADGEGRRLYSVVARGGACGGG 3114  
Db 2526 WHSREVPAKISGTWL---LVVP-----GAADDG---LVALT---SSLVGGG 2565  
Qy 3115 ASGGVMTCHASGVLVEAAAGVVDGLAGVMPRGAVAVDVGVRDLRAGAGCVLGPVFS 3174  
Db 2566 AE-----VVRIGLSEEDPHR-----EDVAQRLANALTDAGL-- 2597  
Qy 3175 GLRAVRDGDLLAEVCLPEANGDAAGLHGLPALLDGVVQPLSVLLPGTGEGGAGFG 3234  
Db 2598 -----GGVLSLLGLDE---SPAPGFSCLP-----TGF----- 2621  
Qy 3235 EGVVRPAVMGVSILHRAGVTGVRVRSVAVGCRGGREAVSVVVGDEAGVPVAVSDRLRLRP 3294  
Db 2622 -----ALTVQL----- 2627  
Qy 3295 VDMQOLRAVSASAGRRGSLYAVQMAEVPVPVCGQAWHEDYGESGGPVPVGVVLRCP 3354  
Db 2628 ---LRAL---RKADVEAPFWA----- 2642  
Qy 3355 DAGAGGGGGGGGGVGVGVGVGLERFAGSRLVVVTRGAVVAGPEDGPVDV 3414  
Db 2643 -----VTRGGVAL--EDVRVSP 2657  
Qy 3415 VGASVMLVRSQAQAEHPDRF-VLLDLTDGTDLDTGAGAGWGVGDSRVAOVA-CGEPQ 3472  
Db 2658 EQALVWGLLVAGLEHPEFPGGLIDLPDWDRL-----GARLAGVLADGEDQ 2706  
Qy 3473 LAVRGERLLAARLKRLESQDVPQORSQDTRARRSDVPAQORSQGVPAARRSDVSGREVLP 3532  
Db 2707 VAIRRGGVFVRLERAGASG-----AGSV----- 2730  
Qy 3533 WLSGGSVLTGGTGVLAGAARHLAGVCGVGRDLLLLVSRGPDAPGAEGLRAELAAAGV 3592  
Db 2731 WRPRGTVLVTGGTGGGLGHVARWLAG-AGAEHVLTSTRGADAPGAGELRAELEALGARV 2789  
Qy 3593 RIVACDVGERRERVLLEGVGPACPLTGVVHAAGVLDDATIASLTPERLGTVPFAAKVDA 3652  
Db 2790 SIUPCDVARDVAVLAGIGGECPLTAVVHAAGVGEAGDVEMGLADFAVLVSAKVRGA 2849  
Qy 3653 LLDDELTRGMELSAFVLFSSAGILGSAGQNYAANAALDALAYRRRAAGLPGVSLAWG 3712  
Db 2850 ANLDELLADSELDFAVMFSSVSVWGAGGQGAAYAAANVLDALAEQRRARRGLVGTAVANG 2909  
Qy 3713 LWEEASGTMCHLACTHRRRIIRSGLHPMSTPDALALFDDAALDRPVLPAUL---RPAP 3769  
Db 2910 PW-AGDMA---AGETGAQLHRMGLASMEFSAALLAQGLALDRDETSLVVADVDMARFAP 2965

Qy 3770 PLP-----PLLODLLPATRRRTTRTTTGGADNGAQLHARLAGOHEQOHTTLLALVRSH 3824  
Db 2966 APTSARRRPLL-DTIDEAPAALETTEGOAGTKGPKVELTORLAGLSKERDDAVLDLVRAE 3024  
Qy 3825 IATVLGHTTPTDTPPDRAFRDLGFDLSLTAVELNRNLSRTTGLRLPTTLAFDHPNPTTLTH 3884  
Db 3025 TAAVLGRDDATALAPSRPQELGFDLSLMAVELNRNLTATGQLPASTTIFDYPNAESLSR 3084  
Qy 3885 HLHTOLOPOPDNAVAPVLAELDKLESALSALDKTDSASERVTLRLKSLMLRW-APQHPT 3943  
Db 3085 HLCALFLP-TETVDSALAEALDRIEQQLSMLTGEAPARDRIATRLRALHEKWNAAAEVPT 3143  
Qy 3944 AESADDDKFTSATBAEIKFKIDNDLGLS 3972  
Db 3144 --GADVLSLDSATHDEIFEIDNELDLS 3170

Search completed: June 17, 2003, 13:09:23  
Job time : 173.193 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 17, 2003, 12:50:57 ; Search time 194.578 Seconds  
(without alignments)  
2720.102 Million cell updates/sec

Title: US-09-914-286-3  
Perfect score: 20829  
Sequence: 1 VQRMGGEPRAAGEVLGV.....FTSATEAEIKFIDNDLGLS 3972

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Databases : A\_Geneseq\_101002:\*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
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5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20829	100.0	3972	21	AA23749 S. avermitilis ave
2	20829	100.0	3972	22	AA65264 Streptomyces averm
3	20817	99.9	3972	22	AA65268 Streptomyces averm
4	12972	62.3	5532	21	AA23752 S. avermitilis ave
5	12972	62.3	5532	22	AA65267 Streptomyces averm
6	11330.5	54.4	6239	21	AA23750 S. avermitilis ave
7	11330.5	54.4	6239	22	AA65265 Streptomyces averm
8	8151	39.1	4551	21	AA18637 Amino acid sequenc
9	8151	39.1	4551	21	AA67201 Narbonolide syntha
10	8148	39.1	4613	21	AAV77192 S. venezuelae macr

11	8148	39.1	4613	21	AAV77200 S. venezuelae pik
12	8148	39.1	4613	21	AAV77180 S. venezuelae pik
13	7705.5	37.0	4472	18	AAW22601 Tylosin synthase
14	7281.5	35.0	5588	20	AAV39301 SpnE a polyketide
15	7281.5	35.0	5588	22	AAV70969 S. spinosa protein
16	7255	34.8	4545	18	AAW22611 Hybrid armg/tylg O
17	7221.5	34.7	6797	22	AAAB31558 Pmaricin biosynth
18	7190.5	34.5	4881	21	AAW23751 S. avermitilis ave
19	7190.5	34.5	4881	22	AA65266 Streptomyces averm
20	7098	34.1	5069	19	AAW52846 A. mediterranei ri
21	7089.5	34.0	11096	22	AAE10129 Streptomyces nous
22	7079	34.0	3739	21	AAAB18638 Amino acid sequenc
23	7079	34.0	3739	21	AAV67202 Narbonolide syntha
24	7041.5	33.8	3816	21	AAV92708 S. avermitilis ave
25	7017	33.7	3739	21	AAV77193 S. venezuelae macr
26	7017	33.7	3739	21	AAV77201 S. venezuelae pik
27	6941.5	33.3	4550	18	AAW23716 platenolide syntha
28	6941.5	33.3	4550	18	AAW22606 platenolide syntha
29	6939.5	33.2	4150	21	AAE10145 Streptomyces nous
30	6804.5	32.7	3170	20	AAV39299 SpnE a polyketide
31	6804.5	32.7	3170	22	AAV70967 S. spinosa protein
32	6736.5	32.3	3724	18	AAW23718 platenolide syntha
33	6736.5	32.3	3724	18	AAW22608 platenolide syntha
34	6652	31.9	7068	22	AAE10142 Streptomyces nous
35	6652	31.9	7068	22	AAE10144 Streptomyces nous
36	6555	31.5	3729	18	AAW22603 Tylosin synthase
37	6555	31.5	3729	18	AAV70968 S. spinosa protein
38	6447	31.0	4924	22	AAV39300 SpnD a polyketide
39	6447	31.0	4928	20	AAV39300 SpnD a polyketide
40	6439	30.9	6095	22	AAU10701 Amino acid sequenc
41	6387	30.7	3567	14	AAV44431 eryA region polyep
42	6383	30.6	4630	21	AAV77177 S. venezuelae vep
43	6344	30.5	4630	18	AAW19629 Streptomyces venez
44	6302.5	30.3	3546	22	AAW82212 polyketide syntha
45	6299.5	30.2	5087	22	AAU10700 Amino acid sequenc

ALIGNMENTS

RESULT 1  
AA23749  
ID AAB23749 standard; Protein; 3972 AA.  
XX  
AC AAB23749;  
XX  
DT 10-JAN-2001 (first entry)  
XX  
DE S. avermitilis avermectin aglycon synthase protein SEQ ID NO:3.  
XX  
KW Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis;  
KW multifunctional enzyme; polyketide; avermectin; veterinary drug;  
KW agrochemical.  
XX  
OS Streptomyces avermitilis.  
XX  
PN WO200050605-A1.  
XX  
PD 31-AUG-2000.  
XX  
PF 23-FEB-2000; 2000WO-JP01041.  
XX  
PR 24-FEB-1999; 99JP-0046961.  
XX  
PA (KITA) KITASATO INST.  
XX  
PI Omura S, Ikeda H;  
XX  
DR WPI: 2000-565458/52.  
DR N-PSDB; AA92301.  
XX  
PT Avermectin aglycone synthase DNA and proteins encoded by all or part of  
PT it for the production of avermectin and its derivatives for drug and

PT agrochemical use -

Claim 32; Page 203-223; 314pp; Japanese.

CC The present sequence represents an avermectin aglycon synthase protein.  
 CC Also described are: (1) polypeptides encoded by all or part of the DNA;  
 CC (2) expression vectors containing the DNA; (3) host cells transformed by  
 CC the vectors; (4) preparation of the polypeptides by culture of the  
 CC transformants; (5) preparation of avermectin aglycon or its derivatives  
 CC by culture of transformed avermectin-producing microorganisms; and (6)  
 CC oligonucleotides of 5-60 bases in length containing sense or antisense  
 CC sequences from the avermectin aglycon synthase DNA. The enzymes are  
 CC useful for the production of modified forms of avermectin and of the  
 CC intermediates in its biosynthesis, for use as drugs, veterinary drugs  
 CC and agrochemicals.

XX Sequence 3972 AA;

Query Match 100.0%; Score 20829; DB 21; Length 3972;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3972; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VORMDGEPRPAAGVILGVADEADGVVFPFGQGPQWPGMRELLDSDVFRSVRAC 60  
 DB 1 VORMDGEPRPAAGVILGVADEADGVVFPFGQGPQWPGMRELLDSDVFRSVRAC 60  
 QY 61 EAAFAFYDWSVEQVLRDSDPAGLDVDPVQPTLFAVMISLAALWRSQGVPCAVLGH 120  
 DB 61 EAAFAFYDWSVEQVLRDSDPAGLDVDPVQPTLFAVMISLAALWRSQGVPCAVLGH 120  
 QY 121 LGEIAAAHVSGSLADAAARVVTLSQAQTTLAGTCAVLSAATPDLLPRIAPTEDNP 180  
 DB 121 LGEIAAAHVSGSLADAAARVVTLSQAQTTLAGTCAVLSAATPDLLPRIAPTEDNP 180  
 QY 181 ARLAAVAVNGPRSTVVGAREAVADLVADLTAAQVTRMIPVDVPAHSPLMTAIBERVVS 240  
 DB 181 ARLAAVAVNGPRSTVVGAREAVADLVADLTAAQVTRMIPVDVPAHSPLMTAIBERVVS 240  
 QY 241 GLLPITPRSRIPFFSHSVTGGRLDTELDAAVYRNWMSSTVFEPAPARLLLOQPKTFVE 300  
 DB 241 GLLPITPRSRIPFFSHSVTGGRLDTELDAAVYRNWMSSTVFEPAPARLLLOQPKTFVE 300  
 QY 301 MSPHPVLTMLQELAPDLGDTTGTADTVIMGLTLLRRQGGTLDHFLTSLAQLRGHGETSAT 360  
 DB 301 MSPHPVLTMLQELAPDLGDTTGTADTVIMGLTLLRRQGGTLDHFLTSLAQLRGHGETSAT 360  
 QY 361 VLSARLTALSPQQSLLDLVRAHTMAVINDDGNERTASDAGPSAFHLGFDVSMGVE 420  
 DB 361 VLSARLTALSPQQSLLDLVRAHTMAVINDDGNERTASDAGPSAFHLGFDVSMGVE 420  
 QY 421 LNRNLSKATGLRLPVTLLFDHTTPAAVARTALGHLEDDTAPVDPSPSGHGTTAAD 480  
 DB 421 LNRNLSKATGLRLPVTLLFDHTTPAAVARTALGHLEDDTAPVDPSPSGHGTTAAD 480  
 QY 481 DPFAIIGMACRPPGGVRSFKDLWELAAAGDGAIGPPTDRGWPTQRHAQDPTQGTFFP 540  
 DB 481 DPFAIIGMACRPPGGVRSFKDLWELAAAGDGAIGPPTDRGWPTQRHAQDPTQGTFFP 540  
 QY 541 QGGFHLDAAHFDAGFFGISPREALAMPQORLLLETSWEAFERAGIDPLSVRSRTGVF 600  
 DB 541 QGGFHLDAAHFDAGFFGISPREALAMPQORLLLETSWEAFERAGIDPLSVRSRTGVF 600  
 QY 601 AGALSFDYGRMDTASGEAAVDEGHILGTGTVSLSGRIAYSGLEGPAITVDVTCGSAS 660  
 DB 601 AGALSFDYGRMDTASGEAAVDEGHILGTGTVSLSGRIAYSGLEGPAITVDVTCGSAS 660  
 QY 661 LVTLHLACOSLSGECTALAGGVSMSTLGMFIEFSRQGLSVDRCKAYSAADAGTCW 720  
 DB 661 LVTLHLACOSLSGECTALAGGVSMSTLGMFIEFSRQGLSVDRCKAYSAADAGTCW 720  
 QY 721 GEGVGMLLVRLSDAVRLGHRVLA VVRGSAVNDQASNGLTAPNGPAQERVIRQALANAG 780  
 DB 721 GEGVGMLLVRLSDAVRLGHRVLA VVRGSAVNDQASNGLTAPNGPAQERVIRQALANAG 780

QY 781 LSVADVDDVVEGHGTGTTLGDPIEAQALLATYQORAGDRPLWLGLSKNSNIGHTMAAGVGG 840  
 DB 781 LSVADVDDVVEGHGTGTTLGDPIEAQALLATYQORAGDRPLWLGLSKNSNIGHTMAAGVGG 840  
 QY 841 VIKWMAALREGVLPRTLHVDPKSPQVDSAGAVRLLTEAVPWPFGDAAGRLRAGVSSFGI 900  
 DB 841 VIKWMAALREGVLPRTLHVDPKSPQVDSAGAVRLLTEAVPWPFGDAAGRLRAGVSSFGI 900  
 QY 901 GGTNAHVILEEPAAGCGVAGGVTLEGAPGLAISVAESAAPVAVSAPVAESVPVPVVP 960  
 DB 901 GGTNAHVILEEPAAGCGVAGGVTLEGAPGLAISVAESAAPVAVSAPVAESVPVPVVP 960  
 QY 961 VVPVYSARSEAGLRAQAEALRYAVRDPVSLADVAGLACGRAVLEHRAVVAADREBL 1020  
 DB 961 VVPVYSARSEAGLRAQAEALRYAVRDPVSLADVAGLACGRAVLEHRAVVAADREBL 1020  
 QY 1021 VQGLGALAAGEPDRVTTGHAPGGDRGVVFPFGQGGQWAGVRLLLASSPVFARMQA 1080  
 DB 1021 VQGLGALAAGEPDRVTTGHAPGGDRGVVFPFGQGGQWAGVRLLLASSPVFARMQA 1080  
 QY 1081 CEEALAPWVDSVVDILRRDAGDAWERAADVVPVLFSVMUSLAALWRSYGIEPDAVLGH 1140  
 DB 1081 CEEALAPWVDSVVDILRRDAGDAWERAADVVPVLFSVMUSLAALWRSYGIEPDAVLGH 1140  
 QY 1141 SQGETAAAHVCGALSLKDAAKTVLRALAAVRCRGGWASVPLPAQVEQLIGERWAGR 1200  
 DB 1141 SQGETAAAHVCGALSLKDAAKTVLRALAAVRCRGGWASVPLPAQVEQLIGERWAGR 1200  
 QY 1201 LMWAAVNGPRSTAVSGDAEDEVILAYCAGTGVARRIPVDYASCHPQVPLRELELLE 1260  
 DB 1201 LMWAAVNGPRSTAVSGDAEDEVILAYCAGTGVARRIPVDYASCHPQVPLRELELLE 1260  
 QY 1261 GDISQPSGVFPFSTVEGTWLDTTTLDAAVYRNHLHQPVRFSDAVQALADDDHRRVFEVS 1320  
 DB 1261 GDISQPSGVFPFSTVEGTWLDTTTLDAAVYRNHLHQPVRFSDAVQALADDDHRRVFEVS 1320  
 QY 1321 PHPTLVPAIEDTETDAEDVTAIGSLRRGDNDRFLTALAHHTTGTGTPTHHHYTH 1380  
 DB 1321 PHPTLVPAIEDTETDAEDVTAIGSLRRGDNDRFLTALAHHTTGTGTPTHHHYTH 1380  
 QY 1381 HHTHPHPTLHDLPTYPFHQHYWLESOPGAGSGGAGAGSGAGSGAGTAGGTAEVES 1440  
 DB 1381 HHTHPHPTLHDLPTYPFHQHYWLESOPGAGSGGAGAGSGAGSGAGTAGGTAEVES 1440  
 QY 1441 RFWDAVARQDLTETVATTLAVPPSAGLTVVPALSAWHRHQDQARINTWTYQETWKPLTL 1500  
 DB 1441 RFWDAVARQDLTETVATTLAVPPSAGLTVVPALSAWHRHQDQARINTWTYQETWKPLTL 1500  
 QY 1501 PTHPHOTWTLIAIPETOTHHPHITNLTNLHHHGTPIPLTLNHTNPNQHLHHTLHHT 1560  
 DB 1501 PTHPHOTWTLIAIPETOTHHPHITNLTNLHHHGTPIPLTLNHTNPNQHLHHTLHHT 1560  
 QY 1561 RQQAQNHHTGATIGLLSLLALDETPHHPHPTPTGTLNLTLTOTHTTPTPLWYATT 1620  
 DB 1561 RQQAQNHHTGATIGLLSLLALDETPHHPHPTPTGTLNLTLTOTHTTPTPLWYATT 1620  
 QY 1621 NATTHPNNDPLTHPTQAOTWGLARTTLLEHPTHTAGIIDLPTTPPHTLQHLTQTLQPH 1680  
 DB 1621 NATTHPNNDPLTHPTQAOTWGLARTTLLEHPTHTAGIIDLPTTPPHTLQHLTQTLQPH 1680  
 QY 1681 HOTQALARTTCTHTRRLTPTTLTPHOPPTPTPHGTTLITGCTGALATHLHHTHHTOPT 1740  
 DB 1681 HOTQALARTTCTHTRRLTPTTLTPHOPPTPTPHGTTLITGCTGALATHLHHTHHTOPT 1740  
 QY 1741 QHLLTSRTGTPHQAQHLTTQLQKQGIHLATITTCDSNPDQLQQLLNTIPQHPPLTVI 1800  
 DB 1741 QHLLTSRTGTPHQAQHLTTQLQKQGIHLATITTCDSNPDQLQQLLNTIPQHPPLTVI 1800  
 QY 1801 HTAGILDDATLTNLTPTQLNNVLRKAHSAHLLHOLTOTHTLTAFLVYSSAAATGAPGQ 1860  
 DB 1801 HTAGILDDATLTNLTPTQLNNVLRKAHSAHLLHOLTOTHTLTAFLVYSSAAATGAPGQ 1860